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                                        GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on:          July 30, 2004, 12:18:33 ; Search time 54 Seconds
                                         (without alignments)
                                          2579.554 Million cell updates/sec

Title:           US-10-018-386-2
Perfect score:   2686
Sequence:        1 MRPLCVTCWWLGLLAAMGAV...........GSYSLKKVVMIRPNPNTFH 493
Scoring table:   BLOSUM62
                 Gapop 10.0 , Gapext 0.5
Searched:        1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters:      1586107

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :       A_Geneseq_29Jan04:*
                 1: geneseqp1980s:*
                 2: geneseqp1990s:*
                 3: geneseqp2000s:*
                 4: geneseqp2001s:*
                 5: geneseqp2002s:*
                 6: geneseqp2003as:*
                 7: geneseqp2003bs:*
                 8: geneseqp2004s:*

          Pred. No. is the number of results predicted by chance to have a
          score greater than or equal to the score of the result being printed,
          and is derived by analysis of the total score distribution.

                                     SUMMARIES

Result            Query
No.    Score   Match  Length  DB  ID          Description
-----  -----   -----  ------  --  --          -----------
  1    2686    100.0   493    2   AAB66340    Human ang
  2    2682    99.9    493    2   AAY05396    Human TIE
  3    2682    99.9    493    3   AAY54999    Human sca
  4    2682    99.9    493    6   AAY70745    PSEQ-3 pr
  5    2682    99.9    493    6   AAB47997    Angiopole
  6    2682    99.9    493    4   AAB31179    Amino aci
  7    2682    99.9    493    6   AAU12305    Human PRO
  8    2682    99.9    493    4   AAB51329    Human 410
  9    2682    99.9    493    5   AAO14786    Human mat
 10    2682    99.9    493    6   ABG80355    Human TIE
 11    2682    99.9    493    6   AAE19825    Human TIE
 12    2682    99.9    493    5   ABO17749    Novel hum
 13    2682    99.9    493    6   ABO25150    Novel hum
 14    2682    99.9    493    6   ADA01417    Human ang
 15    2682    99.9    493    6   ABU81003    Human PRO
 16    2682    99.9    493    6   AAE32417    Human ang
 17    2682    99.9    493    6   ABU66703    Human PRO
 18    2682    99.9    493    6   ABU67268    Novel hum
 19    2682    99.9    493    6   ABU59784    Novel sec
 20    2682    99.9    493    6   ABO24974    Human sec
 21    2682    99.9    493    6   ABU72036    Novel hum
 22    2682    99.9    493    6   ABU67137    Novel hum
 23    2682    99.9    493    6   ABU66979    Human sec
 24    2682    99.9    493    6   ABE30335    Human ARP
 25    2682    99.9    493    6   ABU79779    Human sec
 26    2682    99.9    493    6   ADA45787    Novel hum
 27    2682    99.9    493    6   ADA76218    Human PRO
 28    2682    99.9    493    6   ADA18868    Human PRO
 29    2682    99.9    493    6   ADA61491    Homo sapi
 30    2682    99.9    493    6   ADB19276    Novel hum
 31    2682    99.9    493    6   ADB27817    Human PRO
 32    2682    99.9    493    6   ADA86296    Novel hum
 33    2682    99.9    493    6   ADB15860    Human PRO
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 35    2682    99.9    493    6   ADA67441    Human PRO
 36    2682    99.9    493    6   ADB30448    Novel hum
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 40    2682    99.9    493    6   ADA87399    Novel hum
 41    2682    99.9    493    6   ADB16601    Human PRO
 42    2682    99.9    493    6   ADA91693    Novel hum
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ALIGNMENTS

```
RESULT 1
AAB66340
ID  AAB66340 standard; protein; 493 AA.
XX
AC  AAB66340;
XX
DT  05-APR-2001  (first entry)
XX
DE  Human angiopoietin-7 (ANG-7).
XX
KW  Human; angiopoietin-7; ANG-7; angiogenesis; cancer; wound healing;
KW  diabetic retinopathy; macular degeneration; cardiovascular disease;
KW  reproductive system.
XX
OS  Homo sapiens.
XX
XX
PN  WO20010242434-A1.
XX
PD  11-JAN-2001.
XX
PF  30-JUN-2000; 2000WO-US018170.
XX
PR  02-JUL-1999;  99EP-0113502.
XX
PA  (FARB ) BAYER AG.
XX
PI  Friedrich G, Hagen G, Wick M, Zubov D, Dubois-Stringfellow N;
XX
DR  WPI; 2001-123103/13.
DR  N-PSDB; AAF29738.
XX
PT  Inhibiting angiogenesis for treating cancer, wound healing, diabetic
PT  retinopathies, macular degeneration, cardiovascular diseases, by
PT  administering angiopoietin-7 polypeptide or its fragments.
XX
PS  Claim 2; Fig 2; 86pp; English.
XX
CC  The present invention describes a method of preventing angiogenesis by
CC  administering angiopoietin-7 (ANG-7) nucleic acid, protein, fragment or
CC  derivative. This can be used in the treatment of angiogenesis-related
CC  diseases, including cancer, wound healing, macular degeneration,
CC  cardiovascular diseases, diabetic retinopathies, infections and
CC  conditions of the reproductive system such as regulation of placental
CC  vascularisation and also may be used as an abortifacient. Note: In the
CC  specification, ANG-7 is also referred to as being angiotensin-7
XX
SQ  Sequence 493 AA;
```

RESULT 2

AAY05396

ID   AAY05396 standard; protein; 493 AA.
XX
AC   AAY05396;
XX
DT   01-JUL-1999 (first entry)
XX
DE   Human TIE ligand Nl1 protein sequence.
XX
DE   Human TIE ligand; Nl1; Nl4; Nl5; Nl8; Ig homology domain; angiogenesis;
KW   EGF homology domain; receptor tyrosine kinase; vascular endothelial cell;
KW   early haemopoietic cell; haemopoiesis; neovascularisation; wound healing;
KW   endothelial cell; growth inhibitor; apoptosis inducer; tumour cell;
KW   vasculogenesis; detection; diagnosis; therapy.
XX
OS   Homo sapiens.
XX
PN   WO9915653-A2.
XX
PD   01-APR-1999.
XX
PF   14-SEP-1998; 98WO-US019093.
XX
PR   19-SEP-1997; 97US-0093821.
PR   29-OCT-1997; 97US-00960507.
XX
PA   (GETH) GENENTECH INC.
XX
PI   Godowski PJ, Gurney AL, Hillan K, Botstein D, Goddard A, Roy M;
PI   Ferrara N, Tunas D, Schwall R;
XX

Query Match   100.0%; Score 2686; DB 4; Length 493;
Best Local Similarity 100.0%; Pred. No.6.6e-217;
Matches 493; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   1 MRPLCVTCWWLGLLAAMGAVAVAGQOEDGFEGGTEEGSPREFIYLNRYKRAGESQDKCTYTFIV 60
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Db   1 MRPLCVTCWWLGLLAAMGAVAVAGQOEDGFEGGTEEGSPREFIYLNRYKRAGESQDKCTYTFIV 60

Qy   61 PQQRVTGAICVNSKEPEVLLENRVHKQELELLNNELLKQKRQIETLQQLVKVDGGIVSEV 120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 PQQRVTGAICVNSKEPEVLLENRVHKQELELLNNELLKQKRQIETLQQLVKVDGGIVSEV 120

Qy 121 KLLRKESRNMNSRVTQLYMQLLHEIIRKRDNALELSQLENRILNQTADMLQLASKYKDLE 180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 121 KLLRKESRNMNSRVTQLYMQLLHEIIRKRDNALELSQLENRILNQTADMLQLASKYKDLE 180

Qy 181 HKYQHLATLAHNQSEIIAQLEEHCQRVPSARPVPQPPPAAPPRVYQPPTYNRIINQISTN 240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 181 HKYQHLATLAHNQSEIIAQLEEHCQRVPSARPVPQPPPAAPPRVYQPPTYNRIINQISTN 240

Qy 241 EIQSDQNLKVLPPPLPTMPFLTLTSLPSSTDKPSGPWRDCLQALEDGHDTSSIYLVKPENTN 300
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 241 EIQSDQNLKVLPPPLPTMPFLTLTSLPSSTDKPSGPWRDCLQALEDGHDTSSIYLVKPENTN 300

Qy 301 RLMQVWCDQRHDPGGWTVIQRRLDGSVNFRRNWETYKQGFGNIDGEYWLGLENIYWLINQ 360
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 301 RLMQVWCDQRHDPGGWTVIQRRLDGSVNFRRNWETYKQGFGNIDGEYWLGLENIYWLINQ 360

Qy 361 GNYKLLVTMEDWSGRKVFAEYASFRLEPESEYYKLRLGRYHGNAGDSFTWHNGKQFTTLD 420
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Db 361 GNYKLLVTMEDWSGRKVFAEYASFRLEPESEYYKLRLGRYHGNAGDSFTWHNGKQFTTLD 420

Qy 421 RDHDVYTGNCAHYQKGGWWYNACAHSNLNGVWYRGGHYRSRYQDGVYWAEFRGGSYSLKK 480
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Db 421 RDHDVYTGNCAHYQKGGWWYNACAHSNLNGVWYRGGHYRSRYQDGVYWAEFRGGSYSLKK 480

Qy 481 VVMMIRPNPNTFH 493
          |||||||||||||
Db 481 VVMMIRPNPNTFH 493

RESULT 3

AAY54999

ID   AAY54999 standard; protein; 493 AA.
XX
DR   WPI; 1999-263480/22.
DR   N-PSDB; AAX36341.
XX
PT   New isolated TIE ligand homologs for, e.g. developing products for
PT   treatment of tumors.
XX
PS   Claim 8; Fig 3; 132pp; English.
XX
CC   This sequence is the human tyrosine kinase containing Ig and EGF homology
CC   domains (TIE) ligand of the invention, designated Nl1. The TIE receptors
CC   are receptor tyrosine kinases which are expressed in vascular endothelial
CC   cells and early haemopoietic cells. The TIE receptors are believed to be
CC   actively involved in angiogenesis, and may play a role in haemopoiesis as
CC   well. The TIE ligand homologs can promote the survival and/or growth
CC   and/or differentiation of TIE receptor expressing cells. They can be used
CC   for promoting neovascularisation in wound healing and for promoting
CC   angiogenic processes, such as for inducing collateral vascularisation in
CC   an ischaemic heart or limb, or for promoting bone development and/or
CC   maturation and/or growth in a patient or muscle growth and development.
CC   The TIE ligand homologs and antibodies can inhibit the growth of
CC   endothelial cells and induce apoptosis of cells, particularly tumour
CC   cells. They can inhibit vascularisation, particularly the vascularisation
CC   of tumour cells. The antibodies can also inhibit vascularisation of a
CC   cell in which a gene encoding an Nl1, Nl5, Nl8 or Nl4 polypeptide is
CC   amplified. The products can also be used for detection, diagnosis, drug
CC   screening and production of transgenic animals
XX
SQ   Sequence 493 AA;

Query Match   99.9%; Score 2682; DB 2; Length 493;
Best Local Similarity 99.8%; Pred. No.1.4e-216;
Matches 492; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy   1 MRPLCVTCWWLGLLAAMGAVAVAGQOEDGFEGGTEEGSPREFIYLNRYKRAGESQDKCTYTFIV 60
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 MRPLCVTCWWLGLLAAMGAVAVAGQOEDGFEGGTEEGSPREFIYLNRYKRAGESQDKCTYTFIV 60

Qy   61 PQQRVTGAICVNSKEPEVLLENRVHKQELELLNNELLKQKRQIETLQQLVKVDGGIVSEV 120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 PQQRVTGAICVNSKEPEVLLENRVHKQELELLNNELLKQKRQIETLQQLVKVDGGIVSEV 120

Qy 121 KLLRKESRNMNSRVTQLYMQLLHEIIRKRDNALELSQLENRILNQTADMLQLASKYKDLE 180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 121 KLLRKESRNMNSRVTQLYMQLLHEIIRKRDNALELSQLENRILNQTADMLQLASKYKDLE 180

Qy 181 HKYQHLATLAHNQSEIIAQLEEHCQRVPSARPVPQPPPAAPPRVYQPPTYNRIINQISTN 240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 181 HKYQHLATLAHNQSEIIAQLEEHCQRVPSARPVPQPPPAAPPRVYQPPTYNRIINQISTN 240

Qy 241 EIQSDQNLKVLPPPLPTMPFLTLTSLPSSTDKPSGPWRDCLQALEDGHDTSSIYLVKPENTN 300
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 241 EIQSDQNLKVLPPPLPTMPFLTLTSLPSSTDKPSGPWRDCLQALEDGHDTSSIYLVKPENTN 300

Qy 301 RLMQVWCDQRHDPGGWTVIQRRLDGSVNFRRNWETYKQGFGNIDGEYWLGLENIYWLINQ 360
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 301 RLMQVWCDQRHDPGGWTVIQRRLDGSVNFRRNWETYKQGFGNIDGEYWLGLENIYWLINQ 360

Qy 361 GNYKLLVTMEDWSGRKVFAEYASFRLEPESEYYKLRLGRYHGNAGDSFTWHNGKQFTTLD 420
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 361 GNYKLLVTMEDWSGRKVFAEYASFRLEPESEYYKLRLGRYHGNAGDSFTWHNGKQFTTLD 420

Qy 421 RDHDVYTGNCAHYQKGGWWYNACAHSNLNGVWYRGGHYRSRYQDGVYWAEFRGGSYSLKK 480
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 421 RDHDVYTGNCAHYQKGGWWYNACAHSNLNGVWYRGGHYRSRYQDGVYWAEFRGGSYSLKK 480

Qy 481 VVMMIRPNPNTFH 493
          |||||||||||||
Db 481 VVMMIRPNPNTFH 493

AC   AAY54999;
XX
DT   18-FEB-2000   (first entry)
XX
DE   Human scarface 1 protein sequence.
XX
KW   Scarface 1; human; Sf-1 protein; angiogenesis; wound healing; diagnosis;
KW   tumour growth; cancer; stem cell amplification; endothelial cell;
KW   TIE receptor; neoplastic disease; wound healing; thromboembolic disease;
KW   atherosclerosis; inflammatory disease; neovascularisation; ischaemia;
KW   therapy.
XX
OS   Homo sapiens.
XX
PN   EP962530-A2.
XX
PD   08-DEC-1999.
XX
PF   01-JUN-1999; 99EP-00304239.
XX
PR   02-JUN-1998; 98US-0087710P.
PR   08-JUN-1998; 98US-0088502P.
PR   17-SEP-1998; 98US-0100857P.
XX
PA   (LILI) LILLY & CO ELI.
XX
PI   Heuer JG, Burget SG, Leonard RA, Rosteck PR, Sankhavaram PR;
XX
DR   WPI; 2000-025636/03.
DR   N-PSDB; AAZ40049.
XX
PT   New substantially pure Scarface 1 (Sf-1) protein, useful for screening
PT   compounds for modulating angiogenesis, to enhance wound healing, inhibit
PT   tumor growth and/or to amplify stem cells.
XX
PS   Claim 2; Page 20-22; 25pp; English.
XX
CC   This sequence represents the human Scarface 1 (Sf-1) protein of the
CC   invention. The Sf-1 nucleic acids are useful as probes to isolate
CC   paralogous genes from humans and/or orthologous genes from other
CC   organisms. Sf-1 proteins are also useful to screen for compounds that
CC   bind the peptides as potential pharmaceutical compounds for modulating
CC   angiogenesis. The proteins are useful as therapeutics to enhance wound
CC   healing, for developing compounds for inhibiting tumour growth, for
CC   treating cancer and for use in a method to amplify stem cells. Sf-1
CC   proteins may be further used in the diagnosis and treatment of certain
CC   diseases involving endothelial cells and associated TIE receptors e.g.
CC   neoplastic diseases involving tumour angiogenesis, thromboembolic
CC   diseases, atherosclerosis and inflammatory diseases. In addition the
CC   mammalian ligand may be used to promote proliferation and/or
CC   differentiation of haematopoietic stem cells. Sf-1 may be used to promote
CC   the growth, survival, migration and/or differentiation and/or
CC   stabilisation or destabilisation of cells expressing TIE receptor.
CC   Biologically active Sf-1 may be used in the in vitro maintenance of the
CC   TIE receptor expressing cells in culture. Alternatively Sf-1 may be used
CC   to support cells which are engineered to express TIE receptor and its
CC   cognate receptor may be used in assay systems to identify (ant)agonists
CC   of the TIE receptor. Sf-1 may be administered to promote
CC   healing, for developing compounds for inhibiting tumour growth, for
CC   treating cancer and for use in a method to amplify stem cells. Sf-1
CC   proteins may be further used in the diagnosis and treatment of certain
CC   neovascularisation and especially to treat ischaemia
XX
SQ   Sequence 493 AA;

Query Match   99.9%; Score 2682; DB 3; Length 493;
Best Local Similarity   99.8%; Pred. No. 1.4e-216;
Matches 492; Conservative   1; Mismatches   0; Indels   0; Gaps   0;

Qy   1 MRPLCVTCWWLGLLAAMGAVAGQEDGFEGTEEGSPREFIYLNRYKRAGESQDKCTYTFIV 60
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Db   1 MRPLCVTCWWLGLLAAMGAVAGQEDGFEGTEEGSPREFIYLNRYKRAGESQDKCTYTFIV 60

Qy   61 PQQRVTGAICVNSKEPEVLLENRVHKQELELLNNELLKQKRQIETLQQLVEVDGGIVSEV 120
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Db   61 PQQRVTGAICVNSKEPEVLLENRVHKQELELLNNELLKQKRQIETLQQLVKVDGGIVSEV 120

Qy   121 KLLRKESRNNMNSRVTQLYMQLLHEIIRKRDNALELSQLENRILNQTADMLQLASRYKDLE 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 KLLRKESRNNMNSRVTQLYMQLLHEIIRKRDNALELSQLENRILNQTADMLQLASRYKDLE 180

Qy   181 HKYQHLATLAHNQSEIIAQLEEHCQRVPSARPVPQPPPAAPPRVQPPTYNRIINQISTN 240
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Db   181 HKYQHLATLAHNQSEIIAQLEEHCQRVPSARPVPQPPPAAPPRVQPPTYNRIINQISTN 240

Qy   241 EIQSDQNLKVLPPPLPFTMPTLTLSLPSSTDKPSGPWRDCLQALEDGHDTSSIYLVKPENTN 300
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 EIQSDQNLKVLPPPLPFTMPTLTLSLPSSTDKPSGPWRDCLQALEDGHDTSSIYLVKPENTN 300

Qy   301 RLMQVWCDQRHDPGGWTVIQRRLDGSVNFRNWETYKQGFGNIDGEYWLGLENIYWLTNQ 360
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Db   301 RLMQVWCDQRHDPGGWTVIQRRLDGSVNFRNWETYKQGFGNIDGEYWLGLENIYWLTNQ 360

Qy   361 GNYKLLVTMEDWSGRKVFAEYASFRLEPESSYYKLRLGRYHGNAGDSFTWHNGKQFTTLD 420
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Qy   421 RDHDVYTGNCAHYQKGGWWYNACAHSNLNGVWYRGGHYRSRYQDGVYWAEFRGGSYSLKK 480
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Db   421 RDHDVYTGNCAHYQKGGWWYNACAHSNLNGVWYRGGHYRSRYQDGVYWAEFRGGSYSLKK 480

Qy   481 VVMMIRPNPNTFH 493
              |||||||||||||
Db   481 VVMMIRPNPNTFH 493

RESULT 4
AAY70745
ID   AAY70745 standard; protein; 493 AA.
XX
AC   AAY70745;
XX
DT   24-JUL-2000   (first entry)
XX
DE   PSEQ-3 protein encoded by NSEQ gene associated with matrix remodelling.
XX
KW   NSEQ gene; matrix-remodeling gene; Incyte clone 2268890; cancer;
KW   matrix remodeling disease; cardiomyopathy; arthritis; angiogenesis;
KW   diabetic necrosis; atherosclerosis; fibrosis; ulceration; cytostatic;
KW   cardioactive; antiarthritic; angiogenic; antiarteriosclerotic; antiulcer.
XX
OS   Homo sapiens.
XX
FH   Key   Location/Qualifiers
FH
FT   Peptide   1..22
FT   /label= Signal_peptide
FT   Modified-site   12
FT   /note= "N-myristoylation site"
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FT   /note= "Protein kinase C phosphorylation site"
FT   Modified-site   127
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FT   Modified-site   164
FT   /note= "cAMP- and cGMP-dependent protein kinase
FT   phosphorylation site"
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FT   /note= "N-glycosylation site"
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FT   like factor"
FT   Modified-site   299
FT   /note= "Protein kinase C phosphorylation site"
FT   Region   305..343
FT   /note= "Resembles carboxy-terminal domain signatures of
FT   fibrinogen beta and gamma chains from BLOCK analysis"
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FT   Modified-site   477
FT   /note= "Protein kinase C phosphorylation site"

XX
PN   WO200021986-A2.
XX
PD   20-APR-2000.
XX
PF   06-OCT-1999; 99WO-US023315.
XX
PR   09-OCT-1998; 98US-00169289.
XX
PA   (INCY-) INCYTE PHARM INC.
XX
PI   Walker MG, Volkmuth W, Klingler TM;
XX
DR   WPI; 2000-317934/27.
DR   N-PSDB; AAZ52359.
XX
PS   Claim 1; Page 54-55; 55pp; English.

The present sequence is PSEQ protein encoded by NSEQ gene that is co-expressed with one or more known matrix-remodeling genes in a number of biological samples using an expression vector. The gene, protein, and antibody sequences can be used in the diagnosis, and treatment or prevention of a disease associated with its altered expression. The diseases that can be treated are matrix-remodeling diseases, including

CC   cancer, cardiomyopathy, arthritis, angiogenesis, diabetic necrosis,
CC   atherosclerosis, fibrosis, and ulceration
XX
SQ   Sequence 493 AA;

Protein co-expressed with matrix-remodeling proteins, useful in the diagnosis and treatment of cancer, cardiomyopathy, arthritis, angiogenesis, diabetic necrosis, atherosclerosis, fibrosis, and ulceration.

Query Match   99.9%; Score 2682; DB 3; Length 493;
Best Local Similarity   99.8%; Pred. No. 1.4e-216;
Matches 492; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```
Qy         1 MRPLCVTCWWLGLLAAMGAVAGGEDGFEGTEEGSPREFIYLNRYKRAGESQDKCTYTFIV 60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1 MRPLCVTCWWLGLLAAMGAVAGGEDGFEGTEEGSPREFIYLNRYKRAGESQDKCTYTFIV 60

Qy        61 PQQRVTGAICVNSKEPVLLENRVHKQELELLNNELLKQRQIETLQQLVKDGGIVSEV 120
             |||||||||||||||||||||||||||||||||||||||||||||||: ||||||||
Db        61 PQQRVTGAICVNSKEPVLLENRVHKQELELLNNELLKQRQIETLQQLVEVDGGIVSEV 120

Qy       121 KLLRKESRNNSRVTQLYMQLLHEIIRKRDNALELSQLENRILNQTADMLQLASKYKDLE 180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       121 KLLRKESRNNSRVTQLYMQLLHEIIRKRDNALELSQLENRILNQTADMLQLASKYKDLE 180

Qy       181 HKYQHLATLAHNQSEIIAQLEEHCQRVPSARPVPQPPPAAPPRVYQPPPTNRIINQISTN 240
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       181 HKYQHLATLAHNQSEIIAQLEEHCQRVPSARPVPQPPPAAPPRVYQPPPTNRIINQISTN 240

Qy       241 EIQSDQNLKVLPPPLPTMPLITSLPSSTDKPSGPWRDCLQALEDGHDTSSIYLVKPENTN 300
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       241 EIQSDQNLKVLPPPLPTMPLITSLPSSTDKPSGPWRDCLQALEDGHDTSSIYLVKPENTN 300

Qy       301 RLMQVWCDQRHDPGGWTVIQRRLDGSVNFRNWETYKQGFGNIDGEYWLGLENIYWLTNQ 360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       301 RLMQVWCDQRHDPGGWTVIQRRLDGSVNFRNWETYKQGFGNIDGEYWLGLENIYWLTNQ 360

Qy       361 GNYKLLVTMEDWSGRKVFAEYASFRLEPESEYYKLRLGRYHGNAGDSFTWHNGKQFTTLD 420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       361 GNYKLLVTMEDWSGRKVFAEYASFRLEPESEYYKLRLGRYHGNAGDSFTWHNGKQFTTLD 420

Qy       421 RDHDVYTGNCAHYQKGGWWYNACAHSNLNGVWYRGGHYRSRYQDGVYWAEFRGGSYSLKK 480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       421 RDHDVYTGNCAHYQKGGWWYNACAHSNLNGVWYRGGHYRSRYQDGVYWAEFRGGSYSLKK 480

Qy       481 VVMMIRPNPNTFH 493
             |||||||||||||
Db       481 VVMMIRPNPNTFH 493
```

RESULT 5
AAB47997
ID   AAB47997 standard; protein; 493 AA.
XX
AC   AAB47997;
XX
DT   12-AUG-2002 (first entry)
XX
DE   Angiopoietin-like protein-3, AR3.
XX
KW   Angiopoietin-like protein 2; AR2; angiopoietin-like protein 3; AR3;
KW   apple crisp protein; APPlE; cocoa crisp protein; COCO;
KW   signal sequence cloning; secretory leader motif; angiogenesis;
KW   wound healing; transplantation.
XX
OS   Homo sapiens.
XX
PN   WO200059938-A1.
XX
PD   12-OCT-2000.
XX
PF   31-MAR-2000; 2000WO-US008832.
XX
PR   01-APR-1999; 99US-0126366P.
PR   29-MAR-2000; 2000US-00538361.
XX
PA   (GEMY) GENETICS INST INC.

XX
PI Racie-Collins LA, Lavallie ER;
XX
DR WPI; 2000-664990/64.
DR N-PSDB; AAI72856.
XX
PT New angiopoietin-like proteins 2 and 3, apple crisp and cocoa crisp
PT proteins and polynucleotides, useful in treating e.g. autoimmune
PT diseases, cancer, or central and peripheral nervous system disorders and
PT neuropathies.
XX
PS Claim 31; Page 71-73; 84pp; English.
XX
CC The sequences given in AAB47996-99 show angiopoietin-like protein 2
CC (AR2), angiopoietin-like 3 protein (AR3), apple crisp protein (APPLE), or
CC cocoa crisp protein (COCO), respectively. These sequences were isolated
CC by indirect cloning techniques, e.g. signal sequence cloning, which
CC isolates DNA based on the presence of well known secretory leader motifs.
CC AR2 and AR3 promote angiogenesis and may therefore be used in wound
CC healing and transplantation.
XX
SQ Sequence 493 AA;

Query Match   99.9%; Score 2682; DB 3; Length 493;
Best Local Similarity   99.8%; Pred. No. 1.4e-216;
Matches 492; Conservative   1; Mismatches   0; Indels   0; Gaps   0;

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Qy    1 MRPLCVTCWWLGLLAAMGAVAGQEDGEGTEEGSPREFIYLNRYKRAGESQDKCTYTFIV 60
          ||||||||||||||||||||||||||| |||||||||||||||||||||||||||||||
Db    1 MRPLCVTCWWLGLLAAMGAVAGQEDGFEGTEEGSPREFIYLNRYKRAGESQDKCTYTFIV 60

Qy   61 PQQRVTGAICVNSKEPEVLLENRVHKQELELLNNELLKQKRQIETLLQQLVKVDGGIVSEV 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||:||||||||
Db   61 PQQRVTGAICVNSKEPEVLLENRVHKQELELLNNELLKQKRQIETLLQQLVEVDGGIVSEV 120

Qy  121 KLLRKESRNMNSRVTQLYMQLLHEIIRKRDNALELSQLENRILNQTADMLQLASKYXDLE 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 KLLRKESRNMNSRVTQLYMQLLHEIIRKRDNALELSQLENRILNQTADMLQLASKYXDLE 180

Qy  181 HKYQHLATLAINNQSEIIAQLEEHCQRVPSARPVPQPPPAAPPRVYQPPTYNRIINQISTN 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 HKYQHLATLAINNQSEIIAQLEEHCQRVPSARPVPQPPPAAPPRVYQPPTYNRIINQISTN 240

Qy  241 EIQSDQNLKVLPPPLPTPMPTLTSLPSSTDKFSGPWRDCLQALLEDGHDTSSIYLVKPENTN 300
          ||||||||||||||||||||||||||||||| ||||||||||:|||||||||||||||||
Db  241 EIQSDQNLKVLPPPLPTPMPTLTSLPSSTDKPSGPWRDCLQALEDGHDTSSIYLVKPENTN 300

Qy  301 RLMQVWCDQRHDPGGWTVIQRRLDGSVNFFRNWETYKQGFGNIDGEYWLGLENIYWLTNQ 360
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  301 RLMQVWCDQRHDPGGWTVIQRRLDGSVNFFRNWETYKQGFGNIDGEYWLGLENIYWLTNQ 360

Qy  361 GNYKLLVTMEDWSGRKVFAEYASFRLEPESEYYKLRLGRYHGNAGDSFTWHNGKQFTTLD 420
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy  421 RDHDVYTGNCAHYQKGGWWYNACAHSNLNGVWYRGGHYRSRYQDGVTWAEFRGGSYSLKK 480
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Db  421 RDHDVYTGNCAHYQKGGWWYNACAHSNLNGVWYRGGHYRSRYQDGVTWAEFRGGSYSLKK 480

Qy  481 VVMMIRPNPNTFH 493
          |||||||||||||
Db  481 VVMMIRPNPNTFH 493
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RESULT 6
AAB31179
ID AAB31179 standard; protein; 493 AA.
XX
AC AAB31179;
XX
DT 20-APR-2001 (first entry)
XX
DE Amino acid sequence of human polypeptide PRO196.

KW Human; secreted protein; transmembrane protein; PRO196; PRO444; PRO183;
KW PRO185; PRO210; PRO215; PRO217; PRO242; PRO288; PRO365; PRO1361; PRO1308;
KW PRO183; PRO1272; PRO1419; PRO4999; PRO71170; PRO248; PRO353; PRO1318;
KW PRO1600; PRO99940; PRO533; PRO301; PRO187; PRO337; PRO1411; PRO4356;
KW PRO246; PRO265; PRO941; PRO100096; PRO6003; PRO6004; PRO350; PRO2630;
KW PRO6309; cell death; genetic disorder; transgenic animal; gene therapy.
XX
OS Homo sapiens.
XX
FH Key   Location/Qualifiers
FH
FT Peptide   1..22
FT   /note= "signal peptide"
FT Modified-site   12..18
FT   /note= "N-myristoylation site"
FT Modified-site   18..24
FT   /note= "N-myristoylation site"
FT Modified-site   22..28
FT   /note= "N-myristoylation site"
FT Modified-site   29..35
FT   /note= "N-myristoylation site"
FT Modified-site   114..120
FT   /note= "N-myristoylation site"
FT Modified-site   124..128
FT   /note= "N-myristoylation site"
FT Modified-site   164..168
FT   /note= "cAMP- and cGMP-dependent protein kinase
FT   phosphorylation site"
FT Modified-site   177..184
FT   /note= "N-glycosylation site"
FT Modified-site   192..196
FT   /note= "tyrosine kinase phosphorylation site"
FT Modified-site   341..347
FT   /note= "N-glycosylation site"
FT Modified-site   373..377
FT   /note= "N-myristoylation site"
FT Modified-site   385..394
FT   /note= "amidation site"
FT Modified-site   385..393
FT   /note= "tyrosine kinase phosphorylation site"
FT Modified-site   461..468
FT   /note= "tyrosine kinase phosphorylation site"
FT Modified-site   465..471
FT   /note= "tyrosine kinase phosphorylation site"
FT Modified-site   473..479
FT   /note= "N-myristoylation site"
FT Modified-site   473..479
FT   /note= "N-myristoylation site"
XX
PN WO200077037-A2.
XX
PD 21-DEC-2000.
XX
PF 22-MAY-2000; 2000WO-US014042.
XX
PR 15-JUN-1999; 2000US-0139695P.
PR 20-JUL-1999; 2000US-0145070P.
PR 26-JUL-1999; 2000US-0145698P.
PR 17-AUG-1999; 2000US-0149396P.
PR 01-SEP-1999; 2000US-0020111.
PR 08-SEP-1999; 2000WO-US025594.
PR 15-SEP-1999; 2000US-021090.
PR 15-SEP-1999; 2000US-021547.
PR 30-NOV-1999; 2000US-028313.
PR 01-DEC-1999; 2000US-028301.
PR 02-DEC-1999; 2000US025565.
PR 07-DEC-1999; 99US-0169495P.
PR 05-JAN-2000; 2000WO-US00219.
PR 18-FEB-2000; 2000WO-US004341.
PR 22-FEB-2000; 2000WO-US004414.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005841.
PR 20-MAR-2000; 2000WO-US007377.
PR 30-MAR-2000; 2000WO-US008439.

```
PR   15-MAY-2000; 2000WO-US013358.
PR   17-MAY-2000; 2000WO-US013705.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Ashkenazi AJ, Baker KP, Botstein DA, Desnoyers L, Eaton DL;
PI   Ferrara N, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;
PI   Godowski PJ, Gurney AL, Kljavin IJ, Mather JP, Napier MA, Pan J;
PI   Paoni NF, Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM;
PI   Wood WI, Zhang Z;
XX
DR   WPI; 2001-050091/06.
DR   N-PSDB; AAC86961.
XX
PS   Claim 12; Fig 2; 244pp; English.
XX
PT   The present sequence represents a human secreted and transmembrane
PT   polypeptide. The specification describes human polypeptides, designated
CC   polypeptides. The specification describes human polypeptides, designated
CC   PRO196, PRO183, PRO185, PRO210, PRO215, PRO217, PRO242, PRO288,
CC   PRO365, PRO1361, PRO1308, PRO1163, PRO1272, PRO1419, PRO4999, PRO7170,
CC   PRO248, PRO353, PRO1318, PRO1600, PRO9940, PRO533, PRO301, PRO187,
CC   PRO337, PRO1411, PRO4356, PRO246, PRO265, PRO941, PRO10096, PRO6003,
CC   PRO6004, PRO350, PRO2630 and PRO6309. The biological activity of cells
CC   can be modulated with agents that bind to these polypeptides, resulting
CC   in the death of the cells. The polynucleotides encoding these
CC   polypeptides are useful in the recombinant production of the
CC   polypeptides, as a hybridisation probe to screen libraries to isolate
CC   homologous sequences, or to map the gene. They may also be used for
CC   analysing genetic disorders, and to produce transgenic animals which are
CC   useful for the development and screening of therapeutically useful
CC   reagents. The polynucleotides can also be used in gene therapy e.g. to
CC   replace a defective gene
XX
SQ   Sequence 493 AA;

Query Match             99.9%;  Score 2682;  DB 4;  Length 493;
Best Local Similarity   99.8%;  Pred. No. 1.4e-216;
Matches  492;  Conservative   1;  Mismatches   0;  Indels   0;  Gaps   0;

Qy        1 MRPLCVTCWWLGLLAAMGAVAGQEDGFEGTEGSSPREFIYLNRYKRAGESQDKCTYTFIV 60
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1 MRPLCVTCWWLGLLAAMGAVAGQEDGFEGTEGSSPREFIYLNRYKRAGESQDKCTYTFIV 60

Qy       61 PQQRVTGAICVNSKEPEVLLENRVHKQELELLNNELLKQKRQIETLQQLVKVDGGIVSEV 120
            |||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db       61 PQQRVTGAICVNSKEPEVLLENRVHKQELELLNNELLKQKRQIETLQQLVEVDGGIVSEV 120

Qy      121 KLLRKESRNMNSRVTQLYMQLLHEIIRKRDNALELSQLENRILNQTADMLQLASKYKDLE 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      121 KLLRKESRNMNSRVTQLYMQLLHEIIRKRDNALELSQLENRILNQTADMLQLASKYKDLE 180

Qy      181 HKYQHLATLAHNQSEIIAQLEEHCQRVPSARPVPQPPPAAPPRVYQPPTYNRIINQISTN 240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      181 HKYQHLATLAHNQSEIIAQLEEHCQRVPSARPVPQPPPAAPPRVYQPPTYNRIINQISTN 240

Qy      241 EIQSDQNLKVLPPLPPTMPTLTSLPSSTDKPSGPWRDCLQALEDGHDTSSIYLVKPENTN 300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      241 EIQSDQNLKVLPPLPPTMPTLTSLPSSTDKPSGPWRDCLQALEDGHDTSSIYLVKPENTN 300

Qy      301 RLMQVWCDQRHDPGGWTVIQRRLDGSVNFFRNWETYKQGFGNIDGEYWLGLENIYWLTNQ 360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      301 RLMQVWCDQRHDPGGWTVIQRRLDGSVNFFRNWETYKQGFGNIDGEYWLGLENIYWLTNQ 360

Qy      361 GNYKLLVTMEDWSGRKVFAEYASFRLEPESEYYKLRLGRYHGNAGDSFTWHNGKQFTTLD 420
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      361 GNYKLLVTMEDWSGRKVFAEYASFRLEPESEYYKLRLGRYHGNAGDSFTWHNGKQFTTLD 420

Qy      421 RDHDVYTGNCAHYQKGGWWYNACAHSNLNGVWYRGGHYRSRYQDGVVWAEFRGGSYSLKK 480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      421 RDHDVYTGNCAHYQKGGWWYNACAHSNLNGVWYRGGHYRSRYQDGVVWAEFRGGSYSLKK 480

Qy      481 VVMMIRPNPNTFH 493
            |||||||||||||
Db      481 VVMMIRPNPNTFH 493
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Db       421 RDHDVYTGNCAHYQKGGWWYNACAHSNLNGVWYRGGHYRSRYQDGVVWAEFRGGSYSLKK 480

Qy       481 VVMMIRPNPNTFH 493
             |||||||||||||
Db       481 VVMMIRPNPNTFH 493

RESULT 7
ID   AAU12305 standard; protein; 493 AA.
XX
AC   AAU12305;
XX
DT   24-OCT-2001  (first entry)
XX
DE   Human PRO196 polypeptide sequence.
XX
KW   Human secretory and transmembrane; PRO; mammalian; cancer; lung; breast;
KW   prostate; cervical; tumour necrosis factor-alpha; TNF-alpha; cartilage;
KW   ear; proliferation; glucose; free fatty acid; skeletal muscle; adipocyte;
KW   A-peptide; factor VIIa; gene therapy.
XX
OS   Homo sapiens.
XX
PN   WO200140466-A2.
XX
PD   07-JUN-2001.
XX
PF   01-DEC-2000; 2000WO-US032678.
PR   01-DEC-1999; 99WO-US028301.
PR   01-DEC-1999; 99WO-US028634.
PR   02-DEC-1999; 99WO-US028551.
PR   02-DEC-1999; 99WO-US028564.
PR   02-DEC-1999; 99WO-US028565.
PR   09-DEC-1999; 99US-01702562P.
PR   09-DEC-1999; 99WO-US030095.
PR   16-DEC-1999; 99WO-US030911.
PR   20-DEC-1999; 99WO-US031243.
PR   30-DEC-1999; 99WO-US031274.
PR   30-DEC-1999; 99WO-US031999.
PR   05-JAN-2000; 2000WO-US000219.
PR   06-JAN-2000; 2000WO-US000277.
PR   06-JAN-2000; 2000WO-US000376.
PR   11-FEB-2000; 2000WO-US003565.
PR   18-FEB-2000; 2000WO-US004341.
PR   18-FEB-2000; 2000WO-US004342.
PR   22-FEB-2000; 2000WO-US004414.
PR   24-FEB-2000; 2000WO-US004914.
PR   24-FEB-2000; 2000WO-US005004.
PR   01-MAR-2000; 2000WO-US005601.
PR   02-MAR-2000; 2000WO-US005841.
PR   03-MAR-2000; 2000US-01872202P.
PR   10-MAR-2000; 2000WO-US006319.
PR   15-MAR-2000; 2000WO-US006884.
PR   20-MAR-2000; 2000WO-US007377.
PR   21-MAR-2000; 2000WO-US007532.
PR   30-MAR-2000; 2000WO-US008439.
PR   17-MAY-2000; 2000WO-US013705.
PR   22-MAY-2000; 2000WO-US014042.
PR   30-MAY-2000; 2000WO-US014941.
PR   02-JUN-2000; 2000WO-US015264.
PR   05-JUN-2000; 2000US-02098321.
PR   28-JUL-2000; 2000WO-US020710.
PR   11-AUG-2000; 2000WO-US022031.
PR   23-AUG-2000; 2000WO-US023522.
PR   24-AUG-2000; 2000WO-US023328.
PR   08-NOV-2000; 2000WO-US030952.
PR   10-NOV-2000; 2000WO-US030873.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
```

PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
XX
DR WPI; 2001-408281/43.
DR N-PSDB; AAS21377.
XX
PT Isolated, secretory and transmembrane PRO polypeptide used to detect
PT other PRO polypeptides, link bioactive molecules to cells expressing PRO
PT polypeptides, and detect the presence of mammalian tumors e.g. lung,
PT breast, prostate, cervical.
XX
PS Claim 12; Fig 268; 813pp; English.
XX
CC AAU12172-AAU12446 represent novel human secretory and transmembrane PRO
CC polypeptides. The PRO polypeptides are useful to detect other PRO
CC polypeptides, to link bioactive molecules to cells expressing PRO
CC polypeptides, to modulate biological activities of cells expressing PRO
CC polypeptides, and to detect the presence of mammalian lung, colon,
CC breast, prostate, rectal, cervical or liver tumours by comparing PRO
CC polypeptide expression in a cell sample to that in a control sample. Some
CC of the 275 sequences are also useful to stimulate the release of tumour
CC necrosis factor-alpha (TNF-alpha) from human blood, the proliferation or
CC differentiation of chondrocytes, the proliferation or gene expression in
CC pericyte cells, the release of proteoglycans from cartilage, the
CC proliferation of inner ear utricular supporting cells or of T-
CC lymphocytes, the release of a cytokine from peripheral blood monocytes
CC (PBMCs), or the proliferation of endothelial cells. Some of the PRO
CC polypeptides may modulate glucose or free fatty acid uptake by skeletal
CC muscle cells or by adipocytes; or inhibit binding of A-peptide to factor
CC VIIa. The PRO polypeptides can be used in assays to identify molecules
CC involved in binding interactions. The polynucleotides encoding PRO
CC polypeptides can be used to generate probes, antisense RNA/DNA,
CC transgenic or knock out animals and can be used in gene therapy
XX
SQ Sequence 493 AA;

Query Match   99.8%; Score 2682; DB 4;   Length 493;
Best Local Similarity 99.8%; Pred. No. 1.4e-216;
Matches 492; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```
Qy     1 MRPLCVTCWWLGLLAAMGAVAGQEDGPEGTEEGSPREFIYLNRYKRAGESQDKCTYTFIV 60
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1 MRPLCVTCWWLGLLAAMGAVAGQEDGPEGTEEGSPREFIYLNRYKRAGESQDKCTYTFIV 60

Qy    61 PQQRVTGAICVNSKEPEVLLENRVHKQELELLNNELLKQRQIETLQQLVKVDGGIVSEV 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61 PQQRVTGAICVNSKEPEVLLENRVHKQELELLNNELLKQRQIETLQQLVEVDGGIVSEV 120

Qy   121 KLLRKESRNMNSRVTQLYMQLLHEIIRKRDNALELSQLENRIINQTADMLQLASKYXDLE 180
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 KLLRKESRNMNSRVTQLYMQLLHEIIRKRDNALELSQLENRIINQTADMLQLASKYXDLE 180

Qy   181 HXYQHLATLAHNQSEIIAQLEEHCQRVPSARPVPQPPPAAPPRVYQPPTYNRIINQISTN 240
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 HXYQHLATLAHNQSEIIAQLEEHCQRVPSARPVPQPPPAAPPRVYQPPTYNRIINQISTN 240

Qy   241 EIQSDQNLKVLPPLPTMPTLLTSLPSSTDKPSGPWRDCLQALEDGHDTSSIYLVKPENTN 300
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 EIQSDQNLKVLPPLPTMPTLLTSLPSSTDKPSGPWRDCLQALEDGHDTSSIYLVKPENTN 300

Qy   301 RLMQVWCDQRHDPGGWTVIQRRLDGSVNFFRNWETYKQGFGNIDGEYWLGLENIYWLTNQ 360
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 RLMQVWCDQRHDPGGWTVIQRRLDGSVNFFRNWETYKQGFGNIDGEYWLGLENIYWLTNQ 360

Qy   361 GNYKLLVTMEDWSGRKVFAEYASFRLEPESEYYKLRLGRYHGNAGDSFTWHNGKQFTTLD 420
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 GNYKLLVTMEDWSGRKVFAEYASFRLEPESEYYKLRLGRYHGNAGDSFTWHNGKQFTTLD 420

Qy   421 RDHDVYTGNCAHYQKGGWWYNACAHSNLNGVWYRGGHYRSRYQDGVVWAEFRGGSYSLKX 480
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 RDHDVYTGNCAHYQKGGWWYNACAHSNLNGVWYRGGHYRSRYQDGVVWAEFRGGSYSLKX 480

Qy   481 VVMMIRPNPNTFH 493
           |||||||||||||
Db   481 VVMMIRPNPNTFH 493
```

RESULT 8
AAB51329
ID AAB51329 standard; protein; 493 AA.
XX
AC AAB51329;
XX
DT 02-APR-2001 (first entry)
XX
DE Human 410 angiopoietin-like protein SEQ ID NO:4.
XX
KW Human; 410; NEW; angiopoietin-like protein; angiogenesis.
XX
OS Homo sapiens.
XX
PN JP200300263-A.
XX
PD 31-OCT-2000.
XX
PF 14-APR-1999; 99JP-00107234.
PR 14-APR-1999; 99JP-00107334.
XX
PA (HERI-) HERIKKUSU KENKYUSHO KK.
XX
DR WPI; 2001-151128/16.
DR N-PSDB; AAF26789.
XX
PT New genes encoding angiopoietin-like proteins 410 and NEW, useful for the
PT prevention and treatment of diseases relating to angiogenesis.
XX
PS Claim 1; Page 12-13; 26pp; Japanese.
XX
CC The present invention describes two human angiopoietin-like proteins
CC designated 410 and NEW. The angiopoietin-like proteins can be used for
CC the prevention and treatment of diseases relating to angiogenesis. The
CC present sequence represents the human 410 angiopoietin-like protein
XX
SQ Sequence 493 AA;

Query Match   99.8%; Score 2682; DB 4;   Length 493;
Best Local Similarity 99.8%; Pred. No. 1.4e-216;
Matches 492; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```
Qy     1 MRPLCVTCWWLGLLAAMGAVAGQEDGPEGTEEGSPREFIYLNRYKRAGESQDKCTYTFIV 60
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1 MRPLCVTCWWLGLLAAMGAVAGQEDGPEGTEEGSPREFIYLNRYKRAGESQDKCTYTFIV 60

Qy    61 PQQRVTGAICVNSKEPEVLLENRVHKQELELLNNELLKQRQIETLQQLVEVDGGIVSEV 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61 PQQRVTGAICVNSKEPEVLLENRVHKQELELLNNELLKQRQIETLQQLVEVDGGIVSEV 120

Qy   121 KLLRKESRNMNSRVTQLYMQLLHEIIRKRDNALELSQLENRIINQTADMLQLASKYXDLE 180
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 KLLRKESRNMNSRVTQLYMQLLHEIIRKRDNALELSQLENRIINQTADMLQLASKYXDLE 180

Qy   181 HXYQHLATLAHNQSEIIAQLEEHCQRVPSARPVPQPPPAAPPRVYQPPTYNRIINQISTN 240
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 HXYQHLATLAHNQSEIIAQLEEHCQRVPSARPVPQPPPAAPPRVYQPPTYNRIINQISTN 240

Qy   241 EIQSDQNLKVLPPLPTMPTLLTSLPSSTDKPSGPWRDCLQALEDGHDTSSIYLVKPENTN 300
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 EIQSDQNLKVLPPLPTMPTLLTSLPSSTDKPSGPWRDCLQALEDGHDTSSIYLVKPENTN 300

Qy   301 RLMQVWCDQRHDPGGWTVIQRRLDGSVNFFRNWETYKQGFGNIDGEYWLGLENIYWLTNQ 360
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 RLMQVWCDQRHDPGGWTVIQRRLDGSVNFFRNWETYKQGFGNIDGEYWLGLENIYWLTNQ 360

Qy   361 GNYKLLVTMEDWSGRKVFAEYASFRLEPESEYYKLRLGRYHGNAGDSFTWHNGKQFTTLD 420
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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```
Qy    1 MRPLCVTCWLGLLAAMGAVAQGEDGFEGTEEGSPREFIYLNRYKRAGESQDKCTYTFIV 60

SQ    Sequence 493 AA;

XX    Matches 492; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
CC    Best Local Similarity 99.8%; Pred. No. 1.4e-216;
CC    Query Match 99.9%; Score 2682; DB 5; Length 493;
PS    Example 1; Fig 3; 63pp; English.

CC    associated nucleotide of the invention
CC    present amino acid sequence is encoded by a human matrix-remodeling-
CC    cancer, cardiomyopathy, diabetic necrosis, fibrosis and ulceration). The
CC    with matrix remodeling (e.g. angiogenesis, arthritis, atherosclerosis,
CC    prevention, treatment and evaluation of therapies for diseases associated
CC    nucleotides of the invention are also useful in the diagnosis, prognosis,
CC    to the nucleotides of the invention. The matrix-remodeling-associated
CC    are useful for screening for and purifying ligands that specifically bind
CC    components. The matrix-remodeling-associated nucleotides of the invention
CC    construction, destruction and reorganisation of extracellular matrix
CC    with matrix-remodeling. Matrix-remodeling is associated with the
CC    The invention comprises human nucleotide sequences which are co-expressed

PS    Example; Fig 3; 63pp; English.

PI    (KLIN/) KLINGLER T M.
PA    (VOLK/) VOLKMUTH W.
PA    (WALK/) WALKER M G.

PN    09-OCT-1998; 98US-00169289.

PI    Walker MG, Volkmuth W, Klingler TM;

DR    N-PSDB; AAI42455.
DR    WPI; 2002-338319/37.

PT    cancer.
PT    associated with matrix-remodeling such as angiogenesis, arthritis and
PT    useful in diagnosis, prognosis, prevention and treatment of diseases
PT    New isolated polynucleotide coexpressed with matrix-remodeling genes,

KW    ulceration.
KW    atherosclerosis; cancer; cardiomyopathy; diabetic necrosis; fibrosis;
KW    matrix remodeling-associated disease; angiogenesis; arthritis;
KW    matrix-remodeling-associated nucleotide; screening;
DE    Human; matrix-remodeling gene; extracellular matrix;

DE    Human matrix-remodeling-associated protein 3.

OS    Homo sapiens.

PD    14-FEB-2002.

PN    26-MAR-2001; 2001US-00818143.

PF    14-FEB-2002.

PN    US2002090000-A1.

XX
PR    09-OCT-1998; 98US-00169289.
XX
PD    14-FEB-2002.
XX
PF    26-MAR-2001; 2001US-00818143.
XX

DT    11-JUL-2002 (first entry)

AC    AA014786;

ID    AA014786 standard; protein; 493 AA.

RESULT 9
AA014786
```

```
Qy  361 GNYKLLVTMEDWSGRKVFAEYASFRLEPESEYYKLRLGRYHGNAGDSFTWHNGKQFTTLD 420
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  421 RDHDVYTGNCAHYQKGGWWYNACAHSNLNGVWYRGGHYRSRYQDGVYWAEFRGGSYSLKK 480

Qy  421 RDHDVYTGNCAHYQKGGWWYNACAHSNLNGVWYRGGHYRSRYQDGVYWAEFRGGSYSLKK 480
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  481 VVMMIRPNPNTFH 493

Qy  481 VVMMIRPNPNTFH 493
          ||||||||||||
Db  481 VVMMIRPNPNTFH 493
```

```
Qy    1 MRPLCVTCWLGLLAAMGAVAQGEDGFEGTEEGSPREFIYLNRYKRAGESQDKCTYTFIV 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 MRPLCVTCWLGLLAAMGAVAQGEDGFEGTEEGSPREFIYLNRYKRAGESQDKCTYTFIV 60

PS    Example 1; Fig 3; 85pp; English.

PT    healing and treating ischemic condition of the heart or a limb.
PT    polypeptides which are useful for inducing vascularization for wound
PT    Novel isolated nucleic acid molecules encoding NL4 TIE ligand homologue

DR    N-PSDB; ABS65529.
DR    WPI; 2002-641562/69.

PI    Ferrara N, Tumas D, Schwall R;
PI    Godowski P, Gurney A, Hillan KJ, Botstein D, Goddard A, Roy M;

PA    (GETH ) GENENTECH INC.

PR    29-OCT-1997; 97US-00960507.
PR    19-SEP-1997; 97US-00933821.

PF    19-AUG-1998; 98US-00136801.

PD    02-JUL-2002.

PN    US6413770-B1.

OS    Homo sapiens.

KW    NL8.
KW    ischaemic condition; vulnerary; vasotropic; gene therapy; NL1; NL5;
KW    Human; TIE ligand NL4; vascularisation; wound healing; heart; limb;

DE    Human TIE ligand NL1 protein.

DT    15-NOV-2002 (first entry)

AC    ABG80355;

ID    ABG80355 standard; protein; 493 AA.

RESULT 10
ABG80355
```

```
Qy  481 VVMMIRPNPNTFH 493
          ||||||||||||
Db  481 VVMMIRPNPNTFH 493

Qy  421 RDHDVYTGNCAHYQKGGWWYNACAHSNLNGVWYRGGHYRSRYQDGVYWAEFRGGSYSLKK 480
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  421 RDHDVYTGNCAHYQKGGWWYNACAHSNLNGVWYRGGHYRSRYQDGVYWAEFRGGSYSLKK 480

Qy  361 GNYKLLVTMEDWSGRKVFAEYASFRLEPESEYYKLRLGRYHGNAGDSFTWHNGKQFTTLD 420
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  361 GNYKLLVTMEDWSGRKVFAEYASFRLEPESEYYKLRLGRYHGNAGDSFTWLGLENIYWLTNQ 420

Qy  301 RLMQVWCDQRHDPGGWTVIQRRLDGSVNFRNWETYKQGFGNIDGEYWLGLENIYWLTNQ 360
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  301 RLMQVWCDQRHDPGGWTVIQRRLDGSVNFRNWETYKQGFGNIDGEYWLGLENIYWLTNQ 360

Qy  241 EIQSDQNLKVLPPPLFTMPLITSLPSSTDKPSGPWRDCLQALEDGHDTSSIYLVKPENTN 300
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241 EIQSDQNLKVLPPPLFTMPLITSLPSSTDKPSGPWRDCLQALEDGHDTSSIYLVKPENTN 300

Qy  181 HKYQHLATLAHNQSEIIAQLEEHCQRVPSARPVPQPPPAAPPRVYQPPPTVNRIINQISTN 240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 HKYQHLATLAHNQSEIIAQLEEHCQRVPSARPVPQPPPAAPPRVYQPPPTVNRIINQISTN 240

Qy  121 KLLRKESRNMNSRVTQLYMQLLHEIIRKRDNALELSQLENRILNQTADMLQLASXYKDLE 180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 KLLRKESRNMNSRVTQLYMQLLHEIIRKRDNALELSQLENRILNQTADMLQLASXYKDLE 180

Qy   61 PQQRVTGAICVNSKEPEVLLENRVHKQELELLNNELLKQRQIETLQQLVKVDGGIVSEV 120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 PQQRVTGAICVNSKEPEVLLENRVHKQELELLNNELLKQRQIETLQQLVKVDGGIVSEV 120
```

XX
CC   The present invention relates to a new nucleic acid molecule which
CC   comprises nucleotides 215 to 1252 of fully defined TIE ligand NL4
CC   polynucleotide sequence of 2212 base pairs as given in the specification.
CC   The nucleic acid of the invention encodes NL4 TIE ligand homologue
CC   polypeptide. The invention is useful for expressing NL4 TIE ligand
CC   homologue polypeptide by recombinant techniques. TIE ligand homologue
CC   polypeptide is useful for inducing vascularisation for promoting wound
CC   healing, and for treating ischaemic condition of heart or limb. The
CC   present amino acid sequence represents a human TIE ligand protein, as
CC   described in the invention
XX
SQ   Sequence 493 AA;

Query Match   99.8%; Score 2682; DB 5; Length 493;
Best Local Similarity   99.8%; Pred. No. 1.4e-216;
Matches 492; Conservative   1; Mismatches   0; Indels   0; Gaps   0;

Qy   1 MRPLCVTCWWLGLLAAMGAVAAGQEDGFEGTEEGSPRFFIYLNRYKRAGESQDKCTYTFIV 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 MRPLCVTCWWLGLLAAMGAVAAGQEDGFEGTEEGSPRFFIYLNRYKRAGESQDKCTYTFIV 60

Qy   61 PQQRVTGAICVNSKEPEVLLENRVHKQELELLNNELLKQKRQIETLQQLVKVDGGIVSEV 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 PQQRVTGAICVNSKEPEVLLENRVHKQELELLNNELLKQKRQIETLQQLVKVDGGIVSEV 120

Qy   121 KLLRKESRNMMSRVTQLYMQLLHEIIRKRDNALELSQLENR.INQTADMLQLASKYXDLE 180
              ||||||||||||||||||||||||||||||||||||||||.|||||||||||||||||||
Db   121 KLLRKESRNMMSRVTQLYMQLLHEIIRKRDNALELSQLENR.INQTADMLQLASKYXDLE 180

Qy   181 HKYQHLATLAHNQSEIIAQLEEHCQRVPSARPVPQPPPAAPPRVYQPPTYNRIINQISTN 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 HKYQHLATLAHNQSEIIAQLEEHCQRVPSARPVPQPPPAAPPRVYQPPTYNRIINQISTN 240

Qy   241 EIQSDQNLKVLPPLPTMPTLTSLPSSTDKPSGPWRDCLQALEDGHDTSSIYLVKPENTN 300
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 EIQSDQNLKVLPPLPTMPTLTSLPSSTDKPSGPWRDCLQALEDGHDTSSIYLVKPENTN 300

Qy   301 RLMQVWCDQRHDPGGWTVIQRRLDGSVNFFRNWETYKQGFGNIDGEYWLGLENIYWLTNQ 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 RLMQVWCDQRHDPGGWTVIQRRLDGSVNFFRNWETYKQGFGNIDGEYWLGLENIYWLTNQ 360

Qy   361 GNYKLLVTMEDWSGRKVFAEYASFRLEPESEYYKLRLGRYHGNAGDSFTWHNGKQFTTLD 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 GNYKLLVTMEDWSGRKVFAEYASFRLEPESEYYKLRLGRYHGNAGDSFTWHNGKQFTTLD 420

Qy   421 RDHDVYTGNCAHYQKGGWWYNACAHSNLNGVWYRGGHYRSRYQDGVYWAEFRGGSYSLKK 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 RDHDVYTGNCAHYQKGGWWYNACAHSNLNGVWYRGGHYRSRYQDGVYWAEFRGGSYSLKK 480

Qy   481 VVMMIRPNPNTFH 493
              |||||||||||||
Db   481 VVMMIRPNPNTFH 493

RESULT 11
AAE19825
ID   AAE19825 standard; protein; 493 AA.
XX
AC   AAE19825;
XX
DT   18-JUN-2002 (first entry)
XX
DE   Human TIE ligand NL1 protein.
XX
KW   Human; TIE ligand; NL1; cytostatic; osteopathic; vascularisation; toxin;
KW   muscular; immunoassay; therapeutic; anti-tumour agent; muscle growth;
KW   bone development; maturation; angiogenesis.
XX
OS   Homo sapiens.
XX
XX
PN   US6350450-B1.
XX

PD   26-FEB-2002.
XX
PD   19-AUG-1998; 98US-00136828.
XX
PF   19-SEP-1997; 97US-0059588P.
XX

PR   (GETH) GENENTECH INC.
PA   (GETH) GENENTECH INC.
XX
PI   Godowski PJ, Gurney AL, Goddard A, Hillan K;
XX
DR   WPI; 2002-215264/27.
DR   N-PSDB; AAD31563.
XX
CC
PT   Novel isolated antibody which specifically binds to a mammalian NL1 TIE
PT   ligand useful for immunoassays, delivery of cytotoxic molecules and as
PT   diagnostic agents to detect disease states.
XX
PS   Claim 1; Fig 3; 59pp; English.
XX
CC   The invention relates to an isolated antibody which specifically binds to
CC   a mammalian NL1 TIE (Tyrosine kinase containing Ig and EGF homology
CC   domains) ligand polypeptide which is capable of inducing vascularisation.
CC   The isolated antibody may be used in immunoassays to measure the amount
CC   of a TIE ligand in a biological sample. Additionally, the antibody may be
CC   used for the delivery of cytotoxic molecules, e.g. radioisotopes or
CC   toxins, or therapeutic agents to cells expressing a corresponding TIE
CC   receptor. The therapeutic agents may, for example, be other TIE ligands,
CC   including the TIE-2 ligand, members of the vascular endothelial growth
CC   factor (VEGF) family, or known anti-tumour agents, and agents known to be
CC   associated with muscle growth or development, or bone development,
CC   maturation, or growth. Anti-TIE ligand antibodies are also suitable as
CC   diagnostic agents, to detect disease states associated with the
CC   expression of a TIE (e.g. TIE-2) receptor. These detectably labelled
CC   antibody agonists of a TIE receptor can be used for imaging the presence
CC   of angiogenesis. The present sequence is human TIE ligand NL1 protein
XX
SQ   Sequence 493 AA;

Query Match   99.8%; Score 2682; DB 5; Length 493;
Best Local Similarity   99.8%; Pred. No. 1.4e-216;
Matches 492; Conservative   1; Mismatches   0; Indels   0; Gaps   0;

Qy   1 MRPLCVTCWWLGLLAAMGAVAAGQEDGFEGTEEGSPRFFIYLNRYKRAGESQDKCTYTFIV 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 MRPLCVTCWWLGLLAAMGAVAAGQEDGFEGTEEGSPRFFIYLNRYKRAGESQDKCTYTFIV 60

Qy   61 PQQRVTGAICVNSKEPEVLLENRVHKQELELLNNELLKQKRQIETLQQLVKVDGGIVSEV 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 PQQRVTGAICVNSKEPEVLLENRVHKQELELLNNELLKQKRQIETLQQLVKVDGGIVSEV 120

Qy   121 KLLRKESRNMMSRVTQLYMQLLHEIIRKRDNALELSQLENR.INQTADMLQLASKYXDLE 180
              ||||||||||||||||||||||||||||||||||||||||.|||||||||||||||||||
Db   121 KLLRKESRNMMSRVTQLYMQLLHEIIRKRDNALELSQLENR.INQTADMLQLASKYXDLE 180

Qy   181 HKYQHLATLAHNQSEIIAQLEEHCQRVPSARPVPQPPPAAPPRVYQPPTYNRIINQISTN 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 HKYQHLATLAHNQSEIIAQLEEHCQRVPSARPVPQPPPAAPPRVYQPPTYNRIINQISTN 240

Qy   241 EIQSDQNLKVLPPLPTMPTLTSLPSSTDKPSGPWRDCLQALEDGHDTSSIYLVKPENTN 300
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 EIQSDQNLKVLPPLPTMPTLTSLPSSTDKPSGPWRDCLQALEDGHDTSSIYLVKPENTN 300

Qy   301 RLMQVWCDQRHDPGGWTVIQRRLDGSVNFFRNWETYKQGFGNIDGEYWLGLENIYWLTNQ 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 RLMQVWCDQRHDPGGWTVIQRRLDGSVNFFRNWETYKQGFGNIDGEYWLGLENIYWLTNQ 360

Qy   361 GNYKLLVTMEDWSGRKVFAEYASFRLEPESEYYKLRLGRYHGNAGDSFTWHNGKQFTTLD 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 GNYKLLVTMEDWSGRKVFAEYASFRLEPESEYYKLRLGRYHGNAGDSFTWHNGKQFTTLD 420

Qy   421 RDHDVYTGNCAHYQKGGWWYNACAHSNLNGVWYRGGHYRSRYQDGVYWAEFRGGSYSLKK 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 RDHDVYTGNCAHYQKGGWWYNACAHSNLNGVWYRGGHYRSRYQDGVYWAEFRGGSYSLKK 480

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Qy   481  VVMMIRPNNTFH  493
          ||||||||||||
Db   481  VVMMIRPNNTFH  493

RESULT 12
AB017749
ID   AB017749 standard; protein; 493 AA.
AC   AB017749;
XX
DT   26-AUG-2003 (first entry)
XX
DE   Novel human secreted and transmembrane protein PRO196.
XX
KW   Human; secreted and transmembrane protein; PRO; antiinflammatory;
KW   antiarteriosclerotic; cardiant; anti-infertility; anti-HIV; cytostatic;
KW   antidiabetic; gene therapy; tumour necrosis factor (TNF)-alpha release;
KW   TNF-alpha release; cell proliferation; cell differentiation;
KW   gene expression modulator; proteoglycan release; cytokine release;
KW   tumour; inflammatory disease; organ failure; atherosclerosis;
KW   cardiac injury; infertility; birth defect; premature aging; AIDS;
KW   acquired immunodeficiency syndrome; cancer; diabetic complication;
KW   chromosome mapping; gene mapping; pharmaceutical; diagnostic; biosensor;
KW   bioreactor; tissue typing.
XX
OS   Homo sapiens.
XX
PN   US20032156-A1.
XX
PD   13-FEB-2003.
XX
PF   06-MAY-2002; 2002US-0014D474.
XX
PR   31-MAR-1997; 97WO-US005230.
PR   12-JUN-1998; 98WO-US012456.
PR   14-JUL-1998; 98WO-US014552.
PR   28-AUG-1998; 98WO-US017888.
PR   10-SEP-1998; 98WO-US018824.
PR   14-SEP-1998; 98WO-US019093.
PR   14-SEP-1998; 98WO-US019094.
PR   14-SEP-1998; 98WO-US019177.
PR   16-SEP-1998; 98WO-US019930.
PR   17-SEP-1998; 98WO-US019437.
PR   07-OCT-1998; 98WO-US021141.
PR   29-OCT-1998; 98WO-US022991.
PR   29-OCT-1998; 98WO-US022992.
PR   20-NOV-1998; 98WO-US024855.
PR   01-DEC-1998; 98WO-US025108.
PR   05-JAN-1999; 99WO-US000106.
PR   08-MAR-1999; 99WO-US005028.
PR   10-MAR-1999; 99WO-US005190.
PR   20-APR-1999; 99WO-US008615.
PR   14-MAY-1999; 99WO-US010733.
PR   02-JUN-1999; 99WO-US012252.
PR   01-SEP-1999; 99WO-US020111.
PR   08-SEP-1999; 99WO-US020594.
PR   13-SEP-1999; 99WO-US020944.
PR   15-SEP-1999; 99WO-US021090.
PR   15-SEP-1999; 99WO-US021547.
PR   05-OCT-1999; 99WO-US023089.
PR   29-NOV-1999; 99WO-US028214.
PR   30-NOV-1999; 99WO-US028313.
PR   01-DEC-1999; 99WO-US028409.
PR   01-DEC-1999; 99WO-US028301.
PR   01-DEC-1999; 99WO-US028634.
PR   02-DEC-1999; 99WO-US028551.
PR   02-DEC-1999; 99WO-US028564.
PR   02-DEC-1999; 99WO-US028565.
PR   16-DEC-1999; 99WO-US030095.
PR   20-DEC-1999; 99WO-US030911.
PR   20-DEC-1999; 99WO-US030999.
PR   22-DEC-1999; 99WO-US030720.
PR   30-DEC-1999; 99WO-US031243.
PR   30-DEC-1999; 99WO-US031274.
PR   05-JAN-2000; 2000WO-US000219.
PR   06-JAN-2000; 2000WO-US000277.
PR   06-JAN-2000; 2000WO-US000376.
PR   11-FEB-2000; 2000WO-US003565.
PR   18-FEB-2000; 2000WO-US004341.
PR   22-FEB-2000; 2000WO-US004342.
PR   24-FEB-2000; 2000WO-US004914.
PR   01-MAR-2000; 2000WO-US005601.
PR   02-MAR-2000; 2000WO-US005746.
PR   02-MAR-2000; 2000WO-US005004.
PR   10-MAR-2000; 2000WO-US006319.
PR   15-MAR-2000; 2000WO-US006884.
PR   20-MAR-2000; 2000WO-US007377.
PR   21-MAR-2000; 2000WO-US007532.
PR   30-MAR-2000; 2000WO-US008439.
PR   17-MAY-2000; 2000WO-US013705.
PR   22-MAY-2000; 2000WO-US014042.
PR   30-MAY-2000; 2000WO-US014941.
PR   02-JUN-2000; 2000WO-US015264.
PR   28-JUL-2000; 2000WO-US020710.
PR   11-AUG-2000; 2000WO-US022031.
PR   23-AUG-2000; 2000WO-US023522.
PR   24-AUG-2000; 2000WO-US023328.
PR   08-NOV-2000; 2000WO-US030952.
PR   10-NOV-2000; 2000WO-US030873.
PR   01-DEC-2000; 2000US-US032678.
PR   20-DEC-2000; 2000US-00747259.
PR   20-DEC-2000; 2000WO-US034956.
PR   28-FEB-2001; 2001WO-US006498.
PR   28-FEB-2001; 2001WO-US006520.
PR   01-MAR-2001; 2001WO-US006666.
PR   09-MAR-2001; 2001US-00802706.
PR   14-MAR-2001; 2001US-00808689.
PR   22-MAR-2001; 2001WO-US008366.
PR   05-APR-2001; 2001US-00828366.
PR   10-MAY-2001; 2001US-00854208.
PR   10-MAY-2001; 2001US-00854280.
PR   18-MAY-2001; 2001US-00860216.
PR   30-MAY-2001; 2001US-00860216.
PR   25-MAY-2001; 2001US-00866028.
PR   25-MAY-2001; 2001US-00866034.
PR   20-JUN-2001; 2001US-00885342.
PR   19-JUN-2001; 2001US-00882636.
PR   20-JUN-2001; 2001WO-US019592.
PR   21-JUN-2001; 2001US-00887879.
PR   22-JUN-2001; 2001WO-US020116.
PR   29-JUN-2001; 2001US-00921066.
PR   09-JUL-2001; 2001WO-US021735.
PR   18-JUL-2001; 2001US-00908827.
PR   06-AUG-2001; 2001US-00924419.
PR   09-AUG-2001; 2001US-00927796.
PR   16-AUG-2001; 2001US-00931836.
PR   19-DEC-2001; 2001US-0028072.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
PI   Gerritsen ME, Godard A, Godowski PJ, Gurney AL, Sherwood S;
PI   Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
XX
PT   New secreted and transmembrane PRO nucleic acids, for treating
PT   inflammation, organ failure, atherosclerosis, cardiac injury,
XX
DR   WPI; 2003-341980/32.
DR   N-PSDB; ACD23986.
```

RESULT 13
ABO25150

PT   infertility, birth defects, premature aging, axquired immunodeficiency
PT   syndrome (AIDS), or cancer.
XX
PS   Claim 12; Fig 268; 660pp; English.
XX
CC   The invention describes an isolated nucleic acid (I) comprising, or which
CC   has 80 % sequence identity to, or the full-length coding sequence of, one
CC   of 275 nucleotide sequences, and which encodes a corresponding
CC   polypeptide selected from 275 amino acid sequences, where all sequences
CC   are given in the specification. The polypeptide encoded by (I) is used to
CC   detect PRO polypeptides, link a bioactive molecule to a cell expressing a
CC   PRO polypeptide, modulate a biological activity of a cell, stimulate the
CC   release of tumour necrosis factor (TNF)-alpha from human blood, modulate
CC   the uptake of glucose or free fatty acid by cells, stimulate or inhibit
CC   the proliferation or differentiation of cells or gene expression,
CC   stimulate the release of proteoglycans, stimulate the release of cytokine
CC   from peripheral blood mononuclear cells, inhibit the binding of A-peptide
CC   to factor VIIA, or detect the presence of tumour in a mammal. The nucleic
CC   acid and polypeptide encoded by it, are useful for treating inflammatory
CC   diseases, organ failure, atherosclerosis, cardiac injury, infertility,
CC   birth defects, premature aging, acquired immunodeficiency syndrome
CC   (AIDS), cancer, or diabetic complications. The nucleic acid is useful in
CC   hybridisation probes, in chromosome and gene mapping, and in generating
CC   antisense RNA or DNA. The polypeptides are useful as pharmaceuticals,
CC   diagnostics, biosensors or bioreactors. Both are useful in tissue typing.
CC   This is the amino acid sequence of a novel human secreted and
CC   transmembrane PRO polypeptide
XX
SQ   Sequence 493 AA;

Query Match   99.9%; Score 2682; DB 6; Length 493;
Best Local Similarity   99.8%;
Matches 492; Conservative   1; Mismatches   0; Indels   0; Gaps   0;

Qy   1 MRPLCVTCWWLGLLAAMGAVAGQEDGFEGTEEGSPREFIYLNRYKRAGESQDKCTYTFIV 60
Db   1 MRPLCVTCWWLGLLAAMGAVAGQEDGFEGTEEGSPREFIYLNRYKRAGESQDKCTYTFIV 60

Qy   61 PQQRVTGAICVNSKEPEVLLENRVHKQELELLNNELLKQKRQIETLQQLVKVDGGIVSEV 120
Db   61 PQQRVTGAICVNSKEPEVLLENRVHKQELELLNNELLKQKRQIETLQQLVEVDGGIVSEV 120

Qy   121 KLLRKESRNMNSRVTQLYMQLLHEIIRKRDNALELSQLENRIINQTADMLQLASKYKDLE 180
Db   121 KLLRKESRNMNSRVTQLYMQLLHEIIRKRDNALELSQLENRIINQTADMLQLASKYKDLE 180

Qy   181 HKYQHLATLAHNQSEIIAQLEEHCQRVPSARPVPQPPPAAPPRVYQPPTYNRIINQISTN 240
Db   181 HKYQHLATLAHNQSEIIAQLEEHCQRVPSARPVPQPPPAAPPRVYQPPTYNRIINQISTN 240

Qy   241 EIQSDQNLKVLPPLPTMPTLITSLPSSTDKPSGPWRDCLQALEDGHDTSSIYLVKPENTN 300
Db   241 EIQSDQNLKVLPPLPTMPTLITSLPSSTDKPSGPWRDCLQALEDGHDTSSIYLVKPENTN 300

Qy   301 RLMQVWCDQRHDPGGWTVIQRLLDGSVNFFRNWETYKQGFGNIDGEYWLGLENIYWLTNQ 360
Db   301 RLMQVWCDQRHDPGGWTVIQRLLDGSVNFFRNWETYKQGFGNIDGEYWLGLENIYWLTNQ 360

Qy   361 GNYKLLVTMEDWSGRKVFAEYASFRLEPESEYYKLRLGRYHGNAGDSFTWHNGKQFTTLD 420
Db   361 GNYKLLVTMEDWSGRKVFAEYASFRLEPESEYYKLRLGRYHGNAGDSFTWHNGKQFTTLD 420

Qy   421 RDHDVYTGNCAHYQKGGWWYNACAHSNLNGVWYRGGHYRSRYQDGVYWAEFRGGSYSLKK 480
Db   421 RDHDVYTGNCAHYQKGGWWYNACAHSNLNGVWYRGGHYRSRYQDGVYWAEFRGGSYSLKK 480

Qy   481 VVMMIRPNPNTFH 493
Db   481 VVMMIRPNPNTFH 493

PR   20-DEC-1999; 9WO-US030999.
PR   05-JAN-2000; 2000WO-US000219.
PR   18-FEB-2000; 2000WO-US004341.
PR   18-FEB-2000; 2000WO-US004342.
PR   22-FEB-2000; 2000WO-US004414.
PR   01-MAR-2000; 2000WO-US005601.
PR   02-MAR-2000; 2000WO-US005841.
PR   09-MAR-2000; 2000WO-US006471.
PR   20-MAR-2000; 2000WO-US007377.
PR   30-MAR-2000; 2000WO-US008439.
PR   15-MAY-2000; 2000WO-US013358.
PR   17-MAY-2000; 2000WO-US013705.
PR   22-MAY-2000; 2000WO-US014042.
PR   30-MAY-2000; 2000WO-US014941.
PR   02-JUN-2000; 2000WO-US015264.
PR   11-AUG-2000; 2000WO-US022031.
PR   23-AUG-2000; 2000WO-US023522.
PR   24-AUG-2000; 2000WO-US023328.
PR   01-DEC-2000; 2000WO-US032678.
PR   28-FEB-2001; 2001WO-US006520.
PR   30-MAY-2001; 2001WO-US017443.
PR   01-JUN-2001; 2001WO-US017800.
PR   20-JUN-2001; 2001WO-US019692.
PR   29-JUN-2001; 2001WO-US021066.
PR   09-JUL-2001; 2001WO-US021735.
PR   15-NOV-2001; 2001US-0000279б.
XX
PA   (GETH) GENENTECH INC.
XX
PI   Ashkenazi AJ, Baker KP, Botstein DA, Desnoyers L, Eaton DL;
PI   Ferrara N, Fong S, Gao W, Gerber H, Goddard A;
PI   Godowski PJ, Gurney AL, Kljavin IJ, Mather JP, Napier MA, Pan J;
PI   Paoni NF, Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM;
PI   Wood WI, Zhang Z;
XX
PS   Claim 12; Fig 2; 254pp; English.
XX
PT   New secreted and transmembrane PRO polypeptides, useful for treating
PT   diabetes, retinal disorders and stimulating an immune response.
XX
DR   WPI; 2003-503396/47.
DR   N-PSDB; ACD42312.
XX
CC   The invention describes an isolated polypeptide (I) having at least 80 %
CC   amino acid sequence identity to 30 secreted and transmembrane
CC   polypeptides. PRO polypeptides are also useful for stimulating
CC   hypertrophy of adult heart, for inhibiting vascular endothelial growth
CC   factor stimulated proliferation of endothelial cells, stimulating
CC   proliferation of stimulated T-lymphocytes and for inducing proliferation
CC   of PDB12 pancreatic ductal cells and are thus useful in the treatment of
CC   disorders which involve protein secretion by the pancreas, including
CC   diabetes. PRO polypeptides are useful for inducing vascular permeability
CC   and in enhancing survival of retinal neurons cells and are also useful
CC   for the treatment of retinal disorders. PRO polypeptides are also useful
CC   for stimulating an immune response and inducing inflammation by inducing
CC   mononuclear cell and eosinophil infiltration at the site of infection of
CC   an animal. The PRO polypeptides are further useful for inducing apoptosis
CC   in endothelial cells for inhibiting neoplastic growth. This is the amino
CC   acid sequence of a novel human secreted and transmembrane PRO polypeptide
XX
SQ   Sequence 493 AA;

Query Match   99.9%; Score 2682; DB 6; Length 493;
                        99.8%; Pred. No. 1.4e-216;
Best Local Similarity   99.8%;
Matches 492; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy   1 MRPLCVTCWWLGLLAAMGAVAGGEDGFEGTEEGSPREFIYLNRYKRAGESQDKCYTFIV 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 MRPLCVTCWWLGLLAAMGAVAGGEDGFEGTEEGSPREFIYLNRYKRAGESQDKCYTFIV 60

Qy   61 PQQRVTGAICVNSKEPEVLLENRVHKQELELLNNELLKQKRQIETLQQLVKVDGGIVSEV 120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Db   61 PQQRVTGAICVNSKEPEVLLENRVHKQELELLNNELLKQKRQIETLQQLVEVDGGIVSEV 120

RESULT 14
ADA01417
ADA01417 standard; protein; 493 AA.
ID   ADA01417 standard; protein; 493 AA.
XX
AC   ADA01417;
XX
DT   06-NOV-2003 (first entry)
XX
DE   Human angiopoietin-related protein 2 SEQ ID NO:20.
XX
KW   drug testing; hyperlipidaemia; arteriosclerosis; hyperglycaemia;
KW   antilipaemic; antiarteriosclerotic; antidiabetic; gene therapy; human;
KW   angiopoietin-related protein 2.
XX
OS   Homo sapiens.
XX
XX
PN   WO200210039-A1.
XX
PD   19-DEC-2002.
XX
PF   07-JUN-2002; 2002WO-JP005657.
XX
PR   08-JUN-2001; 2001JP-00173758.
PR   13-JUN-2001; 2001JP-00178548.
PR   13-JUL-2001; 2001JP-00213334.
PR   28-SEP-2001; 2001JP-00300715.
PR   28-SEP-2001; 2001JP-00300716.
PR   22-NOV-2001; 2001JP-00357037.
PR   18-DEC-2001; 2001JP-00384103.
PR   05-APR-2002; 2002JP-00103583.
XX
PA   (SANY) SANKYO CO LTD.
XX
PI   Koishi R, Ando Y, Ono M, Yasumo H, Shimizugawa T, Yoshida K;
PI   Shimamura M, Furukawa H;
XX
DR   WPI; 2003-148803/14.
DR   N-PSDB; ADA01416.
XX
PT   Testing drugs to treat or prevent diseases e.g. hyperlipemia,
PT   arteriosclerosis and hyperglycemia by culturing with transformant cells
PT   then detecting e.g. decrease in mRNA expression dose.
XX

Qy 121 KLLRKESRNMNSRVTQLYMQLLHEIIRKRDNALELSQLENRILNQTADMLQLASKYKDLE 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 121 KLLRKESRNMNSRVTQLYMQLLHEIIRKRDNALELSQLENRILNQTADMLQLASKYKDLE 180

Qy 181 HXYQHLATLAHNQSEIIAQLEEHCQRVPSARPVPQPPPAAPPRVYQPPTYNRRIINQISTN 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Db 181 HXYQHLATLAHNQSEIIAQLEEHCQRVPSARPVPQPPPAAPPRVYQPPTYNRRIINQISTN 240

Qy 241 EIQSDQNLKVLPPPLPTMPLITSLPSSTDKPSPSGPWRDCLQALEDGHDTSSIYLVKPENTN 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 241 EIQSDQNLKVLPPPLPTMPLITSLPSSTDKPSGPWRDCLQALEDGHDTSSIYLVKPENTN 300

Qy 301 RLMQVWCDQRHDPGGWTVIQRRLDGSVNFRNWETYKQGFGNIIDGEYWLGLENIYWLTNQ 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 301 RLMQVWCDQRHDPGGWTVIQRRLDGSVNFRNWETYKQGFGNIIDGEYWLGLENIYWLTNQ 360

Qy 361 GNYKLLVTMEDWSGRKVFAEYASFRLEPESEYYKLRIGRYHGNAGDSFTWHNGKQFTTLD 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 361 GNYKLLVTMEDWSGRKVFAEYASFRLEPESEYYKLRIGRYHGNAGDSFTWHNGKQFTTLD 420

Qy 421 RDHDVYTGNCAHYQKGGWWYNACAHSNLNGVWYRGGHYRSRYQDGVYWAEFRGGSYSLKK 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 421 RDHDVYTGNCAHYQKGGWWYNACAHSNLNGVWYRGGHYRSRYQDGVYWAEFRGGSYSLKK 480

Qy 481 VVMMIRPNPNTFH 493
          |||||||||||||
Db 481 VVMMIRPNPNTFH 493

RESULT 15

ID   ABU81003 standard; protein; 493 AA.

PS   Claim 25; Page 235-237; 279pp; Japanese.

XX

CC   The present invention describes a method for testing drugs that have
CC   activity on treating or preventing at least 1 disease selected from
CC   hyperlipaemia, arteriosclerosis and hyperglycaemia, which comprises
CC   culturing cells originating from a mammal in the presence or absence of a
CC   test substance, and detecting expression dose of the mRNA with any of the
CC   specified nucleotide sequences. More specifically the method comprises:
CC   (a) culturing cells originating from a mammal in the presence or absence
CC   of a test substance; (b) detecting expression dose of the mRNA with any
CC   of the nucleotide sequences (i)-(v) (where t and u are exchangeable): (i)
CC   nucleotides 47-1411 of a 1604 base pair sequence (ADA01398); (ii)
CC   nucleotides 78-1457 of a 1716 base pair sequence (ADA01400); (iii) the
CC   DNA inserted into a phagemid sustaining in the transformant E. coli
CC   pBK/m55-1 SANK 72199 (FERM BP-6940); (iv) the DNA inserted into a
CC   phagemid sustaining in the transformant E. coli pTrip/h55-1 SANK 72299
CC   (FERM BP-6941); or (v) a nucleotide sequence hybridisable with a
CC   polynucleotide containing the antisense sequence of (i)-(iv) under
CC   stringent conditions and encoding a polypeptide with the activity of
CC   increasing neutral lipid concentration in serum; and (c) comparing the
CC   resultant expression doses for selecting a test substance. The nucleotide
CC   sequences (i)-(v) have antilipaemic, antiarteriosclerotic and
CC   antidiabetic activities, and can be used in gene therapy. The method is
CC   for testing drugs to treat or prevent diseases e.g. hyperlipaemia,
CC   arteriosclerosis and hyperglycaemia. The present sequence is used in the
CC   exemplification of the present invention.

XX

SQ   Sequence 493 AA;

Query Match   99.9%; Score 2682; DB 6; Length 493;
Best Local Similarity   99.8%;
Matches 492; Conservative   1; Mismatches   0; Indels   0; Gaps   0;
                        Pred. No. 1.4e-216;

Qy   1 MRPLCVTCWWLGLLAAMGAVAGQEDGFEGTEEGSPREFIYLNRYKRAGESQDKCTYTFIV 60
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 MRPLCVTCWWLGLLAAMGAVAGQEDGFEGTEEGSPREFIYLNRYKRAGESQDKCTYTFIV 60

Qy   61 PQQRVTGAICVNSKEPEVLLENRVHKQELELLNNELLKQKRQIETLQQLVKDGGIVSEV 120
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 PQQRVTGAICVNSKEPEVLLENRVHKQELELLNNELLKQKRQIETLQQLVEVDGGIVSEV 120

Qy   121 KLLRKESRNMMSRVTQLYMQLLHEIIRKRDNALELSQLENRILNQTADMLQLASKYKDLE 180
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 KLLRKESRNMNSRVTQLYMQLLHEIIRKRDNALELSQLENRILNQTADMLQLASKYKDLE 180

Qy   181 HKYQHLATLAHNQSEIIAQLEEHCQRVPSARPVPQPPPAAPPRVYQPPTYNRIINQISTN 240
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 HKYQHLATLAHNQSEIIAQLEEHCQRVPSARPVPQPPPAAPPRVYQPPTYNRIINQISTN 240

Qy   241 EIQSDQNLKVLPPPLPTMPTLTSLPSSTDKPSGPWRDCLQALEDGHDTSSIYLVKPENTN 300
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 EIQSDQNLKVLPPPLPTMPTLTSLPSSTDKPSGPWRDCLQALEDGHDTSSIYLVKPENTN 300

Qy   301 RLMQVWCDQRHDPGGWTVIQRRLDGSVNFFRNWETYKQGFGNIDGEYWLGLENIYWLTNQ 360
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 RLMQVWCDQRHDPGGWTVIQRRLDGSVNFFRNWETYKQGFGNIDGEYWLGLENIYWLTNQ 360

Qy   361 GNYKLLVTMEDWSGRKVFAEYASFRLEPESEYYKLRLGRYHGNAGDSFTWHNGKQFTTLD 420
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 GNYKLLVTMEDWSGRKVFAEYASFRLEPESEYYKLRLGRYHGNAGDSFTWHNGKQFTTLD 420

Qy   421 RDHDVYTGNCAHYQKGGWYNACAHSNLNGVWYRGGHYRSRYQDGVYWAEFRGGSYSLKK 480
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 RDHDVYTGNCAHYQKGGWYNACAHSNLNGVWYRGGHYRSRYQDGVYWAEFRGGSYSLKK 480

Qy   481 VVMMIRPNPNTFH 493
                |||||||||||||
Db   481 VVMMIRPNPNTFH 493

XX

AC   ABU81003;

XX

DT   23-JUN-2003 (first entry)

XX

DE   Human PRO polypeptide #134.

XX

KW   Human; PRO polypeptide; secreted and transmembrane protein; diabetes;
KW   anti-PRO antibody; diagnostic assay; gene expression; diabetes;
KW   bone disorder; cartilage disorder; rheumatoid arthritis; obesity;
KW   sports injury; osteoarthritis; hyper-insulinaemia; hypo-insulinaemia;
KW   hearing loss; coagulation disorder; stroke; heart attack; cardiant;
KW   antidiabetic; anorectic; vulnerary; antiarthritic; osteopathic;
KW   antirheumatic; auditory; cerebroprotective; angiogenic.

XX

OS   Homo sapiens.

XX

PN   US200300431-A1.

XX

PD   02-JAN-2003.

XX

PF   19-DEC-2001; 2001US-00028072.

XX

PR   18-JUN-1997; 97US-00499119P.
PR   26-AUG-1997; 97US-00569794P.
PR   17-SEP-1997; 97US-00593113P.
PR   17-SEP-1997; 97US-00593115P.
PR   17-SEP-1997; 97US-00593117P.
PR   17-SEP-1997; 97US-00599122P.
PR   17-SEP-1997; 97US-00591184P.
PR   17-SEP-1997; 97US-00593263P.
PR   18-SEP-1997; 97US-00593252P.
PR   19-SEP-1997; 97US-00555888P.
PR   24-SEP-1997; 97US-00598366P.
PR   17-OCT-1997; 97US-00622250P.
PR   17-OCT-1997; 97US-00622285P.
PR   17-OCT-1997; 97US-00622287P.
PR   24-OCT-1997; 97US-00637755P.
PR   24-OCT-1997; 97US-00628144P.
PR   24-OCT-1997; 97US-00628156P.
PR   24-OCT-1997; 97US-00630045P.
PR   24-OCT-1997; 97US-00630082P.
PR   24-OCT-1997; 97US-00631127P.
PR   27-OCT-1997; 97US-00633277P.
PR   27-OCT-1997; 97US-00633279P.
PR   27-OCT-1997; 97US-00633292P.
PR   28-OCT-1997; 97US-00633550P.
PR   28-OCT-1997; 97US-00633561P.
PR   29-OCT-1997; 97US-00637704P.
PR   29-OCT-1997; 97US-00633733P.
PR   29-OCT-1997; 97US-00633735P.
PR   29-OCT-1997; 97US-00637738P.
PR   03-NOV-1997; 97US-00642248P.
PR   07-NOV-1997; 97US-00648809P.
PR   07-NOV-1997; 97US-00651866P.
PR   12-NOV-1997; 97US-00655846P.
PR   17-NOV-1997; 97US-00653364P.
PR   21-NOV-1997; 97US-00663364P.
PR   24-NOV-1997; 97US-00665511P.
PR   24-NOV-1997; 97US-00667702P.
PR   24-NOV-1997; 97US-00669122P.
PR   11-DEC-1997; 97US-00692787P.
PR   16-DEC-1997; 97US-00693344P.
PR   11-DEC-1997; 97US-00698944P.
PR   23-JAN-1998; 98US-00723207P.
PR   04-FEB-1998; 98US-00735612P.
PR   09-FEB-1998; 98US-00740086P.
PR   09-FEB-1998; 98US-00740092P.
PR   12-MAR-1998; 98US-00777791P.
PR   20-MAR-1998; 98US-00778904P.
PR   25-MAR-1998; 98US-00792294P.
PR   27-MAR-1998; 98US-00796684P.
PR   27-MAR-1998; 98US-00797928P.
PR   31-MAR-1998; 98US-00801655P.

PR 12-JUN-1998; 98WO-US012456.
PR 14-JUL-1998; 98WO-US014552.
PR 28-AUG-1998; 98WO-US017888.
PR 10-SEP-1998; 98WO-US018824.
PR 14-SEP-1998; 98WO-US019093.
PR 14-SEP-1998; 98WO-US019094.
PR 14-SEP-1998; 98WO-US019177.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98WO-US019437.
PR 07-OCT-1998; 98WO-US021141.
PR 29-OCT-1998; 98WO-US022991.
PR 29-OCT-1998; 98WO-US022992.
PR 20-NOV-1998; 98WO-US024855.
PR 01-DEC-1998; 98WO-US025108.
PR 05-JAN-1999; 99WO-US000106.
PR 08-MAR-1999; 99WO-US005028.
PR 10-MAR-1999; 99WO-US005190.
PR 20-APR-1999; 99WO-US008615.
PR 14-MAY-1999; 99WO-US010733.
PR 02-JUN-1999; 99WO-US012252.
PR 01-SEP-1999; 99WO-US020111.
PR 08-SEP-1999; 99WO-US020594.
PR 13-SEP-1999; 99WO-US020944.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 05-OCT-1999; 99WO-US023089.
PR 29-NOV-1999; 99WO-US028214.
PR 30-NOV-1999; 99WO-US028313.
PR 30-NOV-1999; 99WO-US028409.
PR 01-DEC-1999; 99WO-US028301.
PR 01-DEC-1999; 99WO-US028634.
PR 02-DEC-1999; 99WO-US028851.
PR 02-DEC-1999; 99WO-US028564.
PR 02-DEC-1999; 99WO-US028865.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 20-DEC-1999; 99WO-US031099.
PR 30-DEC-1999; 99WO-US031243.
PR 30-DEC-1999; 99WO-US031274.
PR 05-JAN-2000; 2000WO-US000019.
PR 06-JAN-2000; 2000WO-US000277.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 18-FEB-2000; 2000WO-US004342.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.
PR 24-FEB-2000; 2000WO-US005004.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005746.
XX
PA (GETH) GENENTECH INC.
XX
PI Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
XX
DR WPI; 2003-352836/33.
DR N-PSDB; ACA67127.
XX
PT New isolated PRO polypeptide useful for treating diabetes, rheumatoid
PT arthritis, sports injuries, obesity, hearing loss in mammals, stroke, or
PT heart attack.
XX
PS Claim 12; Fig 268; 643pp; English.
XX
CC The present invention relates to the isolation of novel human PRO
CC polypeptides, and the polynucleotide sequences encoding them. The PRO
CC polypeptides are secreted and transmembrane proteins. The PRO
CC polypeptides and polynucleotides are useful for preparing a medicament
CC useful in the treatment of diabetes, bone and/or cartilage disorders
CC (e.g. rheumatoid arthritis, sports injuries, osteoarthritis), obesity,
CC hyper- or hypo-insulinaemia, hearing loss, and coagulation disorders
CC (e.g. stroke, heart attack). Anti-PRO antibodies are useful in diagnostic
CC assays for PRO, by detecting its expression in specific cells, tissues or
CC serum, and for affinity purification of PRO from recombinant cell culture
CC or natural sources. ABU80870-ABU81144 represent the human PRO
CC polypeptides of the invention. Note: The sequence data for this patent
CC was obtained in electronic format directly from the USPTO web site at
CC seqdata.uspto.gov/psipsDIDentry.html
XX
SQ Sequence 493 AA;

Query Match   99.9%;
Best Local Similarity   99.8%;
Matches 492; Conservative   1; Mismatches   0; Indels   0; Gaps   0;

Qy   1 MRPLCVTCWWLGLLAAMGAVAGQEDGFEGGTEEGSPREFIYLNRYKRAGESQDKCTYTFIV 60
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Db   1 MRPLCVTCWWLGLLAAMGAVAGQEDGFEGGTEEGSPREFIYLNRYKRAGESQDKCTYTFIV 60

Qy   61 PQQRVTGAICVNSKPEVLLENRVHKQELELLNNELLKQRQIETLQQLVKDGGIVSEV 120
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Db   61 PQQRVTGAICVNSKPEVLLENRVHKQELELLNNELLKQRQIETLQQLVEVDGGIVSEV 120

Qy   121 KLLRKESRNMMNSRVTQLYMQLLHEIIRKRDNALELSQLENRILNQTADMLQLASRYKDLE 180
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 KLLRKESRNMMNSRVTQLYMQLLHEIIRKRDNALELSQLENRILNQTADMLQLASRYKDLE 180

Qy   181 HKYQHLATLAAHNQSEIIAQLEEHCQRVPSARPVPQPPPAAPPRVYQPPTYNRIINQISTN 240
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Db   181 HKYQHLATLAAHNQSEIIAQLEEHCQRVPSARPVPQPPPAAPPRVYQPPTYNRIINQISTN 240

Qy   241 EIQSDQNLKVLPPPLPTMPLTLSLPSSTDKPSGPWRDCLQALEDGHDTSSIYLYKPENTN 300
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 EIQSDQNLKVLPPPLPTMPLTLSLPSSTDKPSGPWRDCLQALEDGHDTSSIYLYKPENTN 300

Qy   301 RLMQVWCDQRHDPGGWTVIQRRLDGSVNFFRNWETYKQGFGNIDGEYWLGLENIYWLTNQ 360
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 RLMQVWCDQRHDPGGWTVIQRRLDGSVNFFRNWETYKQGFGNIDGEYWLGLENIYWLTNQ 360

Qy   361 GNYKLLVTMEDWSGRKVFAEYASFRLEPESEYYKLRLGRYHGNADSFTWHNGKQFTLD 420
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 GNYKLLVTMEDWSGRKVFAEYASFRLEPESEYYKLRLGRYHGNADSFTWHNGKQFTLD 420

Qy   421 RDHDVYTGNCAHYQKGGWWYNACAHSNLNGVWYRGGHYRSRYQDGVYWAEFRGGSYSLKK 480
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 RDHDVYTGNCAHYQKGGWWYNACAHSNLNGVWYRGGHYRSRYQDGVYWAEFRGGSYSLKK 480

Qy   481 VVMMIRPNPNTFH 493
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Db   481 VVMMIRPNPNTFH 493

Search completed: July 30, 2004, 12:36:14
Job time : 57 secs

OM protein - protein search, using sw model

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GenCore version 5.1.6

Run on: July 30, 2004, 12:35:14 ; Search time 20 Seconds
                                    (without alignments)
                                    1272.580 Million cell updates/sec

Title: US-10-018-386-2
Perfect score: 2686
Sequence: 1 MRPLCVTCWWLGLLAAMGAV..........GSYSLKKVVMIRPNNTFH 493

Scoring table: BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Issued_Patents_AA:*
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                 2:/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Match Length	DB	DB ID	Description
1	2682	99.9	493	2	US-08-933-821-2	Sequence 2, Appli
2	2682	99.9	493	3	US-08-960-507-2	Sequence 2, Appli
3	2682	99.9	493	4	US-09-136-828-2	Sequence 2, Appli
4	2682	99.9	493	4	US-09-332-928A-2	Sequence 2, Appli
5	2682	99.9	493	4	US-09-136-801-2	Sequence 2, Appli
6	2682	99.9	493	4	US-09-332-929-2	Sequence 2, Appli
7	2682	99.9	493	4	US-09-333-075-2	Sequence 2, Appli
8	2682	99.9	493	4	US-09-202-088A-2	Sequence 2, Appli
9	2682	99.9	493	3	US-09-333-077-2	Sequence 2, Appli
10	1507.5	56.1	491	2	US-08-933-821-4	Sequence 4, Appli
11	1507.5	56.1	491	3	US-08-960-507-4	Sequence 4, Appli
12	1507.5	56.1	491	4	US-09-136-828-4	Sequence 4, Appli
13	1507.5	56.1	491	4	US-09-332-928A-4	Sequence 4, Appli
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15	1507.5	56.1	491	4	US-09-332-929-4	Sequence 4, Appli
16	1507.5	56.1	491	4	US-09-333-075-4	Sequence 4, Appli
17	1507.5	56.1	491	4	US-09-202-088A-4	Sequence 4, Appli
18	1507.5	56.1	491	3	US-09-333-077-4	Sequence 4, Appli
19	1500.5	55.9	491	4	US-09-658-644-2	Sequence 2, Appli
20	1094.5	40.7	470	2	US-08-933-821-6	Sequence 6, Appli
21	1094.5	40.7	470	3	US-08-960-507-6	Sequence 6, Appli
22	1094.5	40.7	470	4	US-09-136-828-6	Sequence 6, Appli
23	1094.5	40.7	470	4	US-09-332-928A-6	Sequence 6, Appli
24	1094.5	40.7	470	4	US-09-136-801-6	Sequence 6, Appli
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29	578	21.5	491	3	US-08-740-223A-13	Sequence 13, Appli
30	578	21.5	491	4	US-09-709-188-13	Sequence 13, Appli
31	578	21.5	491	3	US-08-740-223A-4	Sequence 4, Appli
32	578	21.5	497	4	US-09-709-188-4	Sequence 4, Appli
33	577.5	21.5	498	3	US-08-740-223A-20	Sequence 20, Appli
34	577.5	21.5	498	4	US-09-709-188-20	Sequence 20, Appli
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36	577	21.5	498	4	US-09-709-188-1	Sequence 1, Appli
37	577	21.5	497	2	US-08-418-595-4	Sequence 4, Appli
38	578	21.5	497	2	US-08-665-926-4	Sequence 4, Appli
39	577	21.5	497	3	US-08-348-492-4	Sequence 4, Appli
40	577	21.5	497	4	US-09-162-437-4	Sequence 4, Appli
41	577	21.5	497	4	US-09-442-717-4	Sequence 4, Appli
42	577	21.5	497	4	US-09-689-020-4	Sequence 4, Appli
43	575.5	21.4	498	4	US-09-202-491-6	Sequence 6, Appli
44	575	21.4	490	3	US-08-740-223A-12	Sequence 12, Appli
45	575	21.4	490	4	US-09-709-188-12	Sequence 12, Appli

ALIGNMENTS

RESULT 1
US-08-933-821-2

; Sequence 2, Application US/08933821
; Patent No. 5972338
; GENERAL INFORMATION:
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; TITLE OF INVENTION: Tie Ligands
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/933,821
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Ginger R.
; REGISTRATION NUMBER: 33,055
; REFERENCE/DOCKET NUMBER: P1130
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-3216
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 493 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-933-821-2

Query Match   99.9%; Score 2682; DB 2; Length 493;
Best Local Similarity   99.8%; Pred. No. 4.8e-220;
Matches 492; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy   1 MRPLCVTCWWLGLLAAMGAVAGQEDGFEGTEEGSPREFIYLNRYKRAGESQDKCTYTFIV 60
              MRPLCVTCWWLGLLAAMGAVAGQEDGFEGTEEGSPREFIYLNRYKRAGESQDKCTYTFIV
Db   1 MRPLCVTCWWLGLLAAMGAVAGQEDGFEGTEEGSPREFIYLNRYKRAGESQDKCTYTFIV 60

Qy   61 PQQRVTGAICVNSKEPEVLLENRVHKQELELLNNELLKQKRQIETLQQLVKVDGGIVSEV 120
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Db   61 PQQRVTGAICVNSKEPEVLLENRVHKQELELLNNELLKQKRQIETLQQLVEVDGGIVSEV 120

RESULT 2

US-08-960-507-2

; Sequence 2, Application US/08960507
; Patent No. 6057435
; GENERAL INFORMATION:
;   APPLICANT: Godowski, Paul J.
;   APPLICANT: Gurney, Austin L.
;   TITLE OF INVENTION: Tie Ligands
;   NUMBER OF SEQUENCES: 24
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Genentech, Inc.
;   STREET: 1 DNA Way
;   CITY: South San Francisco
;   STATE: California
;   COUNTRY: USA
;   ZIP: 94080
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: WinPatin (Genentech)
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/960,507
;   FILING DATE:
;   CLASSIFICATION: 536
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Dreger, Ginger R.
;   REGISTRATION NUMBER: 33,055
;   REFERENCE/DOCKET NUMBER: P1130p1
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 650/225-3216
;   TELEFAX: 650/952-9881
US-08-960-507-2
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 493 amino acids
;   TYPE: Amino Acid
;   TOPOLOGY: Linear

Query Match 99.9%; Score 2682; DB 3; Length 493;
Best Local Similarity 99.8%; Pred. No. 4.8e-220;
Matches 492; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Db  121 KLLRKESRNMNSRVTQLYMQLLHEIIRKRDNALELSQLENRILNQTADMLQLASKYKDLE 180

Qy  181 HKYQHLATLAHNQSEIIAQLEEHCQRVPSARPVPQPPPAAPRVYQPPTYNRIINQISTN 240
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Qy  241 EIQSDQNLKVLPPLPTMPTLLTSLPSSTDKPSGPWRDCLQALEDGHDTSSIYLVKPENTN 300
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Db  241 EIQSDQNLKVLPPLPTMPTLLTSLPSSTDKPSGPWRDCLQALEDGHDTSSIYLVKPENTN 300

Qy  301 RLMQVWCDQRHDPGGWTVIQRRLDGSVNFFRNWETYKQGFGNIDGEYWLGLENIYWLTNQ 360
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Qy  361 GNYKLLVTMEDWSGRKVFAEYASFRLEPESEYYKLRLGRYHGNAGDSFTWHNGKQFTTLD 420
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Db  361 GNYKLLVTMEDWSGRKVFAEYASFRLEPESEYYKLRLGRYHGNAGDSFTWHNGKQFTTLD 420

Qy  421 RDHDVYTGNCAHYQKGGWWYNACAHSNLNGVWYRGGHYRSRYQDGVYWAEFRGGSYSLKK 480
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Qy  481 VVMMIRPNPNTFH 493
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Db  481 VVMMIRPNPNTFH 493
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RESULT 3

US-09-136-828-2

; Sequence 2, Application US/09136828
; Patent No. 6350450
; GENERAL INFORMATION:
;   APPLICANT: Godowski, Paul J.
;   APPLICANT: Gurney, Austin L.
;   TITLE OF INVENTION: Tie Ligands
;   NUMBER OF SEQUENCES: 17
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Genentech, Inc.
;   STREET: 1 DNA Way
;   CITY: South San Francisco
;   STATE: California
;   COUNTRY: USA
;   ZIP: 94080
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: WinPatin (Genentech)
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/09/136,828
;   FILING DATE:
;   CLASSIFICATION:
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Dreger, Ginger R.
;   REGISTRATION NUMBER: 33,055
;   REFERENCE/DOCKET NUMBER: P1130R1A
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 650/225-3216
;   TELEFAX: 650/952-9881
US-09-136-828-2
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 493 amino acids
;   TYPE: Amino Acid

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Qy   61 PQQRVTGAICVNSKEPEVLLENRVHKQELELLNNELLKQKRQIETLQQLVEVDGGIVSEV 120
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Db   61 PQQRVTGAICVNSKEPEVLLENRVHKQELELLNNELLKQKRQIETLQQLVEVDGGIVSEV 120

Qy  121 KLLRKESRNMNSRVTQLYMQLLHEIIRKRDNALELSQLENRILNQTADMLQLASKYKDLE 180
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Db  121 KLLRKESRNMNSRVTQLYMQLLHEIIRKRDNALELSQLENRILNQTADMLQLASKYKDLE 180

Qy  181 HKYQHLATLAHNQSEIIAQLEEHCQRVPSARPVPQPPPAAPRVYQPPTYNRIINQISTN 240
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Qy  241 EIQSDQNLKVLPPLPTMPTLLTSLPSSTDKPSGPWRDCLQALEDGHDTSSIYLVKPENTN 300
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Db  241 EIQSDQNLKVLPPLPTMPTLLTSLPSSTDKPSGPWRDCLQALEDGHDTSSIYLVKPENTN 300

Qy  301 RLMQVWCDQRHDPGGWTVIQRRLDGSVNFFRNWETYKQGFGNIDGEYWLGLENIYWLTNQ 360
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Db  301 RLMQVWCDQRHDPGGWTVIQRRLDGSVNFFRNWETYKQGFGNIDGEYWLGLENIYWLTNQ 360

Qy  361 GNYKLLVTMEDWSGRKVFAEYASFRLEPESEYYKLRLGRYHGNAGDSFTWHNGKQFTTLD 420
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Db  361 GNYKLLVTMEDWSGRKVFAEYASFRLEPESEYYKLRLGRYHGNAGDSFTWHNGKQFTTLD 420

Qy  421 RDHDVYTGNCAHYQKGGWWYNACAHSNLNGVWYRGGHYRSRYQDGVYWAEFRGGSYSLKK 480
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Db  421 RDHDVYTGNCAHYQKGGWWYNACAHSNLNGVWYRGGHYRSRYQDGVYWAEFRGGSYSLKK 480

Qy  481 VVMMIRPNPNTFH 493
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Db  481 VVMMIRPNPNTFH 493
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TOPOLOGY: Linear
US-09-136-828-2

Query Match   99.9%;   Score 2682; DB 4;   Length 493;
Best Local Similarity   99.8%;   Pred. No. 4.8e-220;
Matches 492; Conservative   1; Mismatches   0; Indels   0; Gaps   0;

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Db    1 MRPLCVTCWWLGLLAAMGAVAGQEDGFEGTEEGSPREFIYLNRYKRAGESQDKCTYTFIV 60

Qy   61 PQQRVTGAICVNSKEPEVLLENRVHKQELELLNNELLKQRQIETLQQLVKVDGGIVSEV 120
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Db   61 PQQRVTGAICVNSKEPEVLLENRVHKQELELLNNELLKQRQIETLQQLVKVDGGIVSEV 120

Qy  121 KLLRKESRNMNSRVTQLYMQLLHEIIRKRDNALELSQLENRIINQTADMLQLASKYKDLE 180
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Db  121 KLLRKESRNMNSRVTQLYMQLLHEIIRKRDNALELSQLENRIINQTADMLQLASKYKDLE 180

Qy  181 HKYQHLATLAHNQSEIIAQLEEHCQRVPSARPVPQPPPAAPPRVYQPPTYNRIINQISTN 240
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Db  181 HKYQHLATLAHNQSEIIAQLEEHCQRVPSARPVPQPPPAAPPRVYQPPTYNRIINQISTN 240

Qy  241 EIQSDQNLKVLPPLPLPTMPTLTSLPSSTDKPSGPWRDCLQALEDGHDTSSIYLVKPENTN 300
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Db  241 EIQSDQNLKVLPPLPLPTMPTLTSLPSSTDKPSGPWRDCLQALEDGHDTSSIYLVKPENTN 300

Qy  301 RLMQVWCDQRHDPGGWTVIQRRLDGSVNFFRNWETYKQGFGNIDGEYWLGLENIYWLTNQ 360
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Db  301 RLMQVWCDQRHDPGGWTVIQRRLDGSVNFFRNWETYKQGFGNIDGEYWLGLENIYWLTNQ 360

Qy  361 GNYKLLVTMEDWSGRKVFAEYASFRLEPESEYYKLRLGRYHGNAGDSFTWHNGKQFTTLD 420
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Qy  421 RDHDVYTGNCAHYQKGGWWYNACAHSNLNGVWYRGGHYRSRYQDGVYWAEFRGGSYSLKK 480
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Db  421 RDHDVYTGNCAHYQKGGWWYNACAHSNLNGVWYRGGHYRSRYQDGVYWAEFRGGSYSLKK 480

Qy  481 VVMMIRPNPNTFH 493
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Db  481 VVMMIRPNPNTFH 493
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RESULT 4
US-09-332-928A-2
Sequence 2, Application US/09332928A
Patent No. 6368853
GENERAL INFORMATION:
APPLICANT: Godowski, Paul J.
           Gurney, Austin L.
TITLE OF INVENTION: Tie Ligands
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/332,928A
FILING DATE: 14-Jun-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/933,821
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:

NAME: Dreger, Ginger R.
REGISTRATION NUMBER: 33,055
REFERENCE/DOCKET NUMBER: P1130
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-3216
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 493 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-332-928A-2

Query Match   99.9%;   Score 2682; DB 4;   Length 493;
Best Local Similarity   99.8%;   Pred. No. 4.8e-220;
Matches 492; Conservative   1; Mismatches   0; Indels   0; Gaps   0;

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Qy    1 MRPLCVTCWWLGLLAAMGAVAGQEDGFEGTEEGSPREFIYLNRYKRAGESQDKCTYTFIV 60
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Db    1 MRPLCVTCWWLGLLAAMGAVAGQEDGFEGTEEGSPREFIYLNRYKRAGESQDKCTYTFIV 60

Qy   61 PQQRVTGAICVNSKEPEVLLENRVHKQELELLNNELLKQRQIETLQQLVKVDGGIVSEV 120
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Db   61 PQQRVTGAICVNSKEPEVLLENRVHKQELELLNNELLKQRQIETLQQLVKVDGGIVSEV 120

Qy  121 KLLRKESRNMNSRVTQLYMQLLHEIIRKRDNALELSQLENRIINQTADMLQLASKYKDLE 180
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Db  121 KLLRKESRNMNSRVTQLYMQLLHEIIRKRDNALELSQLENRIINQTADMLQLASKYKDLE 180

Qy  181 HKYQHLATLAHNQSEIIAQLEEHCQRVPSARPVPQPPPAAPPRVYQPPTYNRIINQISTN 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 HKYQHLATLAHNQSEIIAQLEEHCQRVPSARPVPQPPPAAPPRVYQPPTYNRIINQISTN 240

Qy  241 EIQSDQNLKVLPPLPLPTMPTLTSLPSSTDKPSGPWRDCLQALEDGHDTSSIYLVKPENTN 300
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241 EIQSDQNLKVLPPLPLPTMPTLTSLPSSTDKPSGPWRDCLQALEDGHDTSSIYLVKPENTN 300

Qy  301 RLMQVWCDQRHDPGGWTVIQRRLDGSVNFFRNWETYKQGFGNIDGEYWLGLENIYWLTNQ 360
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  301 RLMQVWCDQRHDPGGWTVIQRRLDGSVNFFRNWETYKQGFGNIDGEYWLGLENIYWLTNQ 360

Qy  361 GNYKLLVTMEDWSGRKVFAEYASFRLEPESEYYKLRLGRYHGNAGDSFTWHNGKQFTTLD 420
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  361 GNYKLLVTMEDWSGRKVFAEYASFRLEPESEYYKLRLGRYHGNAGDSFTWHNGKQFTTLD 420

Qy  421 RDHDVYTGNCAHYQKGGWWYNACAHSNLNGVWYRGGHYRSRYQDGVYWAEFRGGSYSLKK 480
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  421 RDHDVYTGNCAHYQKGGWWYNACAHSNLNGVWYRGGHYRSRYQDGVYWAEFRGGSYSLKK 480

Qy  481 VVMMIRPNPNTFH 493
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Db  481 VVMMIRPNPNTFH 493
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RESULT 5
US-09-136-801-2
Sequence 2, Application US/09136801
Patent No. 6413770
GENERAL INFORMATION:
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin
APPLICANT: Hillan, Kenneth
APPLICANT: Botstein, David
APPLICANT: Goddard, Audrey
APPLICANT: Roy, Margaret
APPLICANT: Ferrara, Napoleone
APPLICANT: Tumas, Daniel
APPLICANT: Schwall, Ralph
TITLE OF INVENTION: Tie Ligand Homologues
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.

Left column

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;   STREET:  1 DNA Way
;   CITY:  South San Francisco
;   STATE:  California
;   COUNTRY:  USA
;   ZIP:  94080
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE:  3.5 inch, 1.44 Mb floppy disk
;   COMPUTER:  IBM PC compatible
;   OPERATING SYSTEM:  PC-DOS/MS-DOS
;   SOFTWARE:  WinPatin (Genentech)
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER:  US/09/136,801
;   FILING DATE:
;   CLASSIFICATION:
;   ATTORNEY/AGENT INFORMATION:
;   NAME:  Dreger, Ginger R.
;   REGISTRATION NUMBER:  33,055
;   REFERENCE/DOCKET NUMBER:  P1130P2
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE:  650/225-3216
;   TELEFAX:  650/952-9981
; INFORMATION FOR SEQ ID NO:  2:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH:  493 amino acids
;   TYPE:  Amino Acid
;   TOPOLOGY:  Linear
US-09-136-801-2

Query Match             99.9%;  Score 2682;  DB 4;  Length 493;
Best Local Similarity   99.8%;  Pred. No. 4.8e-220;
Matches  492;  Conservative  1;  Mismatches  0;  Indels  0;  Gaps  0;

Qy    1 MRPLCVTCWWLGLLAAMGAVAGQEDGFEGTEEGSPREFIYLNRYKRAGESQDKCTYTFIV 60
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 MRPLCVTCWWLGLLAAMGAVAGQEDGFEGTEEGSPREFIYLNRYKRAGESQDKCTYTFIV 60

Qy   61 PQQRVTGAICVNSKEPEVLLENRVHKQELELLNNELLKQRQIETLQQLVKYDGGIVSEV 120
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Db   61 PQQRVTGAICVNSKEPEVLLENRVHKQELELLNNELLKQRQIETLQQLVEVDGGIVSEV 120

Qy  121 KLLRKESRNMNSRVTQLYMQLLHEIIRKRDNALELSQLENRIINQTADMLQLASKYKDLE 180
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 KLLRKESRNMNSRVTQLYMQLLHEIIRKRDNALELSQLENRIINQTADMLQLASKYKDLE 180

Qy  181 HKYQHLATLAHNQSEIIAQLEEHCQRVPSARPVPQPPPAAPPRVYQPPTYNRIINQISTN 240
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Db  181 HKYQHLATLAHNQSEIIAQLEEHCQRVPSARPVPQPPPAAPPRVYQPPTYNRIINQISTN 240

Qy  241 EIQSDQNLKVLPPPLPTMPTLTSLPSSTDKPSGGPWRDCLQALEDGHDTSSIYLVKPENTN 300
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241 EIQSDQNLKVLPPPLPTMPTLTSLPSSTDKPSGGPWRDCLQALEDGHDTSSIYLVKPENTN 300

Qy  301 RLMQVWCDQRHDPGGWTVIQRRLDGSVNFFRNWETYKQGFGNIDGEYWLGLENIYWLTNQ 360
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  301 RLMQVWCDQRHDPGGWTVIQRRLDGSVNFFRNWETYKQGFGNIDGEYWLGLENIYWLTNQ 360

Qy  361 GNYKLLVTMEDWSGRKVFAEYASFRLEPESEYYKLRLGRYHGNAGDSFTWHNGKQFTTLD 420
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  361 GNYKLLVTMEDWSGRKVFAEYASFRLEPESEYYKLRLGRYHGNAGDSFTWHNGKQFTTLD 420

Qy  421 RDHDVYTGNCAHYQKGGWWYNACAHSNLNGVWYRGGHYRSRYQDGVYWAEFRGGSYSLKK 480
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  421 RDHDVYTGNCAHYQKGGWWYNACAHSNLNGVWYRGGHYRSRYQDGVYWAEFRGGSYSLKK 480

Qy  481 VVMMIRPNPNTFH 493
         |||||||||||||
Db  481 VVMMIRPNPNTFH 493


RESULT 6
US-09-332-929-2
; Sequence 2, Application US/09332929
; Patent No. 6420542
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Right column

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; GENERAL INFORMATION:
;   APPLICANT:  Godowski, Paul J.
;   APPLICANT:  Gurney, Austin L.
;   TITLE OF INVENTION:  Tie Ligands
;   NUMBER OF SEQUENCES:  17
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE:  Genentech, Inc.
;   STREET:  1 DNA Way
;   CITY:  South San Francisco
;   STATE:  California
;   COUNTRY:  USA
;   ZIP:  94080
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE:  3.5 inch, 1.44 Mb floppy disk
;   COMPUTER:  IBM PC compatible
;   OPERATING SYSTEM:  PC-DOS/MS-DOS
;   SOFTWARE:  WinPatin (Genentech)
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER:  US/09/332,929
;   FILING DATE:
;   CLASSIFICATION:
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER:  08/933,821
;   FILING DATE:
;   ATTORNEY/AGENT INFORMATION:
;   NAME:  Dreger, Ginger R.
;   REGISTRATION NUMBER:  33,055
;   REFERENCE/DOCKET NUMBER:  P1130
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE:  650/225-3216
;   TELEFAX:  650/952-9981
; INFORMATION FOR SEQ ID NO:  2:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH:  493 amino acids
;   TYPE:  Amino Acid
;   TOPOLOGY:  Linear
US-09-332-929-2

Query Match             99.9%;  Score 2682;  DB 4;  Length 493;
Best Local Similarity   99.8%;  Pred. No. 4.8e-220;
Matches  492;  Conservative  1;  Mismatches  0;  Indels  0;  Gaps  0;

Qy    1 MRPLCVTCWWLGLLAAMGAVAGQEDGFEGTEEGSPREFIYLNRYKRAGESQDKCTYTFIV 60
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Db    1 MRPLCVTCWWLGLLAAMGAVAGQEDGFEGTEEGSPREFIYLNRYKRAGESQDKCTYTFIV 60

Qy   61 PQQRVTGAICVNSKEPEVLLENRVHKQELELLNNELLKQRQIETLQQLVKYDGGIVSEV 120
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Db   61 PQQRVTGAICVNSKEPEVLLENRVHKQELELLNNELLKQRQIETLQQLVEVDGGIVSEV 120

Qy  121 KLLRKESRNMNSRVTQLYMQLLHEIIRKRDNALELSQLENRIINQTADMLQLASKYKDLE 180
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 KLLRKESRNMNSRVTQLYMQLLHEIIRKRDNALELSQLENRIINQTADMLQLASKYKDLE 180

Qy  181 HKYQHLATLAHNQSEIIAQLEEHCQRVPSARPVPQPPPAAPPRVYQPPTYNRIINQISTN 240
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 HKYQHLATLAHNQSEIIAQLEEHCQRVPSARPVPQPPPAAPPRVYQPPTYNRIINQISTN 240

Qy  241 EIQSDQNLKVLPPPLPTMPTLTSLPSSTDKPSGGPWRDCLQALEDGHDTSSIYLVKPENTN 300
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Db  241 EIQSDQNLKVLPPPLPTMPTLTSLPSSTDKPSGGPWRDCLQALEDGHDTSSIYLVKPENTN 300

Qy  301 RLMQVWCDQRHDPGGWTVIQRRLDGSVNFFRNWETYKQGFGNIDGEYWLGLENIYWLTNQ 360
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Db  301 RLMQVWCDQRHDPGGWTVIQRRLDGSVNFFRNWETYKQGFGNIDGEYWLGLENIYWLTNQ 360

Qy  361 GNYKLLVTMEDWSGRKVFAEYASFRLEPESEYYKLRLGRYHGNAGDSFTWHNGKQFTTLD 420
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Db  361 GNYKLLVTMEDWSGRKVFAEYASFRLEPESEYYKLRLGRYHGNAGDSFTWHNGKQFTTLD 420

Qy  421 RDHDVYTGNCAHYQKGGWWYNACAHSNLNGVWYRGGHYRSRYQDGVYWAEFRGGSYSLKK 480
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Db  421 RDHDVYTGNCAHYQKGGWWYNACAHSNLNGVWYRGGHYRSRYQDGVYWAEFRGGSYSLKK 480
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Qy  481 VVMMIRPNPNTFH 493
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Db  481 VVMMIRPNPNTFH 493
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RESULT 7
US-09-333-075-2
; Sequence 2, Application US/09333075
; Patent No. 6492331
; GENERAL INFORMATION:
;   APPLICANT: Godowski, Paul J.
;   APPLICANT: Gurney, Austin L.
;   TITLE OF INVENTION: Tie Ligands
;   NUMBER OF SEQUENCES: 17
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Genentech, Inc.
;   STREET: 1 DNA Way
;   CITY: South San Francisco
;   STATE: California
;   COUNTRY: USA
;   ZIP: 94080
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: WinPatin (Genentech)
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/09/333,075
;   FILING DATE:
;   CLASSIFICATION:
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 08/933,821
;   FILING DATE:
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Dreger, Ginger R.
;   REGISTRATION NUMBER: 33,055
;   REFERENCE/DOCKET NUMBER: P1130
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 650/225-3216
;   TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 2:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 493 amino acids
;   TYPE: Amino Acid
;   TOPOLOGY: Linear
US-09-333-075-2

  Query Match   99.9%; Score 2682; DB 4; Length 493;
  Best Local Similarity   99.8%; Pred. No. 4.8e-220;
  Matches 492; Conservative   1; Mismatches   0; Indels   0; Gaps   0;

Qy   1 MRPLCVTCWWLGLLAAMGAVAGQEDGFEGTEEGSPREFIYLNRYKRAGESQDKCTYTFIV 60
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Db   1 MRPLCVTCWWLGLLAAMGAVAGQEDGFEGTEEGSPREFIYLNRYKRAGESQDKCTYTFIV 60

Qy   61 PQQRVTGAICVNSKEPEVLLENRVHKQELELLNNELLKQKROIETLQQLVKVDGGIVSEV 120
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Db   61 PQQRVTGAICVNSKEPEVLLENRVHKQELELLNNELLKQKROIETLQQLVEVDGGIVSEV 120

Qy 121 KLLRKESRNMNSRVTQLYMQLLHEIIRKRDNALELSQLENRIINQTADMLQLASKYKDLE 180
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Qy 181 HKYQHLATLAHNQSEIIAQLEEHCQRVPSARPVPQPPPAAPPRVYQPPTYNRIINQISTN 240
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Db 181 HKYQHLATLAHNQSEIIAQLEEHCQRVPSARPVPQPPPAAPPRVYQPPTYNRIINQISTN 240

Qy 241 EIQSDQNLKVLPPPLPTMPTLTSLPSSTDKPSGPWRDCLQALEDGHDTSSIYLVKPENTN 300
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Db 241 EIQSDQNLKVLPPPLPTMPTLTSLPSSTDKPSGPWRDCLQALEDGHDTSSIYLVKPENTN 300

Qy 301 RLMQVWCDQRHDPGGWTVIQRRLDGSVNFRNWETYKQGFGNIDGEYWLGLENIYWLTNQ 360
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Db 301 RLMQVWCDQRHDPGGWTVIQRRLDGSVNFRNWETYKQGFGNIDGEYWLGLENIYWLTNQ 360
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RESULT 8
US-09-202-088A-2
; Sequence 2, Application US/09202088A
; Patent No. 6551822
; GENERAL INFORMATION:
;   APPLICANT: Godowski, Paul J.
;   APPLICANT: Gurney, Austin L.
;   APPLICANT: Hillan, Kenneth
;   APPLICANT: Botstein, David
;   APPLICANT: Goddard, Audrey
;   APPLICANT: Roy, Margaret
;   APPLICANT: Ferrara, Napoleone
;   APPLICANT: Tumas, Daniel
;   APPLICANT: Schwall, Ralph
;   TITLE OF INVENTION: TIE LIGAND HOMOLOGUES
;   FILE REFERENCE: P1130P3US
;   CURRENT APPLICATION NUMBER: US/09/202,088A
;   CURRENT FILING DATE: 1998-12-08
;   PRIOR APPLICATION NUMBER: PCT/US98/19093
;   PRIOR FILING DATE: 1998-09-14
;   NUMBER OF SEQ ID NOS: 35
; SEQ ID NO 2
;   LENGTH: 493
;   TYPE: PRT
;   ORGANISM: Homo Sapiens
US-09-202-088A-2

  Query Match            99.9%;  Score 2682;  DB 4;  Length 493;
  Best Local Similarity   99.8%;  Pred. No. 4.8e-220;
  Matches  492;  Conservative   1;  Mismatches   0;  Indels   0;  Gaps   0;

Qy    1 MRPLCVTCWWLGLLAAMGAVAGQEDGFEGTEEGSPREFIYLNRYKRAGESQDKCTYTFIV 60
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Db    1 MRPLCVTCWWLGLLAAMGAVAGQEDGFEGTEEGSPREFIYLNRYKRAGESQDKCTYTFIV 60

Qy   61 PQQRVTGAICVNSKEPEVLLENRVHKQELELLNNELLKQKROIETLQQLVKVDGGIVSEV 120
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Db   61 PQQRVTGAICVNSKEPEVLLENRVHKQELELLNNELLKQKROIETLQQLVEVDGGIVSEV 120

Qy  121 KLLRKESRNMNSRVTQLYMQLLHEIIRKRDNALELSQLENRIINQTADMLQLASKYKDLE 180
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 KLLRKESRNMNSRVTQLYMQLLHEIIRKRDNALELSQLENRIINQTADMLQLASKYKDLE 180

Qy  181 HKYQHLATLAHNQSEIIAQLEEHCQRVPSARPVPQPPPAAPPRVYQPPTYNRIINQISTN 240
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 HKYQHLATLAHNQSEIIAQLEEHCQRVPSARPVPQPPPAAPPRVYQPPTYNRIINQISTN 240

Qy  241 EIQSDQNLKVLPPPLPTMPTLTSLPSSTDKPSGPWRDCLQALEDGHDTSSIYLVKPENTN 300
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241 EIQSDQNLKVLPPPLPTMPTLTSLPSSTDKPSGPWRDCLQALEDGHDTSSIYLVKPENTN 300

Qy  301 RLMQVWCDQRHDPGGWTVIQRRLDGSVNFRNWETYKQGFGNIDGEYWLGLENIYWLTNQ 360
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  301 RLMQVWCDQRHDPGGWTVIQRRLDGSVNFRNWETYKQGFGNIDGEYWLGLENIYWLTNQ 360

Qy  361 GNYKLLVTMEDWSGRKVFAEYASFRLEPESEYYKLRLGRYHGNAGDSFTWHNGKQFTLLD 420
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  361 GNYKLLVTMEDWSGRKVFAEYASFRLEPESEYYKLRLGRYHGNAGDSFTWHNGKQFTLLD 420

Qy  421 RDHDVYTGNCAHYQKGGWWYNACAHSNLNGVWYRGGHYRSRYQDGVYWAEFRGGSYSLKK 480
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  421 RDHDVYTGNCAHSNLNGVWYRGGHYRSRYQDGVYWAEFRGGSYSLKK 480

Qy  481 VVMMIRPNPNTFH 493
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Left column

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Db  361 GNYKLLVTMEDWSGRKVFAEYASFRLEPESSEYYKLRLGRYHGNAGDSFTWHNGKQFTTLD 420
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Db  421 RDHDVYTGNCAHYQKGGWWYNACAHSNLNGVWYRGGHYRSRYQDGVYWAEFRGGSYSLKK 480
Qy  481 VVMMIRPNPNTFH 493
Db  481 VVMMIRPNPNTFH 493
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RESULT 9
US-09-333-077-2
; Sequence 2, Application US/09333077
; Patent No. 6586397
; GENERAL INFORMATION:
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; TITLE OF INVENTION: Tie Ligands
; NUMBER OF SEQUENCES: 17
; CURRENT APPLICATION DATA:
; CURRENT APPLICATION NUMBER: US/09/333,077
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/933,821
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Ginger R.
; REGISTRATION NUMBER: 33,055
; REFERENCE/DOCKET NUMBER: P1130
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-3216
; TELEFAX: 650/952-9881
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatin (Genentech)
; SEQUENCE CHARACTERISTICS:
; LENGTH: 493 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-09-333-077-2

Query Match   99.9%; Score 2682;   DB 4;   Length 493;
Best Local Similarity 99.8%; Pred. No. 4.8e-220;
Matches 492; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Qy    1 MRPLCVTCWLGLLAAMGAVAGQEDGFEGTEGSSPREIYLNRYKRAGESQDKCTYTFIV  60
Db    1 MRPLCVTCWLGLLAAMGAVAGQEDGFEGTEGSSPREFIYLNRYKRAGESQDKCTYTFIV  60

Qy   61 PQORVTGAICVNSKEPEVLLENRVHKQELELLNNELLKQKRQIETLLQQLVKVDGGIVSEV 120
Db   61 PQORVTGAICVNSKEPEVLLENRVHKQELELLNNELLKQKRQIETLLQQLVEVDGGIVSEV 120

Qy  121 KLLRKESRNMNSRVTQLYMQLLHEIIRKRDNALELSQLENRIILNQTADMLQLASKYKDLE 180
Db  121 KLLRKESRNMNSRVTQLYMQLLHEIIRKRDNALELSQLENRIILNQTADMLQLASKYKDLE 180

Qy  181 HKYQHLATLAHNQSEIIAQLEEHCQRVPSARPVYQPPPAAPRVYQPPTYNRIINQISTN 240
Db  181 HKYQHLATLAHNQSEIIAQLEEHCQRVPSARPVYQPPPAAPRVYQPPTYNRIINQISTN 240
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Right column

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Qy  301 RLMQVWCDQRHDPGGWTVIQRRLDGSVNFFRNWETYKQGFGNIIDGEYWLGLENIYWLINQ 360
Db  301 RLMQVWCDQRHDPGGWTVIQRRLDGSVNFFRNWETYKQGFGNIIDGEYWLGLENIYWLINQ 360

Qy  361 GNYKLLVTMEDWSGRKVFAEYASFRLEPESEYYKLRLGRYHGNAGDSFTWHNGKQFTTLD 420
Db  361 GNYKLLVTMEDWSGRKVFAEYASFRLEPESSEYYKLRLGRYHGNAGDSFTWHNGKQFTTLD 420

Qy  421 RDHDVYTGNCAHYQKGGWWYNACAHSNLNGVWYRGGHYRSRYQDGVYWAEFRGGSYSLKK 480
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Qy  481 VVMMIRPNPNTFH 493
Db  481 VVMMIRPNPNTFH 493
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RESULT 10
US-08-933-821-4
; Sequence 4, Application US/08933821
; Patent No. 5972338
; GENERAL INFORMATION:
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; TITLE OF INVENTION: Tie Ligands
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/933,821
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Ginger R.
; REGISTRATION NUMBER: 33,055
; REFERENCE/DOCKET NUMBER: P1130
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-3216
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 491 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-933-821-4

Query Match   56.1%; Score 1507.5; DB 2; Length 491;
Best Local Similarity 58.6%; Pred. No. 5e-120;
Matches 290; Conservative 69; Mismatches 109; Indels 27; Gaps 9;

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Qy    9 WWLGLLAAMGAVAGQEDGFEGTEGSSPREF------IYLNRYKRAGESQD---KCTYTFIVP  61
Db    6 WTLGVLFFLLVDTGHCRG--------GQFKIKINQRRYPRATDGKERAXKCAYTFLVP  56

Qy   62 QQRVTGAICVNSKEPEV-LLENRVHKQELELLNNELLKQKRQIETLLQQLVKVDGGIVSEV 120
Db   57 EQRITGPICVNTKGQDASTIKDMITRMDLENLKDVLSRQXREIDVLQLVVDGNIVNEV 116

Qy  121 KLLRKESRNMNSRVTQLYMQLLHEIIRKRDNALELSQLENRILNQTADMLQLASKYKDLE 180
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RESULT 11
US-08-960-507-4
Sequence 4, Application US/08960507
Patent No. 6057435
GENERAL INFORMATION:
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
TITLE OF INVENTION: Tie Ligands
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/960,507
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Dreger, Ginger R.
REGISTRATION NUMBER: 33,055
REFERENCE/DOCKET NUMBER: P1130p1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-3216
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 491 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-960-507-4

Query Match   56.1%; Score 1507.5; DB 3; Length 491;
Best Local Similarity 58.6%; Pred. No. 5e-120;
Matches 290; Conservative 69; Mismatches 109; Indels 27; Gaps 9;

Qy   9 WWLGLLAAMGAVAGQEDGFEGTEEGSPREF----IYLNRYKRAGESQD--KCTYTFIVP 61
            |:||:| :| ||||:|||:| :: :: ||:|||||
Db   117 KLIRKESRNMNSRVTQLYMQLLHEIIRKRDNSLELSQLENKILNVTTEMLKMATRYRELE 176

Qy   117 KLIRKESRNMNSRVTQLYMQLLHEIIRKRDNSLELSQLENKILNVTTEMLKMATRYRELE 176
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   177 VRYASLIDLVNNQSVMTLLEEQCLRIFSRQDTHVSPPLVQVVPQHI--PNSQQYTPGLL 234

Qy   177 VRYASLIDLVNNQSVMTLLEEQCLRIFSRQDTHVSPPLVQVVPQHI--PNSQQYTPGLL 234
            |||||||||||||||||||||||||||||||||||||||||||||| :||||||||||
Db   235 GGNEIQRDPGYPRDLMPPPDLATSPTKSPFKIPPVTFINEGPFKDCQQAKEAGHSVSGIY 294

Qy   235 GGNEIQRDPGYPRDLMPPPDLATSPTKSPFKIPPVTFINEGPFKDCQQAKEAGHSVSGIY 294
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   295 MIKPENSNGPMQLWCENSLDPGGWTVIQKRTDGSVNFFRNWENYKKGFGNIDGEYWLGLE 354

Qy   295 MIKPENSNGPMQLWCENSLDPGGWTVIQKRTDGSVNFFRNWENYKKGFGNIDGEYWLGLE 354
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   355 NIYMLSNQDNYKLLIELEDWSDKKVYAEYSSFRLEPESSEYYKIRLGRYHGNAGDSFTWHN 414

Qy   355 NIYMLSNQDNYKLLIELEDWSDKKVYAEYSSFRLEPESSEYYKIRLGRYHGNAGDSFTWHN 414
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   415 GKQFTTLDRDHDVYTGNCAHYQKGGWWYNACAHSNLNGVWYRGGHYRSRYQDGVYWAEFR 472

Qy   353 NIYWLTNQGNYKLLVTMEDWSGRKVFAEYASFRLEPESSEYYKIRLGRYHGNAGDSFTWHN 412
            ||:||:|||||||:|:||||:|:||||||||||||||||||||:||||||||||||||||
Db   413 GKQFTTLDRDHDVYTGNCAHYQKGGWWYNACAHSNLNGVWYRGGHYRSRYQDGVYWAEFR 472

Qy   413 GKQFTTLDRDHDVYTGNCAHYQKGGWWYNACAHSNLNGVWYRGGHYRSRYQDGVYWAEFR 472
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   473 GGSYSLKKVVMMIRP 487

Qy   415 GKQFTTLDRDKDMYAGNCAHFHKGGWWYNACAHSNLNGVWYRGGHYRSKHQDGIFWAEYR 474
            |||||||:||||:|:|||:|:|||||||||||||||||||||||||||| :||||:|
Db   475 GGSYSLRAVQMMIKP 489

Qy   473 GGSYSLKKVVMMIRP 487
            ||||||:.||:||:|
Db   475 GGSYSLRAVQMMIKP 489

RESULT 12
US-09-136-828-4
Sequence 4, Application US/09136828
Patent No. 6350450
GENERAL INFORMATION:
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
TITLE OF INVENTION: Tie Ligands
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/136,828
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Dreger, Ginger R.
REGISTRATION NUMBER: 33,055
REFERENCE/DOCKET NUMBER: P1130R1A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-3216
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 491 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-09-136-828-4

Qy   6 WTLGVLFFLVDTGHCRG---------GQFKIKKINQRRYPRATDGKEEAAKKCAYTFLVP 56
            |:||||||:||:||:: |||:|||:|||::||||||::|||||||||||
Db   62 QQRVTGAICIVNSKEPEV-LLENRVHKQELELLNNELLKQEKQIETLQQLVKVDGGIVSEV 120

Qy   62 QQRVTGAICIVNSKEPEV-LLENRVHKQELELLNNELLKQEKQIETLQQLVKVDGGIVSEV 120
            :|||:||||:||:|||: ||||:||:|:||:|:||:|||:||:|||||:|:|||:|:|
Db   177 EQRITGPICVNTKGQDASTIKDMITRMDLENLKDVLSRQKREIDVLQLVVDVDGNIIVEV 116

Qy   57 EQRITGPICVNTKGQDASTIKDMITRMDLENLKDVLSRQKREIDVLQLVVDVDGNIIVEV 116
            :||:|||||||:||||:||||||||::||||:|||::||::|||||:|||:||||:|:||
Db   117 KLIRKESRNMNSRVTQLYMQLLHEIIRKRDNALELSQLENRILNQTADMLQLASKYKDLE 180

Qy   121 KLIRKESRNMNSRVTQLYMQLLHEIIRKRDNALELSQLENRILNQTADMLQLASKYKDLE 180
            ||||||||||||||||||||||||||||||:|||||||||:|||:|:||:||::|||:||
Db   181 HKYQHLATLAHNQSEIIAQLEEHCQRVPSARVPQPP----AAPPRVYQPPTYNRIINQI 237

Qy   57 EQRITGPICVNTKGQDASTIKDMITRMDLENLKDVLSRQKREIDVLQLVVDVDGNIIVEV 116

Qy   117 KLIRKESRNMNSRVTQLYMQLLHEIIRKRDNSLELSQLENKILNVTTEMLKMATRYRELE 176
            ||||||||||||||||||||||||||||||:|||||||||:||||:|:||:||:|||:||
Db   181 HKYQHLATLAHNQSEIIAQLEEHCQRVPSARVPQPP----AAPPRVYQPPTYNRIINQI 237

Qy   177 VRYASLIDLVNNQSVMTLLEEQCLRIFSRQDTHVSPPLVQVVPQHI--PNSQQYTPGLL 234

Qy   181 HKYQHLATLAHNQSEIIAQLEEHCQRVPSARVPQPP----AAPPRVYQPPTYNRIINQI 237
            |||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db   235 GGNEIQRDPGYPRDLMPPPDLATSPTKSPFKIPPVTFINEGPFKDCQQAKEAGHSVSGIY 294

Qy   235 GGNEIQRDPGYPRDLMPPPDLATSPTKSPFKIPPVTFINEGPFKDCQQAKEAGHSVSGIY 294
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   293 LVKPENTNRLMQVWCDQRHDPGGWTVIQRRLDGSVNFFRNWETYKKQFGNIDGEYWLGLE 352

Qy   293 LVKPENTNRLMQVWCDQRHDPGGWTVIQRRLDGSVNFFRNWETYKKQFGNIDGEYWLGLE 352

Qy   238 STNEIQSDQNL--KVLPPP-LPTMPTLT--SLPSSTDKPSGPWRDCLQALEDGHDTSSIY 292

Qy   295 MIKPENSNGPMQLWCENSLDPGGWTVIQKRTDGSVNFFRNWENYKKGFGNIDGEYWLGLE 354

Qy   355 NIYMLSNQDNYKLLIELEDWSDKKVYAEYSSFRLEPESSEYYKIRLGRYHGNAGDSFTWHN 414

Qy   353 NIYWLTNQGNYKLLVTMEDWSGRKVFAEYASFRLEPESSEYYKIRLGRYHGNAGDSFTWHN 412

Qy   238 STNEIQSDQNL--KVLPPP-LPTMPTLT--SLPSSTDKPSGPWRDCLQALEDGHDTSSIY 292

Qy   413 GKQFTTLDRDHDVYTGNCAHYQKGGWWYNACAHSNLNGVWYRGGHYRSRYQDGVYWAEFR 472

Qy   415 GKQFTTLDRDKDMYAGNCAHFHKGGWWYNACAHSNLNGVWYRGGHYRSKHQDGIFWAEYR 474

Qy   473 GGSYSLKKVVMMIRP 487
            |||||:.||:||:|
Db   475 GGSYSLRAVQMMIKP 489

RESULT 13
US-09-332-928A-4
Sequence 4, Application US/09332928A
Patent No. 6368853
GENERAL INFORMATION:
; APPLICANT: Gurney, Austin L.
; APPLICANT: Godowski, Paul J.
; TITLE OF INVENTION: Tie Ligands
; NUMBER OF SEQUENCES: 17
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/09/332,928A
;   FILING DATE: 14-Jun-1999
;   CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 08/933,821
;   FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
;   NAME: Dreger, Ginger R.
;   REGISTRATION NUMBER: 33,055
; CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Genentech, Inc.
;   STREET: 1 DNA Way
;   CITY: South San Francisco
;   STATE: California
;   COUNTRY: USA
;   ZIP: 94080
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: WinPatin (Genentech)

Query Match   56.1%; Score 1507.5; DB 4; Length 491;
Best Local Similarity   58.6%; Pred. No. 5e-120;
Matches 290; Conservative 69; Mismatches 109; Indels 27; Gaps 9;

Qy   9 WWLGLLAAMGAVAGQEDGFEGTEEGSPREF-----IYLNRYKRAGESQD---KCTYFIVP 61
          ::||:|| |||: ::| |:::::::|:|| ||||||:||||||| |:||:|||
Db   6 WTLGVLFFLLVDTGHCRG---------------GQFKIKKINQRRYPRATDGKEEAKKCAYTFLVP 56

Qy   62 QQRVTGAICVNSKEPEV-LLENRVHKQELELLNNELLKQKRQIETLQQLVKVDGGIVSEV 120
          :::|||:||:|||::|: ::::|:|: :|::|||||||||||||||||:|:::||:|::
Db   57 EQRITGPICVNTKGQDASTIKDMITRMDLENLKDVLSRQKREIDVLQLVVDGNIVNEV 116

Qy   121 KLLRKESRNMNSRVTQLYMQLLHEIIRKRDNALELSQLENRIILNQTADMLQLASKYKDLE 180
          ||||||||||||||||||||||||||||||||||||||||||||||||:||||||||||||
Db   117 KLLRKESRNMNSRVTQLYMQLLHEIIRKRDNSLELSQLENKILNVTTEMLKMATYRELE 176

Qy   181 HKYQHLATLAHNQSEIIAQLEEHCQRVPSARPVPQPPP---AAPPRVYQPPTYNRIINQI 237
          |||||||||||||||||||||||||||||||||||||| :|:||:||||||||||||:
Db   177 VKYASLTDLVNNQSVMTLLEEQCLRIFSRQDTHVSPPLVQVVPQHI--PNSQQYTPGLL 234

Qy   238 STNEIQSDQNL--KVLPPP-LPTMPTLT--SLPSSTDKPSGPWRDCLQALEDGHDTSSIY 292
          :|:||:|:|| ||:||| |||||||| :||||||||| |:||||||:||||::|||
Db   235 GGNEIQRDPGYPRDLMPPDLAISPTKSPFKIPPVTFINEGPFKDCQQAKEAGHSVSGIY 294

Qy   293 LVKPENTNRLMQVWCDQRHDPGGWTVIQRRLDGSVNFFRNWETYKQGFGNIDGEYWLGLE 352
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   295 MIKPENSNGPMQLWCENSLDPGGWTVIQKRTDGSVNFFRNWENYKKGFGNIDGEYWLGLE 354

Qy   353 NIYWLTNQGNYKLLVTMEDWSGRKVFAEYASFRLEPESEYYKLRLGRYHGNAGDSFTWHN 412
          |||||:|||||||||||||||||||||||||||||||||||||:||||||||||||||||
Db   355 NIYMLSNQDNYKLLIELEDWSDKKVYAEYSSFRLEPESEFYRLRLGTYQGNAGDSMWWHN 414

Qy   413 GKQFTTLDRDHDVYTGNCAHYQKGGWWYNACAHSNLNGVWYRGGHYRSRYQDGVYWAEFR 472
          ||||||||||||:||||||||||||||||||||||||||||||||||||:||||||||||
Db   415 GKQFTTLDRDKDMYAGNCAHFHKGGWWYNACAHSNLNGVWYRGGHYRSKHQDGIFWAEYR 474

Qy   473 GGSYSLKKVVMMIRP 487
          |||||:|| ||:| |
Db   475 GGSYSLRAVQMMIKP 489

RESULT 14
US-09-136-801-4
; Sequence 4, Application US/09136801
; Patent No. 6413770
; GENERAL INFORMATION:
;   APPLICANT: Godowski, Paul J.
;   APPLICANT: Gurney, Austin
;   APPLICANT: Hillan, Kenneth
;   APPLICANT: Botstein, David
;   APPLICANT: Goddard, Audrey
;   APPLICANT: Roy, Margaret
;   APPLICANT: Ferrara, Napoleone
;   APPLICANT: Tumas, Daniel
;   APPLICANT: Schwall, Ralph
;   TITLE OF INVENTION: Tie Ligand Homologues
;   NUMBER OF SEQUENCES: 35
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Genentech, Inc.
;   STREET: 1 DNA Way
;   CITY: South San Francisco

Query Match   56.1%; Score 1507.5; DB 4; Length 491;
Best Local Similarity   58.6%; Pred. No. 5e-120;
Matches 290; Conservative 69; Mismatches 109; Indels 27; Gaps 9;

Qy   9 WWLGLLAAMGAVAGQEDGFEGTEEGSPREF-----IYLNRYKRAGESQD---KCTYFIVP 61
          ::||:|| |||: ::| |:::::::|:|| ||||||:||||||| |:||:|||
Db   6 WTLGVLFFLLVDTGHCRG---------------GQFKIKKINQRRYPRATDGKEEAKKCAYTFLVP 56

Qy   62 QQRVTGAICVNSKEPEV-LLENRVHKQELELLNNELLKQKRQIETLQQLVKVDGGIVSEV 120
          :::|||:||:|||::|: ::::|:|: :|::|||||||||||||||||:|:::||:|::
Db   57 EQRITGPICVNTKGQDASTIKDMITRMDLENLKDVLSRQKREIDVLQLVVDGNIVNEV 116

Qy   121 KLLRKESRNMNSRVTQLYMQLLHEIIRKRDNALELSQLENRIILNQTADMLQLASKYKDLE 180
          ||||||||||||||||||||||||||||||||||||||||||||||||:||||||||||||
Db   117 KLLRKESRNMNSRVTQLYMQLLHEIIRKRDNSLELSQLENKILNVTTEMLKMATYRELE 176

Qy   181 HKYQHLATLAHNQSEIIAQLEEHCQRVPSARPVPQPPP---AAPPRVYQPPTYNRIINQI 237
          |||||||||||||||||||||||||||||||||||||| :|:||:||||||||||||:
Db   177 VKYASLTDLVNNQSVMTLLEEQCLRIFSRQDTHVSPPLVQVVPQHI--PNSQQYTPGLL 234

Qy   238 STNEIQSDQNL--KVLPPP-LPTMPTLT--SLPSSTDKPSGPWRDCLQALEDGHDTSSIY 292
          :|:||:|:|| ||:||| |||||||| :||||||||| |:||||||:||||::|||
Db   235 GGNEIQRDPGYPRDLMPPDLAISPTKSPFKIPPVTFINEGPFKDCQQAKEAGHSVSGIY 294

Qy   293 LVKPENTNRLMQVWCDQRHDPGGWTVIQRRLDGSVNFFRNWETYKQGFGNIDGEYWLGLE 352
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   295 MIKPENSNGPMQLWCENSLDPGGWTVIQKRTDGSVNFFRNWENYKKGFGNIDGEYWLGLE 354

Qy   353 NIYWLTNQGNYKLLVTMEDWSGRKVFAEYASFRLEPESEYYKLRLGRYHGNAGDSFTWHN 412
          |||||:|||||||||||||||||||||||||||||||||||||:||||||||||||||||
Db   355 NIYMLSNQDNYKLLIELEDWSDKKVYAEYSSFRLEPESEFYRLRLGTYQGNAGDSMWWHN 414

Qy   413 GKQFTTLDRDHDVYTGNCAHYQKGGWWYNACAHSNLNGVWYRGGHYRSRYQDGVYWAEFR 472
          ||||||||||||:||||||||||||||||||||||||||||||||||||:||||||||||
Db   415 GKQFTTLDRDKDMYAGNCAHFHKGGWWYNACAHSNLNGVWYRGGHYRSKHQDGIFWAEYR 474

Qy   473 GGSYSLKKVVMMIRP 487
          |||||:|| ||:| |
Db   475 GGSYSLRAVQMMIKP 489

STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/136,801
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Dreger, Ginger R.
REGISTRATION NUMBER: 33,055
REFERENCE/DOCKET NUMBER: P1130P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-3216
TELEFAX: 650/952-9981
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 491 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-09-136-801-4

Query Match   56.1%; Score 1507.5; DB 4; Length 491;
Best Local Similarity 58.6%; Pred. No. 5e-120;
Matches 290; Conservative 69; Mismatches 109; Indels 27; Gaps 9;

```
Qy   9 WWLGLLAAMGAVAGQEDGFEGTEEGSPREF----IYLNRYKRAGESQD---KCTYTPIVP  61
Db   6 WTLGVLFLLVDTGHCRG--------GQFKIKKINQRYRPRATDGKEBAAKCCAYTFLVP  56

Qy  62 QQRVTGAICVNSKEPEV-LLENRVHKQELELLNNELLKQRQIETLQQLVKVDGGIVSEV 120
Db  57 EQRITGPICVNTKGQDASTIKDMITRMDLENLKDVLSRQKREIDVLQLVVDVDGNIVNEV 116

Qy 121 KLLRKESRNMNSRVTQLYMQLLHEIIRKRDNALELSQLENRILNQTADMLQLASKYKDLE 180
Db 117 KLLRKESRNMNSRVTQLIYMQLLHEIIRKRDNSLELSQLENKILNVTTEMLKVATRYRELE 176

Qy 181 HKYQHLATLAHNQSEIIAQLEEHCQRVPSARPVQPQPP---AAPPRVYQPPYNRIINQI 237
Db 177 VKYASLIDLVNNQSVMITLLEEQCLRIFSRQDTHVSPFLVQVVPQHI--PNSQQYTPGLL 234

Qy 238 STNEIQSDQNL--KVLPPP-LPTMPTLT--SLPSSTDKPSGPWRDCLQALEDGHDTSSIY 292
Db 235 GGNEIQRDPGYRDLMPPPDLAITSPTKSPFKIPPVTFINEGPFKDCQQAKEAGHSVSGIY 294

Qy 293 LVKPENTNRLMQVWCDQRHDPGGWTVIQRRLDGSVNFRNWETYKQGFGNIDGEYWLGLE 352
Db 295 MIKPENSNGPMQLWCENSLDPGGWTVIQKRTDGSVNFPRNWENYKKGFGNIDGEYWLGLE 354

Qy 353 NIYWLTNQGNYKLLVTMEDWSGRKVFAEYASFRLEPESEYYKLRLGRYHGNAGDSFTWHN 412
Db 355 NIYMLSNQDNYKLLIELEDWSDKKVYAEYSSFRLEPESEFYRLRLGTIYQGNAGDSMWWHN 414

Qy 413 GKQFTTLDRDHDVYTGNCAHYQKGGWWWNACAHSNLNGVWYRGGHYRSRYQDGVYWAEFR 472
Db 415 GKQFTTLDRDKDMYAGNCAHFHKGGWWYNACAHSNLNGVWYRGGHYRSKHQDGIFWAEYR 474

Qy 473 GGSYSLKKVVMMIRP 487
Db 475 GGSYSLRAVQMMIKP 489
```

RESULT 15
US-09-332-929-4
Sequence 4, Application US/09332929
Patent No. 6420542
GENERAL INFORMATION:
APPLICANT: Godowski, Paul J.

APPLICANT: Gurney, Austin L.
TITLE OF INVENTION: Tie Ligands
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/332,929
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/933,821
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Dreger, Ginger R.
REGISTRATION NUMBER: 33,055
REFERENCE/DOCKET NUMBER: P1130
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-3216
TELEFAX: 650/952-9981
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 491 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-09-332-929-4

Query Match   56.1%; Score 1507.5; DB 4; Length 491;
Best Local Similarity 58.6%; Pred. No. 5e-120;
Matches 290; Conservative 69; Mismatches 109; Indels 27; Gaps 9;

```
Qy   9 WWLGLLAAMGAVAGQEDGFEGTEEGSPREF----IYLNRYKRAGESQD---KCTYTPIVP  61
Db   6 WTLGVLFLLVDTGHCRG--------GQFKIKKINQRYRPRATDGKEBAAKCCAYTFLVP  56

Qy  62 QQRVTGAICVNSKEPEV-LLENRVHKQELELLNNELLKQRQIETLQQLVKVDGGIVSEV 120
Db  57 EQRITGPICVNTKGQDASTIKDMITRMDLENLKDVLSRQKREIDVLQLVVDVDGNIVNEV 116

Qy 121 KLLRKESRNMNSRVTQLYMQLLHEIIRKRDNALELSQLENRILNQTADMLQLASKYKDLE 180
Db 117 KLLRKESRNMNSRVTQLIYMQLLHEIIRKRDNSLELSQLENKILNVTTEMLKVATRYRELE 176

Qy 181 HKYQHLATLAHNQSEIIAQLEEHCQRVPSARPVQPQPP---AAPPRVYQPPYNRIINQI 237
Db 177 VKYASLIDLVNNQSVMITLLEEQCLRIFSRQDTHVSPFLVQVVPQHI--PNSQQYTPGLL 234

Qy 238 STNEIQSDQNL--KVLPPP-LPTMPTLT--SLPSSTDKPSGPWRDCLQALEDGHDTSSIY 292
Db 235 GGNEIQRDPGYRDLMPPPDLAITSPTKSPFKIPPVTFINEGPFKDCQQAKEAGHSVSGIY 294

Qy 293 LVKPENTNRLMQVWCDQRHDPGGWTVIQRRLDGSVNFRNWETYKQGFGNIDGEYWLGLE 352
Db 295 MIKPENSNGPMQLWCENSLDPGGWTVIQKRTDGSVNFPRNWENYKKGFGNIDGEYWLGLE 354

Qy 353 NIYWLTNQGNYKLLVTMEDWSGRKVFAEYASFRLEPESEYYKLRLGRYHGNAGDSFTWHN 412
Db 355 NIYMLSNQDNYKLLIELEDWSDKKVYAEYSSFRLEPESEFYRLRLGTIYQGNAGDSMWWHN 414

Qy 413 GKQFTTLDRDHDVYTGNCAHYQKGGWWWNACAHSNLNGVWYRGGHYRSRYQDGVYWAEFR 472
Db 415 GKQFTTLDRDKDMYAGNCAHFHKGGWWYNACAHSNLNGVWYRGGHYRSKHQDGIFWAEYR 474

Qy 473 GGSYSLKKVVMMIRP 487
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Db |||||||:|||:|
       475 GGSYSLRAVQMMIKP 489

Search completed: July 30, 2004, 12:38:31
Job time : 21 secs

OM protein - protein search, using sw model

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                GenCore version 5.1.6
                Copyright (c) 1993 - 2004 Compugen Ltd.

Run on:         July 30, 2004, 12:37:34 ; Search time 46 Seconds
                                          (without alignments)
                                          3361.863 Million cell updates/sec

Title:          US-10-018-386-2
Perfect score:  2686
Sequence:       1 MRPLCVTCWWLGLLAAMGAV..........GSYSLKKVVMMIRPNPNTFH 493

Scoring table:  BLOSUM62
                Gapop 10.0 , Gapext 0.5

Searched:       1291235 seqs, 313682936 residues

Total number of hits satisfying chosen parameters:    1291235

Post-processing: Minimum Match 0%
Maximum Match 100%
Minimum DB seq length: 0
Maximum DB seq length: 200000000

Database :      Published Applications_AA:*
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                4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
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               18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*
                   Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2682	99.9	493	9	US-09-818-143-23	Sequence 23, Appl
2	2682	99.9	493	9	US-09-832-355A-113	Sequence 113, Appl
3	2682	99.9	493	10	US-09-983-000A-8	Sequence 8, Appli
4	2682	99.9	493	12	US-10-147-493-268	Sequence 268, App
5	2682	99.9	493	12	US-10-145-127-268	Sequence 268, App
6	2682	99.9	493	12	US-10-160-503-268	Sequence 268, App
7	2682	99.9	493	12	US-10-143-118-268	Sequence 268, App
8	2682	99.9	493	12	US-10-144-993-268	Sequence 268, App
9	2682	99.9	493	12	US-10-787-268	Sequence 268, App
10	2682	99.9	493	12	US-10-140-024-268	Sequence 268, App
11	2682	99.9	493	12	US-10-158-808-268	Sequence 268, App
12	2682	99.9	493	12	US-10-152-405-268	Sequence 268, App
13	2682	99.9	493	12	US-10-127-552A-268	Sequence 268, App
14	2682	99.9	493	12	US-10-127-900A-268	Sequence 268, App
15	2682	99.9	493	12	US-10-128-685A-268	Sequence 268, App

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16  2682  99.9  493  12  US-10-131-820A-268    Sequence 268, App
17  2682  99.9  493  12  US-10-142-886-268     Sequence 268, App
18  2682  99.9  493  12  US-10-146-728-268     Sequence 268, App
19  2682  99.9  493  12  US-10-146-786-268     Sequence 268, App
20  2682  99.9  493  12  US-10-147-499-268     Sequence 268, App
21  2682  99.9  493  12  US-10-157-798-268     Sequence 268, App
22  2682  99.9  493  13  US-10-066-500-4       Sequence 4, Appli
23  2682  99.9  493  14  US-10-028-072-268     Sequence 268, App
24  2682  99.9  493  14  US-10-121-049-268     Sequence 268, App
25  2682  99.9  493  14  US-10-123-904-268     Sequence 268, App
26  2682  99.9  493  14  US-10-140-470-268     Sequence 268, App
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31  2682  99.9  493  14  US-10-066-273-4       Sequence 4, Appli
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33  2682  99.9  493  14  US-10-137-865-268     Sequence 268, App
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35  2682  99.9  493  14  US-10-142-431-268     Sequence 268, App
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41  2682  99.9  493  14  US-10-142-419-268     Sequence 268, App
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45  2682  99.9  493  14  US-10-141-755-268     Sequence 268, App
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ALIGNMENTS

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RESULT 1
US-09-818-143-23
Sequence 23, Application US/09818143
Patent No. US2002001900A1
GENERAL INFORMATION:
; APPLICANT: Walker, Michael G.
; APPLICANT: Volkmuth, Wayne
; APPLICANT: Klingler, Tod M.
; TITLE OF INVENTION: POLYNUCLEOTIDES COEXPRESSED WITH MATRIX-REMODELING GENES
; FILE REFERENCE: PB-0004 CIP
; CURRENT APPLICATION NUMBER: US/09/818,143
; CURRENT FILING DATE: 2001-03-26
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PERL Program
; SEQ ID NO 23
; LENGTH: 493
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: -
US-09-818-143-23
; OTHER INFORMATION: 2268890CD1

Query Match             99.9%;  Score 2682;  DB 9;  Length 493;
Best Local Similarity   99.8%;
Matches  492;  Conservative    1;  Mismatches   0;  Indels   0;  Gaps   0;
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Qy     61  PQQRVTGAICVNSKEPEVLLENRVHKQELELLNNELLKQRQIETLQQLVRVDGGIVSEV   120
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Qy    121  KLLRKESRNMNSRVTQLYMQLLHEIIRKRDNALELSQLENRILNQTADMLQLASKYXDLE   180
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RESULT 2
US-09-832-355A-113
Sequence 113, Application US/0983235SA
Publication No. US20030027751A1
GENERAL INFORMATION:
APPLICANT: Kovesdi, Imre
APPLICANT: Kessler, Paul
TITLE OF INVENTION: VEGF FUSION PROTEINS
FILE REFERENCE: 205654
CURRENT APPLICATION NUMBER: US/09/832,355A
CURRENT FILING DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 126
SOFTWARE: Patentin version 3.0
SEQ ID NO 113
LENGTH: 493
TYPE: PRT
ORGANISM: Homo sapiens
US-09-832-355A-113

Query Match   99.9%;   Score 2682;   DB 10;   Length 493;
Best Local Similarity   99.8%;   Pred. No. 4.9e-210;
Matches   492;   Conservative   1;   Mismatches   0;   Indels   0;   Gaps   0;

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Qy   61  PQQRVTGAICVNSKEPEVLLENRVHKQELELLNNELLKQKRQIETLQQLVKVDGGIVSEV  120
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Db   61  PQQRVTGAICVNSKEPEVLLENRVHKQELELLNNELLKQKRQIETLQQLVEVDGGIVSEV  120

Qy  121  KLLRKESRNMNSRVTQLYMQLLHEIIRKRDNALELSQLENRILNQTADMLQLASKYKDLE  180
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Db  121  KLLRKESRNMNSRVTQLYMQLLHEIIRKRDNALELSQLENRILNQTADMLQLASKYKDLE  180

Qy  181  HKYQHLATLAHNQSEIIAQLEEHCQRVPSARPVPQPPPAAPRVYQPPTYNRIINQISTN  240
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Qy  241  EIQSDQNLKVLPPPLPTMPTLITSLPSSTDKPSGGPWRDCLQALEDGHDTSSIYLVKPENTN  300
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Db  241  EIQSDQNLKVLPPPLPTMPTLITSLPSSTDKPSGGPWRDCLQALEDGHDTSSIYLVKPENTN  300

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Qy  361  GNYKLLVTMEDWSGRKVFAEYASFRLEPESEYYKLRLGRYHGNAGDSFTWHNGKQFTTLD  420
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Db  361  GNYKLLVTMEDWSGRKVFAEYASFRLEPESEYYKLRLGRYHGNAGDSFTWHNGKQFTTLD  420

Qy  421  RDHDVYTGNCAHYQKGGWWYNACAHSNLNGVWYRGGHYRSRYQDGVYWAEFRGGSYSLKK  480
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Db  421  RDHDVYTGNCAHYQKGGWWYNACAHSNLNGVWYRGGHYRSRYQDGVYWAEFRGGSYSLKK  480

Qy  481  VVMMIRPNPNTFH  493
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Db  481  VVMMIRPNPNTFH  493
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RESULT 3
US-09-983-000A-8
Sequence 8, Application US/0998300A
Publication No. US20030118585A1
GENERAL INFORMATION:
APPLICANT: AGY Therapeutics
APPLICANT: Melcher, Thorsten
APPLICANT: Mueller, Sabine
APPLICANT: Chin, Daniel
TITLE OF INVENTION: USE OF PROTEIN BIOMOLECULAR TARGETS IN THE TREATMENT AND VISUALIZI...
TITLE OF INVENTION: OF BRAIN TUMORS
FILE REFERENCE: 263/180 -- PEagleman -- AGY
CURRENT APPLICATION NUMBER: US/09/983,000A
CURRENT FILING DATE: 2001-10-17
NUMBER OF SEQ ID NOS: 35
SOFTWARE: Patentin version 3.1
SEQ ID NO 8
LENGTH: 493
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: gene
LOCATION: (1)..(493)
OTHER INFORMATION: Angiopoietin-like 2 (ANGPTL2), protein
NAME/KEY: SIGNAL
LOCATION: (1)..(22)
OTHER INFORMATION: Potential
NAME/KEY: CHAIN
LOCATION: (23)..(493)
OTHER INFORMATION: Angiopoietin-related protein 2
NAME/KEY: DOMAIN
LOCATION: (76)..(115)
OTHER INFORMATION: Coiled Coil (potential)
NAME/KEY: DOMAIN
LOCATION: (152)..(206)
OTHER INFORMATION: Coiled Coil (potential)
NAME/KEY: DOMAIN
LOCATION: (438)..(450)
OTHER INFORMATION: Fibrinogen C-terminal
NAME/KEY: CARBOHYD
LOCATION: (164)..(164)
OTHER INFORMATION: N-linked (GLCNAC...) (potential)
NAME/KEY: CARBOHYD
LOCATION: (192)..(192)
OTHER INFORMATION: N-linked (GLCNAC...) (potential)
US-09-983-000A-8

Query Match   99.9%;   Score 2682;   DB 10;   Length 493;
Best Local Similarity   99.8%;   Pred. No. 4.9e-210;
Matches   492;   Conservative   1;   Mismatches   0;   Indels   0;   Gaps   0;

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Qy   61  PQQRVTGAICVNSKEPEVLLENRVHKQELELLNNELLKQKRQIETLQQLVKVDGGIVSEV  120
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Db   61  PQQRVTGAICVNSKEPEVLLENRVHKQELELLNNELLKQKRQIETLQQLVEVDGGIVSEV  120

Qy  121  KLLRKESRNMNSRVTQLYMQLLHEIIRKRDNALELSQLENRILNQTADMLQLASKYKDLE  180
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Qy  421  RDHDVYTGNCAHYQKGGWWYNACAHSNLNGVWYRGGHYRSRYQDGVYWAEFRGGSYSLKK  480
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Qy  481  VVMMIRPNPNTFH  493
Db  481  VVMMIRPNPNTFH  493
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RESULT 4

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US-10-147-493-268
; Sequence 268, Application US/10147493
; Publication No. US20040029217A1
; GENERAL INFORMATION:
; APPLICANT: Baker,Kevin P.
; APPLICANT: Beresini,Maureen
; APPLICANT: DeForge,Laura
; APPLICANT: Desnoyers,Luc
; APPLICANT: Filvaroff,Ellen
; APPLICANT: Gao,Wei-Qiang
; APPLICANT: Gerritsen,Mary E.
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Gurney,Austin L.
; APPLICANT: Sherwood,Steven
; APPLICANT: Smith,Victoria
; APPLICANT: Stewart,Timothy A.
; APPLICANT: Tumas,Daniel
; APPLICANT: Watanabe,Colin K
; APPLICANT: Wood,William
; APPLICANT: Zhang,Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330R1C345
; CURRENT APPLICATION NUMBER: US/10/147,493
; CURRENT FILING DATE: 2002-05-17
; PRIOR APPLICATION removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NO: 550
; SEQ ID NO 268
; LENGTH: 493
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-147-493-268

  Query Match             99.9%;  Score 2682;  DB 12;  Length 493;
  Best Local Similarity   99.8%;  Pred. No. 4.9e-210;
  Matches   492;  Conservative    1;  Mismatches   0;  Indels   0;  Gaps   0;

Qy    1 MRPLCVTCWWLGLLAAMGAVAGQEDGFEGTEEGSPREFIYLNRYKRAGESQDKCTYTFIV 60
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Db    1 MRPLCVTCWWLGLLAAMGAVAGQEDGFEGTEEGSPREFIYLNRYKRAGESQDKCTYTFIV 60

Qy   61 PQQRVTGAICVNSKEPEVLLENRVHKQELELLNNELLKQKRQIETLQQLVEUDGGIVSEV 120
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Db   61 PQQRVTGAICVNSKEPEVLLENRVHKQELELLNNELLKQKRQIETLQQLVEUDGGIVSEV 120

Qy  121 KLLRKESRNMNSRVTQLYMQLLHEIIRKRDNALELSQLENRILNQTADMLQLASKYKDLE 180
Db  121 KLLRKESRNMNSRVTQLYMQLLHEIIRKRDNALELSQLENRILNQTADMLQLASKYKDLE 180

Qy  181 HKYQHLATLAINQSEIIAQLEEHCQRVPSARPVPQPPPAAPPRVYQPPTYNRIINQISTN 240
Db  181 HKYQHLATLAINQSEIIAQLEEHCQRVPSARPVPQPPPAAPPRVYQPPTYNRIINQISTN 240

Qy  241 EIQSDQNLKVLPPLPTMPLTLSLPSSTDKPSGPWRDCLQALEDGHDTSSIYLVKPENTN 300
Db  241 EIQSDQNLKVLPPLPTMPLTLSLPSSTDKPSGPWRDCLQALEDGHDTSSIYLVKPENTN 300

Qy  301 RLMQVWCDQRHDPGGWTVIQRRLDGSVNFFRNWETYKQGFGNIDGEYWLGLENIYWLTNQ 360
Db  301 RLMQVWCDQRHDPGGWTVIQRRLDGSVNFFRNWETYKQGFGNIDGEYWLGLENIYWLTNQ 360

Qy  361 GNYKLLVTMEDWSGRKVFAEYASFRLEPESEYYKLRLGRYHGNAGDSFTWHNGKQFTTLD 420
Db  361 GNYKLLVTMEDWSGRKVFAEYASFRLEPESEYYKLRLGRYHGNAGDSFTWHNGKQFTTLD 420

Qy  421 RDHDVYTGNCAHYQKGGWWYNACAHSNLNGVWYRGGHYRSRYQDGVYWAEFRGGSYSLKK 480
Db  421 RDHDVYTGNCAHYQKGGWWYNACAHSNLNGVWYRGGHYRSRYQDGVYWAEFRGGSYSLKK 480

Qy  481 VVMMIRPNPNTFH 493
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RESULT 5

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US-10-145-127-268
; Sequence 268, Application US/10145127
; Publication No. US20040033558A1
; GENERAL INFORMATION:
; APPLICANT: Baker,Kevin P.
; APPLICANT: Beresini,Maureen
; APPLICANT: DeForge,Laura
; APPLICANT: Desnoyers,Luc
; APPLICANT: Filvaroff,Ellen
; APPLICANT: Gao,Wei-Qiang
; APPLICANT: Gerritsen,Mary E.
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Gurney,Austin L.
; APPLICANT: Sherwood,Steven
; APPLICANT: Smith,Victoria
; APPLICANT: Stewart,Timothy A.
; APPLICANT: Tumas,Daniel
; APPLICANT: Watanabe,Colin K
; APPLICANT: Wood,William
; APPLICANT: Zhang,Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330R1C252
; CURRENT APPLICATION NUMBER: US/10/145,127
; CURRENT FILING DATE: 2002-05-13
; PRIOR APPLICATION removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NO: 550
; SEQ ID NO 268
; LENGTH: 493
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-145-127-268

  Query Match             99.9%;  Score 2682;  DB 12;  Length 493;
  Best Local Similarity   99.8%;  Pred. No. 4.9e-210;
  Matches   492;  Conservative    1;  Mismatches   0;  Indels   0;  Gaps   0;

Qy    1 MRPLCVTCWWLGLLAAMGAVAGQEDGFEGTEEGSPREFIYLNRYKRAGESQDKCTYTFIV 60
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Db    1 MRPLCVTCWWLGLLAAMGAVAGQEDGFEGTEEGSPREFIYLNRYKRAGESQDKCTYTFIV 60

Qy  121 KLLRKESRNMNSRVTQLYMQLLHEIIRKRDNALELSQLENRILNQTADMLQLASKYKDLE 180
Db  121 KLLRKESRNMNSRVTQLYMQLLHEIIRKRDNALELSQLENRILNQTADMLQLASKYKDLE 180

Qy  181 HKYQHLATLAINQSEIIAQLEEHCQRVPSARPVPQPPPAAPPRVYQPPTYNRIINQISTN 240
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Qy  241 EIQSDQNLKVLPPLPTMPLTLSLPSSTDKPSGPWRDCLQALEDGHDTSSIYLVKPENTN 300
Db  241 EIQSDQNLKVLPPLPTMPLTLSLPSSTDKPSGPWRDCLQALEDGHDTSSIYLVKPENTN 300

Qy  301 RLMQVWCDQRHDPGGWTVIQRRLDGSVNFFRNWETYKQGFGNIDGEYWLGLENIYWLTNQ 360
Db  301 RLMQVWCDQRHDPGGWTVIQRRLDGSVNFFRNWETYKQGFGNIDGEYWLGLENIYWLTNQ 360

Qy  361 GNYKLLVTMEDWSGRKVFAEYASFRLEPESEYYKLRLGRYHGNAGDSFTWHNGKQFTTLD 420
Db  361 GNYKLLVTMEDWSGRKVFAEYASFRLEPESEYYKLRLGRYHGNAGDSFTWHNGKQFTTLD 420

Qy  421 RDHDVYTGNCAHYQKGGWWYNACAHSNLNGVWYRGGHYRSRYQDGVYWAEFRGGSYSLKK 480
Db  421 RDHDVYTGNCAHYQKGGWWYNACAHSNLNGVWYRGGHYRSRYQDGVYWAEFRGGSYSLKK 480

Qy  481 VVMMIRPNPNTFH 493
Db  481 VVMMIRPNPNTFH 493
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RESULT 6
US-10-160-503-268
; Sequence 268, Application US/10160503
; Publication No. US20040033559A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330R1C446
; CURRENT APPLICATION NUMBER: US/10/160,503
; CURRENT FILING DATE: 2002-05-30
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 268
; LENGTH: 493
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-160-503-268

Query Match   99.9%;
Best Local Similarity 99.8%;
Matches 492; Conservative   1; Mismatches   0; Indels   0; Gaps   0;
Score 2682; DB 12; Length 493; Pred. No. 4.9e-210;

```
Qy    1  MRPLCVTCWMLGLLAAMGAVAGQOEDGFEGGTEEGSPREFIYLNRYKRAGESQDKCTYTFIV   60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1  MRPLCVTCWMLGLLAAMGAVAGQOEDGFEGGTEEGSPREFIYLNRYKRAGESQDKCTYTFIV   60

Qy   61  PQQRVTGAICVNSKEPEVLLENRVHKQELELLNNELLKQKRQIETLQQLVKVDGGIVSEV  120
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61  PQQRVTGAICVNSKEPEVLLENRVHKQELELLNNELLKQKRQIETLQQLVKVDGGIVSEV  120

Qy  121  KLLRKESRNMNSRVTQLYMQLLHEIIRKDNALELSQLENRILNQTADMLQLASKYKDLE  180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121  KLLRKESRNMNSRVTQLYMQLLHEIIRKDNALELSQLENRILNQTADMLQLASKYKDLE  180

Qy  181  HKYQHLATLAHNQSEIIAQLEEHCQRVPSARPVPQPPPAAPPRVYQPPTYNRIINQISTN  240
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181  HKYQHLATLAHNQSEIIAQLEEHCQRVPSARPVPQPPPAAPPRVYQPPTYNRIINQISTN  240

Qy  241  EIQSDQNLKVLPPPLPTMPTLTTSLPSSTDKPSGPWRDCLQALEDGHDTSSIYLVKPENTN  300
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241  EIQSDQNLKVLPPPLPTMPTLTTSLPSSTDKPSGPWRDCLQALEDGHDTSSIYLVKPENTN  300

Qy  301  RLMQVWCDQRHDPGGWTVIQRRLDGSVNFRNWETYKQGFGNIDGEYWLGLENIYWLTNQ  360
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  301  RLMQVWCDQRHDPGGWTVIQRRLDGSVNFRNWETYKQGFGNIDGEYWLGLENIYWLTNQ  360

Qy  361  GNYKLLVTMEDWSGRKVFAEYASFRLEPESEYYKLRLGRYHGNAGDSFTWHNGKQFTTLD  420
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  361  GNYKLLVTMEDWSGRKVFAEYASFRLEPESEYYKLRLGRYHGNAGDSFTWHNGKQFTTLD  420

Qy  421  RDHDVYTGNCAHYQKGGWWYNACAHSNLNGVWYRGGHYRSRYQDGVYWAEFRGGSYSLKK  480
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  421  RDHDVYTGNCAHYQKGGWWYNACAHSNLNGVWYRGGHYRSRYQDGVYWAEFRGGSYSLKK  480

Qy  481  VVMMIRPNPNTFH  493
         |||||||||||||
Db  481  VVMMIRPNPNTFH  493
```

RESULT 7
US-10-143-118-268
; Sequence 268, Application US/10143118
; Publication No. US20040038335A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330R1C228
; CURRENT APPLICATION NUMBER: US/10/143,118
; CURRENT FILING DATE: 2002-05-09
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 268
; LENGTH: 493
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-143-118-268

Query Match   99.9%;
Best Local Similarity 99.8%;
Matches 492; Conservative   1; Mismatches   0; Indels   0; Gaps   0;
Score 2682; DB 12; Length 493; Pred. No. 4.9e-210;

```
Db    1  MRPLCVTCWMLGLLAAMGAVAGQOEDGFEGGTEEGSPREFIYLNRYKRAGESQDKCTYTFIV   60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   61  PQQRVTGAICVNSKEPEVLLENRVHKQELELLNNELLKQKRQIETLQQLVKVDGGIVSEV  120
Db   61  PQQRVTGAICVNSKEPEVLLENRVHKQELELLNNELLKQKRQIETLQQLVKVDGGIVSEV  120

Qy  121  KLLRKESRNMNSRVTQLYMQLLHEIIRKDNALELSQLENRILNQTADMLQLASKYKDLE  180
Db  121  KLLRKESRNMNSRVTQLYMQLLHEIIRKDNALELSQLENRILNQTADMLQLASKYKDLE  180

Qy  181  HKYQHLATLAHNQSEIIAQLEEHCQRVPSARPVPQPPPAAPPRVYQPPTYNRIINQISTN  240
Db  181  HKYQHLATLAHNQSEIIAQLEEHCQRVPSARPVPQPPPAAPPRVYQPPTYNRIINQISTN  240

Qy  241  EIQSDQNLKVLPPPLPTMPTLTTSLPSSTDKPSGPWRDCLQALEDGHDTSSIYLVKPENTN  300
Db  241  EIQSDQNLKVLPPPLPTMPTLTTSLPSSTDKPSGPWRDCLQALEDGHDTSSIYLVKPENTN  300

Qy  301  RLMQVWCDQRHDPGGWTVIQRRLDGSVNFRNWETYKQGFGNIDGEYWLGLENIYWLTNQ  360
Db  301  RLMQVWCDQRHDPGGWTVIQRRLDGSVNFRNWETYKQGFGNIDGEYWLGLENIYWLTNQ  360

Qy  361  GNYKLLVTMEDWSGRKVFAEYASFRLEPESEYYKLRLGRYHGNAGDSFTWHNGKQFTTLD  420
Db  361  GNYKLLVTMEDWSGRKVFAEYASFRLEPESEYYKLRLGRYHGNAGDSFTWHNGKQFTTLD  420

Qy  421  RDHDVYTGNCAHYQKGGWWYNACAHSNLNGVWYRGGHYRSRYQDGVYWAEFRGGSYSLKK  480
Db  421  RDHDVYTGNCAHYQKGGWWYNACAHSNLNGVWYRGGHYRSRYQDGVYWAEFRGGSYSLKK  480

Qy  481  VVMMIRPNPNTFH  493
Db  481  VVMMIRPNPNTFH  493
```

RESULT 8

US-10-144-993-268

Sequence 268, Application US/10144993

Publication No. US20040038336A1

GENERAL INFORMATION:

```
Qy     1 MRPLCVTCWWLGLLAAMGAVAGQEDGFEGTEEGSSPREFIYLNRYKRAGESQDKCTYTFIV 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1 MRPLCVTCWWLGLLAAMGAVAGQEDGFEGTEEGSSPREFIYLNRYKRAGESQDKCTYTFIV 60

Qy    61 PQQRVTGAICVNSKEPEVLLENRVHKQELELLNNELLKQKRQIETLQQLVKVDGGIVSEV 120
          |||||||||||||||||||||||||||||||||||||||||||||||:|||||||||
Db    61 PQQRVTGAICVNSKEPEVLLENRVHKQELELLNNELLKQKRQIETLQQLVEVDGGIVSEV 120

Qy   121 KLLRKESRNMNSRVTQLYMQLLHEIIRKRDNALELSQLENRIINQTADMLQLASKYXDLE 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 KLLRKESRNMNSRVTQLYMQLLHEIIRKRDNALELSQLENRIINQTADMLQLASKYXDLE 180

Qy   181 HKYQHLATLAHNQSEIIAQLEEHCQRVPSARPVPQPPPAAPPRVYQPPTYNRIINQISTN 240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 HKYQHLATLAHNQSEIIAQLEEHCQRVPSARPVPQPPPAAPPRVYQPPTYNRIINQISTN 240

Qy   241 EIQSDQNLKVLPPFLPTMPTLITSLPSSTDKPSGPWRDCLQALEDGHDTSSIYLVKPENTN 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 EIQSDQNLKVLPPFLPTMPTLITSLPSSTDKPSGPWRDCLQALEDGHDTSSIYLVKPENTN 300

Qy   301 RLMQVWCDQRHDPGGWTVIQRRLDGSVNFRNWETYKQGFGNIDGEYWLGLENIYWLTNQ 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 RLMQVWCDQRHDPGGWTVIQRRLDGSVNFRNWETYKQGFGNIDGEYWLGLENIYWLTNQ 360

Qy   361 GNYKLLVTMEDWSGRKVFAEYASFRLEPESEYYKLRLGRYHGNAGDSFTWHNGKQFTTLD 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 GNYKLLVTMEDWSGRKVFAEYASFRLEPESEYYKLRLGRYHGNAGDSFTWHNGKQFTTLD 420

Qy   421 RDHDVYTGNCAHYQKGGWWYNACAHSNLNGVWYRGGHYRSRYQDGVYWAEFRGGSYSLKK 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 RDHDVYTGNCAHYQKGGWWYNACAHSNLNGVWYRGGHYRSRYQDGVYWAEFRGGSYSLKK 480

Qy   481 VVMMIRPNPNTFH 493
          |||||||||||||
Db   481 VVMMIRPNPNTFH 493
```

APPLICANT: Baker,Kevin P.
APPLICANT: Beresini,Maureen
APPLICANT: DeForge,Laura
APPLICANT: Desnoyers,Luc
APPLICANT: Filvaroff,Ellen
APPLICANT: Gao,Wei-Qiang
APPLICANT: Gerritsen,Mary E.
APPLICANT: Goddard,Audrey
APPLICANT: Godowski,Paul J.
APPLICANT: Gurney,Austin L.
APPLICANT: Sherwood,Steven
APPLICANT: Smith,Victoria
APPLICANT: Stewart,Timothy A.
APPLICANT: Tumas,Daniel
APPLICANT: Watanabe,Colin K
APPLICANT: Wood,William
APPLICANT: Zhang,Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C261
CURRENT APPLICATION NUMBER: US20040038336A1
CURRENT FILING DATE: 2002-05-13
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 268
LENGTH: 493
TYPE: PRT
ORGANISM: Homo Sapien
US-10-144-993-268

RESULT 9

US-10-158-787-268

Sequence 268, Application US/10158787

Publication No. US20040039164A1

GENERAL INFORMATION:

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Query Match   99.9%; Score 2682; DB 12; Length 493;
Best Local Similarity   99.8%; Pred. No. 4.9e-210;
Matches 492; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy     1 MRPLCVTCWWLGLLAAMGAVAGQEDGFEGTEEGSSPREFIYLNRYKRAGESQDKCTYTFIV 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1 MRPLCVTCWWLGLLAAMGAVAGQEDGFEGTEEGSSPREFIYLNRYKRAGESQDKCTYTFIV 60

Qy    61 PQQRVTGAICVNSKEPEVLLENRVHKQELELLNNELLKQKRQIETLQQLVKVDGGIVSEV 120
          |||||||||||||||||||||||||||||||||||||||||||||||:|||||||||
Db    61 PQQRVTGAICVNSKEPEVLLENRVHKQELELLNNELLKQKRQIETLQQLVEVDGGIVSEV 120

Qy   121 KLLRKESRNMNSRVTQLYMQLLHEIIRKRDNALELSQLENRIINQTADMLQLASKYXDLE 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 KLLRKESRNMNSRVTQLYMQLLHEIIRKRDNALELSQLENRIINQTADMLQLASKYXDLE 180

Qy   181 HKYQHLATLAHNQSEIIAQLEEHCQRVPSARPVPQPPPAAPPRVYQPPTYNRIINQISTN 240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 HKYQHLATLAHNQSEIIAQLEEHCQRVPSARPVPQPPPAAPPRVYQPPTYNRIINQISTN 240

Qy   241 EIQSDQNLKVLPPFLPTMPTLITSLPSSTDKPSGPWRDCLQALEDGHDTSSIYLVKPENTN 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 EIQSDQNLKVLPPFLPTMPTLITSLPSSTDKPSGPWRDCLQALEDGHDTSSIYLVKPENTN 300

Qy   301 RLMQVWCDQRHDPGGWTVIQRRLDGSVNFRNWETYKQGFGNIDGEYWLGLENIYWLTNQ 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 RLMQVWCDQRHDPGGWTVIQRRLDGSVNFRNWETYKQGFGNIDGEYWLGLENIYWLTNQ 360

Qy   361 GNYKLLVTMEDWSGRKVFAEYASFRLEPESEYYKLRLGRYHGNAGDSFTWHNGKQFTTLD 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 GNYKLLVTMEDWSGRKVFAEYASFRLEPESEYYKLRLGRYHGNAGDSFTWHNGKQFTTLD 420

Qy   421 RDHDVYTGNCAHYQKGGWWYNACAHSNLNGVWYRGGHYRSRYQDGVYWAEFRGGSYSLKK 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 RDHDVYTGNCAHYQKGGWWYNACAHSNLNGVWYRGGHYRSRYQDGVYWAEFRGGSYSLKK 480

Qy   481 VVMMIRPNPNTFH 493
          |||||||||||||
Db   481 VVMMIRPNPNTFH 493
```

APPLICANT: Baker,Kevin P.
APPLICANT: Beresini,Maureen
APPLICANT: DeForge,Laura
APPLICANT: Desnoyers,Luc
APPLICANT: Filvaroff,Ellen
APPLICANT: Gao,Wei-Qiang
APPLICANT: Gerritsen,Mary E.
APPLICANT: Goddard,Audrey
APPLICANT: Godowski,Paul J.
APPLICANT: Gurney,Austin L.
APPLICANT: Sherwood,Steven
APPLICANT: Smith,Victoria
APPLICANT: Stewart,Timothy A.
APPLICANT: Tumas,Daniel
APPLICANT: Watanabe,Colin K
APPLICANT: Wood,William
APPLICANT: Zhang,Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C449
CURRENT APPLICATION NUMBER: US/10/158,787
CURRENT FILING DATE: 2003-04-03
PRIOR APPLICATION NUMBER: 60/049911
PRIOR APPLICATION NUMBER: 60/049911
PRIOR FILING DATE: 1997-06-18
PRIOR FILING DATE: 1997-06-18
PRIOR APPLICATION NUMBER: 60/056974
PRIOR FILING DATE: 1997-08-26
PRIOR APPLICATION NUMBER: 60/059913

Left column

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; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 268
; LENGTH: 493
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-158-787-268

Query Match       99.9%;  Score 2682;  DB 12;  Length 493;
Best Local Similarity 99.8%;  Pred. No. 4.9e-210;
Matches 492;  Conservative 1;  Mismatches 0;  Indels 0;  Gaps 0;

Qy    1 MRPLCVTCWWLGLLAAMGAVAVAGQEDGFEGTEEGSPREFIYLNRYKRAGESQDKCTYTFIV 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 MRPLCVTCWWLGLLAAMGAVAVAGQEDGFEGTEEGSPREFIYLNRYKRAGESQDKCTYTFIV 60

Qy   61 PQQRVTGAICVNSKEPEVLLENRVHKQELELLNNELLKQKRQIETLQQLVKVDGGIVSEV 120
        |||||||||||||||||||||||||||||||||||||||||||||||::||||||||||
Db   61 PQQRVTGAICVNSKEPEVLLENRVHKQELELLNNELLKQKRQIETLQQLVEVDGGIVSEV 120

Qy  121 KLLRKESRNMNSRVTQLYMQLLHEIIRKRDNALELSQLENRILNQTADMLQLASKYKDLE 180
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 KLLRKESRNMNSRVTQLYMQLLHEIIRKRDNALELSQLENRILNQTADMLQLASKYKDLE 180

Qy  181 HKYQHLATLAHNQSEIIAQLEEHCQRVPSARPVPQPPPAAPRRVYQPPTYNRIINQISTN 240
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 HKYQHLATLAHNQSEIIAQLEEHCQRVPSARPVPQPPPAAPRRVYQPPTYNRIINQISTN 240

Qy  241 EIQSDQNLKVLPPPLPTMPTLITSLPSSTDKPSGPWRDCLQALEDGHDTSSIYLVKPENTN 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241 EIQSDQNLKVLPPPLPTMPTLITSLPSSTDKPSGPWRDCLQALEDGHDTSSIYLVKPENTN 300

Qy  301 RLMQVWCDQRHDPGGWTVIQRRLDGSVNFRNWETYKQGFGNIDGEYWLGLENIYWLTNQ 360
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  301 RLMQVWCDQRHDPGGWTVIQRRLDGSVNFRNWETYKQGFGNIDGEYWLGLENIYWLTNQ 360

Qy  361 GNYKLLVTMEDWSGRKVFAEYASFRLEPESEYYKLRLGRYHGNAGDSFTWHNGKQFTTLD 420
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  361 GNYKLLVTMEDWSGRKVFAEYASFRLEPESEYYKLRLGRYHGNAGDSFTWHNGKQFTTLD 420

Qy  421 RDHDVYTGNCAHYQKGGWWYNACAHSNLNGVWYRGGHYRSRYQDGVYWAEFRGGSYSLKK 480
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  421 RDHDVYTGNCAHYQKGGWWYNACAHSNLNGVWYRGGHYRSRYQDGVYWAEFRGGSYSLKK 480

Qy  481 VVMMIRPNPNTFH 493
        |||||||||||||
Db  481 VVMMIRPNPNTFH 493
```

```
RESULT 10
US-10-140-024-268
Sequence 268, Application US/10140024
; Publication No. US20040058424A1
; GENERAL INFORMATION:
; APPLICANT: Baker,Kevin P.
; APPLICANT: Beresini,Maureen
; APPLICANT: DeForge,Laura
; APPLICANT: Desnoyers,Luc
```

Right column

```
; APPLICANT: Filvaroff,Ellen
; APPLICANT: Gao,Wei-Qiang
; APPLICANT: Gerritsen,Mary E.
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Gurney,Austin L.
; APPLICANT: Sherwood,Steven
; APPLICANT: Smith,Victoria
; APPLICANT: Stewart,Timothy A.
; APPLICANT: Tumas,Daniel
; APPLICANT: Watanabe,Colin K
; APPLICANT: Wood,William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330R1C69
; CURRENT APPLICATION NUMBER: US/10/140,024
; CURRENT FILING DATE: 2002-05-06
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 268
; LENGTH: 493
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-140-024-268

Query Match       99.9%;  Score 2682;  DB 12;  Length 493;
Best Local Similarity 99.8%;  Pred. No. 4.9e-210;
Matches 492;  Conservative 1;  Mismatches 0;  Indels 0;  Gaps 0;

Qy    1 MRPLCVTCWWLGLLAAMGAVAVAGQEDGFEGTEEGSPREFIYLNRYKRAGESQDKCTYTFIV 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 MRPLCVTCWWLGLLAAMGAVAVAGQEDGFEGTEEGSPREFIYLNRYKRAGESQDKCTYTFIV 60

Qy   61 PQQRVTGAICVNSKEPEVLLENRVHKQELELLNNELLKQKRQIETLQQLVKVDGGIVSEV 120
        |||||||||||||||||||||||||||||||||||||||||||||||::||||||||||
Db   61 PQQRVTGAICVNSKEPEVLLENRVHKQELELLNNELLKQKRQIETLQQLVEVDGGIVSEV 120

Qy  121 KLLRKESRNMNSRVTQLYMQLLHEIIRKRDNALELSQLENRILNQTADMLQLASKYKDLE 180
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 KLLRKESRNMNSRVTQLYMQLLHEIIRKRDNALELSQLENRILNQTADMLQLASKYKDLE 180

Qy  181 HKYQHLATLAHNQSEIIAQLEEHCQRVPSARPVPQPPPAAPRRVYQPPTYNRIINQISTN 240
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 HKYQHLATLAHNQSEIIAQLEEHCQRVPSARPVPQPPPAAPRRVYQPPTYNRIINQISTN 240

Qy  241 EIQSDQNLKVLPPPLPTMPTLITSLPSSTDKPSGPWRDCLQALEDGHDTSSIYLVKPENTN 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241 EIQSDQNLKVLPPPLPTMPTLITSLPSSTDKPSGPWRDCLQALEDGHDTSSIYLVKPENTN 300

Qy  301 RLMQVWCDQRHDPGGWTVIQRRLDGSVNFRNWETYKQGFGNIDGEYWLGLENIYWLTNQ 360
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  301 RLMQVWCDQRHDPGGWTVIQRRLDGSVNFRNWETYKQGFGNIDGEYWLGLENIYWLTNQ 360

Qy  361 GNYKLLVTMEDWSGRKVFAEYASFRLEPESEYYKLRLGRYHGNAGDSFTWHNGKQFTTLD 420
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  361 GNYKLLVTMEDWSGRKVFAEYASFRLEPESEYYKLRLGRYHGNAGDSFTWHNGKQFTTLD 420

Qy  421 RDHDVYTGNCAHYQKGGWWYNACAHSNLNGVWYRGGHYRSRYQDGVYWAEFRGGSYSLKK 480
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  421 RDHDVYTGNCAHYQKGGWWYNACAHSNLNGVWYRGGHYRSRYQDGVYWAEFRGGSYSLKK 480

Qy  481 VVMMIRPNPNTFH 493
        |||||||||||||
Db  481 VVMMIRPNPNTFH 493
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RESULT 11
US-10-140-808-268
Sequence 268, Application US/10140808
; Publication No. US20030017563A1
; GENERAL INFORMATION:
; APPLICANT: Baker,Kevin P.
```

APPLICANT: Beresini,Maureen
APPLICANT: DeForge,Laura
APPLICANT: Desnoyers,Luc
APPLICANT: Filvaroff,Ellen
APPLICANT: Gao,Wei-Qiang
APPLICANT: Gerritsen,Mary E.
APPLICANT: Goddard,Audrey
APPLICANT: Godowski,Paul J.
APPLICANT: Gurney,Austin L.
APPLICANT: Sherwood,Steven
APPLICANT: Smith,Victoria
APPLICANT: Stewart,Timothy A.
APPLICANT: Tumas,Daniel
APPLICANT: Watanabe,Colin K
APPLICANT: Wood,William
APPLICANT: Zhang,Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330R1C182
; CURRENT APPLICATION NUMBER: US/10/140,808
; CURRENT FILING DATE: 2002-05-07
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 268
; LENGTH: 493
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-140-808-268

Query Match   99.9%; Score 2682; DB 12; Length 493;
Best Local Similarity 99.8%; Pred. No. 4.9e-210;
Matches 492; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Qy    1 MRPLCVTCWWLGLLAAMGAVAGQEDGFEGSTEEGSPREFIYLNRYKRAGESQDKCTYTFIV  60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 MRPLCVTCWWLGLLAAMGAVAGQEDGFEGSTEEGSPREFIYLNRYKRAGESQDKCTYTFIV  60

Qy   61 PQQRVTGAICVNSKEPEVLLENRVHKQELELLINNELLKQKRQIETLQQLVEVDGGIVSEV 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 PQQRVTGAICVNSKEPEVLLENRVHKQELELLINNELLKQKRQIETLQQLVEVDGGIVSEV 120

Qy  121 KLLRKESRNMNSRVTQLYMQLLHEIIRKDNALELSQLENRILNQTADMLQLASKYKDLE  180
          |||||||||||||||||||||:||||||||||||||||||||||||||||||||||||
Db  121 KLLRKESRNMNSRVTQLYMQLLHEIIRKDNALELSQLENRILNQTADMLQLASKYKDLE  180

Qy  181 HKYQHLATLAHNQSEIIAQLEEHCQRVPSARPVPQPPPAAPRVYQPPTYNRIINQISTN  240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 HKYQHLATLAHNQSEIIAQLEEHCQRVPSARPVPQPPPAAPRVYQPPTYNRIINQISTN  240

Qy  241 EIQSDQNLKVLPPPLPTMPTLTSLPSSTDKPSGPWRDCLQALEDGHDTSSIVLVKPENTN 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241 EIQSDQNLKVLPPPLPTMPTLTSLPSSTDKPSGPWRDCLQALEDGHDTSSIVLVKPENTN 300

Qy  301 RLMQVWCDQRHDPGGWTVIQRRLDGSVNFFRNWETYKQGFGNIDGEYWLGLENIYWLTNQ 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  301 RLMQVWCDQRHDPGGWTVIQRRLDGSVNFFRNWETYKQGFGNIDGEYWLGLENIYWLTNQ 360

Qy  361 GNYKLLVTMEDWSGRKVFAEYASFRLEPESEYYKLRLGRYHGNAGDSFTWHNGKQFTTLD 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  361 GNYKLLVTMEDWSGRKVFAEYASFRLEPESEYYKLRLGRYHGNAGDSFTWHNGKQFTTLD 420

Qy  421 RDHDVYTGNCAHYQKGGWWYNACAHSNLNGVWYRGGHYRSRYQDGVTWAEFRGGSYSLKK 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  421 RDHDVYTGNCAHYQKGGWWYNACAHSNLNGVWYRGGHYRSRYQDGVTWAEFRGGSYSLKK 480

Qy  481 VVNMIRPNPNTFH 493
          |||||||||||||
Db  481 VVNMIRPNPNTFH 493
```

; Publication No. US20030211571A1
; GENERAL INFORMATION:
APPLICANT: Baker,Kevin P.
APPLICANT: Beresini,Maureen
APPLICANT: DeForge,Laura
APPLICANT: Desnoyers,Luc
APPLICANT: Filvaroff,Ellen
APPLICANT: Gao,Wei-Qiang
APPLICANT: Gerritsen,Mary E.
APPLICANT: Goddard,Audrey
APPLICANT: Godowski,Paul J.
APPLICANT: Gurney,Austin L.
APPLICANT: Sherwood,Steven
APPLICANT: Smith,Victoria
APPLICANT: Stewart,Timothy A.
APPLICANT: Tumas,Daniel
APPLICANT: Watanabe,Colin K
APPLICANT: Wood,William
APPLICANT: Zhang,Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330R1C383
; CURRENT APPLICATION NUMBER: US/10/152,405
; CURRENT FILING DATE: 2002-05-20
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 268
; LENGTH: 493
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-152-405-268

Query Match   99.9%; Score 2682; DB 12; Length 493;
Best Local Similarity 99.8%; Pred. No. 4.9e-210;
Matches 492; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Qy    1 MRPLCVTCWWLGLLAAMGAVAGQEDGFEGSTEEGSPREFIYLNRYKRAGESQDKCTYTFIV  60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 MRPLCVTCWWLGLLAAMGAVAGQEDGFEGSTEEGSPREFIYLNRYKRAGESQDKCTYTFIV  60

Qy   61 PQQRVTGAICVNSKEPEVLLENRVHKQELELLINNELLKQKRQIETLQQLVEVDGGIVSEV 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 PQQRVTGAICVNSKEPEVLLENRVHKQELELLINNELLKQKRQIETLQQLVEVDGGIVSEV 120

Qy  121 KLLRKESRNMNSRVTQLYMQLLHEIIRKDNALELSQLENRILNQTADMLQLASKYKDLE  180
          |||||||||||||||||||||:||||||||||||||||||||||||||||||||||||
Db  121 KLLRKESRNMNSRVTQLYMQLLHEIIRKDNALELSQLENRILNQTADMLQLASKYKDLE  180

Qy  181 HKYQHLATLAHNQSEIIAQLEEHCQRVPSARPVPQPPPAAPRVYQPPTYNRIINQISTN  240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 HKYQHLATLAHNQSEIIAQLEEHCQRVPSARPVPQPPPAAPRVYQPPTYNRIINQISTN  240

Qy  241 EIQSDQNLKVLPPPLPTMPTLTSLPSSTDKPSGPWRDCLQALEDGHDTSSIVLVKPENTN 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241 EIQSDQNLKVLPPPLPTMPTLTSLPSSTDKPSGPWRDCLQALEDGHDTSSIVLVKPENTN 300

Qy  301 RLMQVWCDQRHDPGGWTVIQRRLDGSVNFFRNWETYKQGFGNIDGEYWLGLENIYWLTNQ 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  301 RLMQVWCDQRHDPGGWTVIQRRLDGSVNFFRNWETYKQGFGNIDGEYWLGLENIYWLTNQ 360

Qy  361 GNYKLLVTMEDWSGRKVFAEYASFRLEPESEYYKLRLGRYHGNAGDSFTWHNGKQFTTLD 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  361 GNYKLLVTMEDWSGRKVFAEYASFRLEPESEYYKLRLGRYHGNAGDSFTWHNGKQFTTLD 420

Qy  421 RDHDVYTGNCAHYQKGGWWYNACAHSNLNGVWYRGGHYRSRYQDGVTWAEFRGGSYSLKK 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  421 RDHDVYTGNCAHYQKGGWWYNACAHSNLNGVWYRGGHYRSRYQDGVTWAEFRGGSYSLKK 480

Qy  481 VVNMIRPNPNTFH 493
          |||||||||||||
Db  481 VVNMIRPNPNTFH 493
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RESULT 12
US-10-152-405-268
; Sequence 268, Application US/10152405

RESULT 13
US-10-127-852A-268
; Sequence 268, Application US/10127852A
; Publication No. US20030203428A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330R1C88
; CURRENT APPLICATION NUMBER: US/10/127,852A
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 268
; LENGTH: 493
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-127-852A-268

Query Match   99.9%;   Score 2682; DB 12; Length 493;
Best Local Similarity 99.8%;   Pred. No. 4.9e-210;
Matches 492;   Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy   1 MRPLCVTCWWLGLLAAMGAVAGQEDGFEGTEEGSPREFIYLNRYKRAGESQDKCTYTFIV 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 MRPLCVTCWWLGLLAAMGAVAGQEDGFEGTEEGSPREFIYLNRYKRAGESQDKCTYTFIV 60

Qy   61 PQQRVTGAICVNSKPEVLLENRVHKQELELLNNELLKQKRQIETLQQLVKVDGGIVSEV 120
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 PQQRVTGAICVNSKPEVLLENRVHKQELELLNNELLKQKRQIETLQQLVEVDGGIVSEV 120

Qy   121 KLLRKESRNMNSRVTQLYMQLLHEIIRKRDNALELSQLENRINQTADMLQLASKYKDLE 180
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 KLLRKESRNMNSRVTQLYMQLLHEIIRKRDNALELSQLENRINQTADMLQLASKYKDLE 180

Qy   181 HKYQHLATLAHNQSEIIAQLEEHCQRVPSARPVPQPPPAAPPRVYQPPTYNRIINQISTN 240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 HKYQHLATLAHNQSEIIAQLEEHCQRVPSARPVPQPPPAAPPRVYQPPTYNRIINQISTN 240

RESULT 14
US-10-127-900A-268
; Sequence 268, Application US/10127900A
; Publication No. US20030203429A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330R1C81
; CURRENT APPLICATION NUMBER: US/10/127,900A
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 268

Qy   241 EIQSDQNLKVLPPPLPTMPTLTSLPPSTDKPSGPWRDCLQALEDGHDTSSIYLVKPENTN 300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 EIQSDQNLKVLPPPLPTMPTLTSLPPSTDKPSGPWRDCLQALEDGHDTSSIYLVKPENTN 300

Qy   301 RLMQVWCDQRHDPGGWTVIQRRLDGSVNFFRNWETYKQGFGNIDGEYWLGLENIYWLTNQ 360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 RLMQVWCDQRHDPGGWTVIQRRLDGSVNFFRNWETYKQGFGNIDGEYWLGLENIYWLTNQ 360

Qy   361 GNYKLLVTMEDWSGRKVFAEYASFRLEPESEYYKLRLGRYHGNAGDSFTWHNGKQFTTLD 420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 GNYKLLVTMEDWSGRKVFAEYASFRLEPESEYYKLRLGRYHGNAGDSFTWHNGKQFTTLD 420

Qy   421 RDHDVYTGNCAHYQKGGWWYNACAHSNLNGVWYRGGHYRSRYQDGVYYWAEFRGGSYSLKK 480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 RDHDVYTGNCAHYQKGGWWYNACAHSNLNGVWYRGGHYRSRYQDGVYYWAEFRGGSYSLKK 480

Qy   481 VVMMIRPNPNTFH 493
            |||||||||||||
Db   481 VVMMIRPNPNTFH 493

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;  LENGTH: 493
;  TYPE: PRT
;  ORGANISM: Homo Sapien
US-10-127-900A-268

   Query Match      99.9%;  Score 2682;  DB 12;  Length 493;
   Best Local Similarity   99.8%;  Pred. No. 4.9e-210;
   Matches    492;  Conservative    1;  Mismatches   0;  Indels   0;  Gaps   0;

Qy     1 MRPLCVTCWWLGLLAAMGAVAGQEDGFEGTEEGSPREFIYLNRYKRAGESQDKCTYTFIV 60
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1 MRPLCVTCWWLGLLAAMGAVAGQEDGFEGTEEGSPREFIYLNRYKRAGESQDKCTYTFIV 60

Qy    61 PQQRVTGAICVNSKEPEVLLENRVHKQELELLNNELLKQKRQIETLQQLVKVDGGIVSEV 120
          |||||||||||||||||||||||||||||||||||:|||||||||||||||||||||||
Db    61 PQQRVTGAICVNSKEPEVLLENRVHKQELELLNNELLKQKRQIETLQQLVEVDGGIVSEV 120

Qy   121 KLLRKESRNMNSRVTQLYMQLLHEIIRKRDNALELSQLENRIINQTADMLQLASKYKDLE 180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 KLLRKESRNMNSRVTQLYMQLLHEIIRKRDNALELSQLENRIINQTADMLQLASKYKDLE 180

Qy   181 HKYQHLATLAINQSEIIAQLEEHCQRVPSARPVPQPPPAAPPRVYQPPTYNRIINQISTN 240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 HKYQHLATLAINQSEIIAQLEEHCQRVPSARPVPQPPPAAPPRVYQPPTYNRIINQISTN 240

Qy   241 EIQSDQNLKVLPPPLPTMPTLITSLPSSTDKPSGPWRDCLQALEDGHDTSSIYLVKPENTN 300
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 EIQSDQNLKVLPPPLPTMPTLITSLPSSTDKPSGPWRDCLQALEDGHDTSSIYLVKPENTN 300

Qy   301 RLMQVWCDQRHDPGGWTVIQRRLDGSVNFFRNWETYKQGFGNIDGEYWLGLENIYWLTNQ 360
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 RLMQVWCDQRHDPGGWTVIQRRLDGSVNFFRNWETYKQGFGNIDGEYWLGLENIYWLTNQ 360

Qy   361 GNYKLLVTMEDWSGRKVFAEYASFRLEPESEYYKLRLGRYHGNAGDSFTWHNGKQFTTLD 420
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 GNYKLLVTMEDWSGRKVFAEYASFRLEPESEYYKLRLGRYHGNAGDSFTWHNGKQFTTLD 420

Qy   421 RDHDVYTGNCAHYQKGGWWYNACAHSNLNGVWYRGGHYRSRYQDGVYWAEFRGGSYSLKK 480
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 RDHDVYTGNCAHYQKGGWWYNACAHSNLNGVWYRGGHYRSRYQDGVYWAEFRGGSYSLKK 480

Qy   481 VVMMIRNPNTFH 493
          ||||||||||||
Db   481 VVMMIRNPNTFH 493
```

```
US-10-128-685A-268

   Query Match      99.9%;  Score 2682;  DB 12;  Length 493;
   Best Local Similarity   99.8%;  Pred. No. 4.9e-210;
   Matches    492;  Conservative    1;  Mismatches   0;  Indels   0;  Gaps   0;

Qy     1 MRPLCVTCWWLGLLAAMGAVAGQEDGFEGTEEGSPREFIYLNRYKRAGESQDKCTYTFIV 60
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1 MRPLCVTCWWLGLLAAMGAVAGQEDGFEGTEEGSPREFIYLNRYKRAGESQDKCTYTFIV 60

Qy    61 PQQRVTGAICVNSKEPEVLLENRVHKQELELLNNELLKQKRQIETLQQLVKVDGGIVSEV 120
          |||||||||||||||||||||||||||||||||||:|||||||||||||||||||||||
Db    61 PQQRVTGAICVNSKEPEVLLENRVHKQELELLNNELLKQKRQIETLQQLVEVDGGIVSEV 120

Qy   121 KLLRKESRNMNSRVTQLYMQLLHEIIRKRDNALELSQLENRIINQTADMLQLASKYKDLE 180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 KLLRKESRNMNSRVTQLYMQLLHEIIRKRDNALELSQLENRIINQTADMLQLASKYKDLE 180

Qy   181 HKYQHLATLAINQSEIIAQLEEHCQRVPSARPVPQPPPAAPPRVYQPPTYNRIINQISTN 240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 HKYQHLATLAINQSEIIAQLEEHCQRVPSARPVPQPPPAAPPRVYQPPTYNRIINQISTN 240

Qy   241 EIQSDQNLKVLPPPLPTMPTLITSLPSSTDKPSGPWRDCLQALEDGHDTSSIYLVKPENTN 300
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 EIQSDQNLKVLPPPLPTMPTLITSLPSSTDKPSGPWRDCLQALEDGHDTSSIYLVKPENTN 300

Qy   301 RLMQVWCDQRHDPGGWTVIQRRLDGSVNFFRNWETYKQGFGNIDGEYWLGLENIYWLTNQ 360
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 RLMQVWCDQRHDPGGWTVIQRRLDGSVNFFRNWETYKQGFGNIDGEYWLGLENIYWLTNQ 360

Qy   361 GNYKLLVTMEDWSGRKVFAEYASFRLEPESEYYKLRLGRYHGNAGDSFTWHNGKQFTTLD 420
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 GNYKLLVTMEDWSGRKVFAEYASFRLEPESEYYKLRLGRYHGNAGDSFTWHNGKQFTTLD 420

Qy   421 RDHDVYTGNCAHYQKGGWWYNACAHSNLNGVWYRGGHYRSRYQDGVYWAEFRGGSYSLKK 480
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 RDHDVYTGNCAHYQKGGWWYNACAHSNLNGVWYRGGHYRSRYQDGVYWAEFRGGSYSLKK 480

Qy   481 VVMMIRNPNTFH 493
          ||||||||||||
Db   481 VVMMIRNPNTFH 493
```

OM protein - protein search, using sw model

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Run on: July 30, 2004, 12:32:34 ; Search time 18 Seconds

Title: US-10-018-386-2

Perfect score: 2686

Sequence: 1 MRPLCVTCWWLGLLAAMGAV..........GSYSLKKVVMMIRPNPNTFH 493

2634.579 Million cell updates/sec   (without alignments)   (with alignments)

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
PIR_78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	length	DB	ID	Description
1	533	19.8	312	2	JN0596	fibrinogen-related
2	526.5	19.6	491	1	FGHUB	fibrinogen beta ch
3	524.5	19.5	468	1	FGBOB	fibrinogen beta ch
4	520.5	19.4	866	2	D44234	fibrinogen alpha c
5	512.5	19.1	479	2	A25052	fibrinogen beta ch
6	503	18.7	463	2	A38463	fibrinogen beta ch
7	501	18.7	437	1	FGHUG	fibrinogen gamma-A
8	501	18.7	453	2	FGHUGB	fibrinogen gamma-A
9	501	18.7	453	2	A05299	fibrinogen gamma-A
10	500	18.6	328	2	A35084	fibrinogen beta ch
11	495	18.4	282	2	A32670	fibrinogen-related
12	489.5	18.2	438	2	A45445	fibrinogen gamma c
13	488	18.2	1356	2	B47172	janusin precursor,
14	484.5	18.0	326	2	S61517	ficolin-beta - pig
15	483.5	18.0	326	2	A27447	ficolin-1 precurso
16	483	18.0	432	2	A47172	cytotoxic T-lympho
17	482.5	18.0	334	2	JC5980	transforming growt
18	480.5	17.9	439	2	I37391	ficolin-A precurso
19	480.5	17.9	1353	2	JH0675	ficolin-like pr
20	479.5	17.9	432	2	I56934	restrictin precurs
21	476.5	17.7	444	2	S05313	fibrinogen alpha-I
22	465.5	17.3	441	2	A41932	fibrinogen gamma-B
23	463.5	17.3	432	1	FGLMGS	fibrinogen gamma c
24	459	17.1	437	1	FGRTGA	fibrinogen gamma-B
25	455.5	17.1	445	1	FGRTGB	fibrinogen gamma-B
26	455.5	17.0	417	2	S65944	tenascin-X - pig
27	452	16.8	860	2	I48839	tenascin-X - mouse
28	451.5	16.8	3566	1	A40701	tenascin-X precurs
29	451.5	16.8	4135	2	T42629	tenascin-X - bovin

ALIGNMENTS

RESULT 1
JN0596
fibrinogen-related protein HFREP-1 precursor - human
C;Species: Homo sapiens (man)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 21-Jul-2000
A;Accession: JN0596
R;Yamamoto, T.; Gotoh, M.; Sasaki, H.; Terada, M.; Kitajima, M.; Hirohashi, S.
Biochem. Biophys. Res. Commun. 193, 681-687, 1993
A;Title: Molecular cloning and initial characterization of a novel fibrinogen-related ge
A;Cross-references: GB:D14446; NID:g393314; PIDN:BAA03336.1; PID:g393315
A;Experimental source: liver
C;Superfamily: fibrinogen beta/gamma homology
A;Accession: JN0596
F;1-17/Domain: signal sequence #status predicted <SIG>
F;18-312/Product: fibrinogen-related protein HFREP-1 #status predicted <MAT>
F;80-305/Domain: fibrinogen beta/gamma homology <FBG>

Query Match   19.8%;   Score 533;   DB 2;   Length 312;
Best Local Similarity   39.3%;   Pred. No. 1.9e-27;
Matches 110;   Conservative 41;   Mismatches 89;   Indels 40;   Gaps 9;

```
Qy    232 RINQISTNEIQ-----SDQNLKVLPPPLPTMPTLTISLPSSSTDKPSGPWRDCLQALEDGHD 287
              ||||||     ||:|                    |:|
Db     50 KIKQLLQENEVQPLDKGDED------------------TVVDLGSKRQ----YADCSEIFNDGYK 92

Qy    288 TSSIYLVKPENINRLMQYWCDCQRHDPGGWTVIQRRLDGSVNFFRNWETYKQFGNI---D 344
              |||| :||      |:|   :|: ||||||||||||||||||||:    |:|
Db     93 LSGPYKIKPLQSPAEFSYYCDM-SDGGGWTVIQRRSDGSENFNRGWKDYENGFGNFVQKH 151

Qy    345 GEYWLGLENIYWLITNQGNYKLLVTMEDWSGRKVFAEYASFRLEPESEYYKLRLGRYHGNA 404
              ||||||||||:|| :||:||||||:||:||||:     :|::  | :::||||| :||||
Db    152 GEYWLGNKNLHFLITTQEDYTLKIDLADFEKNSRYAQYKNFKVGDEKNFYELNIGEYSGTA 211

Qy    405 GDSFT------W--HNGKQFTTLDRDHDVTGNCAHYQKGGWWYNACAHSNLNGVWY 453
              |||     :  ||     |||||||||||||:|  |:||||||| ||: |||||
Db    212 GDSLAGNFHPEVQWWASHQRMKFSTWDRDHDNYEGNCAEEDQSGWWFNRCHSANLNGVYY 271

Qy    454 RGGHYRSRYQDGVYWAAFRGGSYSLKKVVMMIRPN----PN 490
              :|: |:|||:||         || |:|||:|||||    :|
Db    272 -SGPYAKTDNGIVWYTWHGWWYSLKSVVMKIRPNDFIPN 310
```

RESULT 2
FGHUB
fibrinogen beta chain precursor [validated] - human
N;Alternate names: coagulation factor I
N;Contains: fibrinopeptide B
C;Species: Homo sapiens (man)
C;Date: 24-Apr-1984 #sequence_revision 31-Mar-1993 #text_change 08-Dec-2000

30	450.5	16.8	1810	2	A32230	tenascin precursor
31	448	16.7	4006	2	T09070	probable tenascin
32	444.5	16.5	220	2	S28170	tenascin homolog -
33	434.5	16.2	1746	1	S19694	tenascin precursor
34	423.5	15.8	2019	1	JQ1322	tenascin precursor
35	421.5	15.7	2201	2	A32160	tenascin-C - human
36	391.5	14.6	1914	2	T42635	tenascin Y precurs
37	388.5	14.5	774	2	T26827	tenascin-C - chick
38	257.5	9.6	463	2	A39832	scabrous locus (sc
39	235.5	8.8	127	2	PC2036	hypothetical prote
40	188.5	7.0	431	2	T29850	hypothetical prote
41	174	6.5	452	2	T26827	hypothetical prote
42	172.5	6.4	933	2	A31930	cytotactin - chick
43	156.5	5.8	77	2	I51647	tenascin - African
44	155	5.8	146	2	T32255	hypothetical prote
45	153	5.7	744	2	F95013	pneumococcal surfa

C;Accession: B43568; A90469; B90469; I37389; A94433; A90437; A94309; G54223; A03121; B37
R;Chung, D.W.; Harris, J.E.; Davie, E.W.
Adv. Exp. Med. Biol. 281, 39-48, 1990
A;Title: Nucleotide sequences of the three genes coding for human fibrinogen.
A;Reference number: B43568; MUID:91344740; PMID:2102623
A;Accession: B43568
A;Molecule type: DNA
A;Residues: 9-191,'P',193-491 <CHU>
R;Chung, D.W.; Que, B.G.; Rixon, M.W.; Mace Jr., M.; Davie, E.W.
Biochemistry 22, 3244-3250, 1983
A;Title: Characterization of complementary deoxyribonucleic acid and genomic deoxyribonu
A;Reference number: A90469; MUID:83283433; PMID:6668356
A;Accession: A90469
A;Molecule type: DNA
A;Residues: 1-38 <CH1>
A;Accession: B90469
A;Molecule type: mRNA
A;Residues: 9-191,'A',193-491 <CH2>
A;Cross-references: GB:00129; NID:g182429; PIDN:AAA52429.1; PID:g182430
R;Huber, P.; Dalton, J.; Courtois, G.; Laurent, M.; Assouline, Z.; Marguerie, G.
Nucleic Acids Res. 15, 1615-1625, 1987
A;Title: Characterization of the 5'-flanking region for the human fibrinogen beta gene.
A;Reference number: I37389; MUID:87146483; PMID:3029722
A;Accession: I37389
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-38 <HUB>
A;Cross-references: EMBL:X05018; NID:g31400; PIDN:CAA28674.1; PID:g31401
R;Watt, K.W.K.; Takagi, T.; Doolittle, R.F.
Biochemistry 18, 68-76, 1979
A;Title: Amino acid sequence of the beta chain of human fibrinogen.
A;Reference number: A90437; MUID:79124640; PMID:420779
A;Accession: A90437
A;Molecule type: protein
A;Residues: 31-144,'QF',147-231,'D',233-330,'E',332-491 <HEN>
A;Molecule type: protein
A;Accession: A94433
A;Contents: carbohydrate binding
A;Residues: 31-137,'QS',140-144,'QF',147-491 <HUB>
R;Blomback, B.; Hessel, B.; Hogg, D.
Thromb. Res. 8, 639-658, 1976
A;Title: Disulfide bridges in NH-2-terminal part of human fibrinogen.
A;Reference number: A94309; MUID:76225080; PMID:936108
A;Contents: disulfide bonds
A;Accession: A94309
A;Molecule type: protein
A;Residues: 31-112,'E',114-137 <KUN>
R;Kunitake, S.T.; Carilli, C.T.; Lau, K.; Protter, A.A.; Naya-Vigne, J.; Kane, J.P.
Biochemistry 33, 1988-1993, 1994
A;Title: Identification of proteins associated with apolipoprotein A-I-containing lipopr
A;Reference number: A54223; MUID:94162201; PMID:8117655
A;Accession: G54223
A;Molecule type: protein
A;Residues: 164-174 <KUN>
A;Note: identification of tryptic peptides from high-density lipoproteins
R;Henschen, A.; Lottspeich, F.; Kehl, M.; Southan, C.
Ann. N.Y. Acad. Sci. 408, 28-43, 1983
A;Title: Covalent structure of fibrinogen.
A;Reference number: A90037; MUID:83254370; PMID:6575689
A;Contents: annotation; review, disulfide bonds
R;Gardlund, B.; Hessel, B.; Marguerie, G.; Murano, G.; Blomback, B.
Eur. J. Biochem. 77, 595-610, 1977
A;Title: Primary structure of human fibrinogen. Characterization of disulfide-containing
A;Reference number: A91249; MUID:77245999; PMID:891553
A;Contents: annotation; disulfide bonds
R;Doolittle, R.F.; Takagi, T.; Watt, H.; Bouma III, H.; Cottrell, B.A.; Cassman, K.G.; G
in Regulatory Proteolytic Enzymes and Their Inhibitors, Magnusson, S.; Ottesen, M.; Fol
A;Title: The structures of fibrinogen and fibrin.
A;Reference number: A94437

A;Contents: annotation; disulfide bonds
R;Doolittle, R.F.
Annu. Rev. Biochem. 53, 195-229, 1984
A;Title: Fibrinogen and fibrin
A;Reference number: A90041; MUID:84305751; PMID:6383194
A;Contents: annotation; review, EM structure, polymerization, ligands
R;Chung, D.W.; Rixon, M.W.; Que, B.G.; Davie, E.W.
Ann. N.Y. Acad. Sci. 408, 449-456, 1983
A;Title: Cloning of fibrinogen genes and their cDNA.
A;Reference number: A90038; MUID:83254384; PMID:6575700
A;Contents: annotation
R;Kirschbaum, N.E.; Budzynski, A.Z.
J. Biol. Chem. 265, 13669-13676, 1990
A;Title: A unique proteolytic fragment of human fibrinogen containing the Aalpha COOH-te
A;Reference number: A37117; MUID:90337977; PMID:2143188
A;Contents: annotation; hementin cleavage site
A;Note: hementin, a protease from Haementeria ghilianii, the giant South American leech,
C;Comment: The conversion of fibrinogen to fibrin is triggered by thrombin, which cleave
ization sites responsible for the formation of the soft clot.
C;Comment: The soft clot is converted into the hard clot by factor XIIIa (fibrin-stabili
ger) and between alpha chains (weaker) of different monomers.
C;Comment: All fibrinogen chains are synthesized in the liver.
C;Genetics:
A;Gene: GDB;FGB
A;Cross-references: GDB:119130; OMIM:134830
A;Map position: 4q28-4q28
A;Introns: 38/3; 102/3; 164/1; 240/1; 278/1; 320/1; 415/2
C;Complex: The fibrinogen molecule is a hexamer containing two sets of alpha (see PIR:FG
ins are contained in the core. Two three-chain coiled coils emerge from this core and co
from the distal domain nodes.
C;Function:
A;Description: fibrinogen cleaved by thrombin yields monomers that are polymerized into
A;Pathway: blood coagulation
C;Superfamily: fibrinogen beta chain; fibrinogen beta/gamma homology <FDR>
C;Superfamily: fibrinogen beta chain; fibrinogen beta/gamma homology <FBG>
C;Keywords: blood coagulation; coiled coil; glycoprotein; liver; plasma; pyroglutamic ac
F;1-30/Domain: (or 4-30 or 15-30) signal sequence #status predicted <SIG>
F;31-491/Product: fibrinogen beta chain #status experimental <FGB>
F;31-44/Product: fibrinopeptide B #status experimental <APT>
F;45-491/Product: fibrin beta chain #status experimental <FGB>
F;45-47/Region: polymerization site
F;99-228/Domain: fibrinogen beta/gamma homology <FDR>
F;238-487/Domain: fibrinogen beta/gamma homology <FBG>
F;31/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status experimen
F;44-45/Cleavage site: Arg-Gly (thrombin) (to alpha-55) #status experimental
F;95/Disulfide bonds: interchain (to alpha-55) #status experimental
F;106/Disulfide bonds: interchain (to gamma-68) #status experimental
F;110/Disulfide bonds: interchain (to gamma-45) #status experimental
F;223/Disulfide bonds: interchain (to alpha-184) #status experimental
F;227/Disulfide bonds: interchain (to gamma-161) #status experimental
F;231-316,241-270,424-437/Disulfide bonds: #status experimental
F;394/Binding site: carbohydrate (Asn) (covalent) #status experimental

```
Query Match    19.6%;   Score 526.5;  DB 1;  Length 491;
Best Local Similarity  30.3%;   Pred. No. 9.2e-27;
Matches  138;  Conservative  64;  Mismatches 114;  Indels 139;  Gaps 16;

Qy     92 LNNELLKQKRQIETLQQLVKVDGGIVSEVKLLRKESRNMNSRVTQL-----YMQLLHEI 145
             |||:|  |   ||   : | |||:||    | ||
Db    112 LQEALLQQERPIRN-----SVD-------------ELNNNVEAVSQTSSSSFQYMYLLKDL 154

Qy    146 IRKRDNALE--------LSQLENRIL-----NQTADMLQLASKYKDLEHKYQHLAT 188
Db    155 WQKRQKQVKDNENVNNEYSSELEKQLYIDETVNSNIPTNLRVLRSILENLRSKIQKL-- 212

Qy    189 LAHNQSEIIAQLEEHCQRVPSARPVPQPPPAAPRVYQPPTYNRIINQISTNEIQSDQNL 248
Db    213 -----ESDVSAQM-EYC-RTPCT------------------------VSCN------- 232

Qy    249 KVLPPPLPTMPTLTISLPSSTDKPSGPWRDCLQALEDGHDTSSIYLVKPENTNRLMQVWCD 308
Db    233 ------IPVV---------------SG--KECEEIRKGGETSEMYLIQPDSSVKPYRVYCD 271

Qy    309 QRHDPGGWTVIQRRLDGSVNFFRNWETYKQGFGNI----------------DGEYWLGLENIYW 356
```

```
Qy   272 MNTENGGWTVIQNRQDGSVDFGRKDWDPYKQGFPGNVATNTDGKNYCGLPGEWLGNDKISQ 331
             |||||||:    :         |||    ||||:
Db   357 LTNQGNYKLLVTMEDWSGRKVPAFYASFRLEPESEYKIRLGRYHGNAGD------------ 406

Qy   332 LTRMGPTELLIEMEDWKGDKYKAHYGGFTVQNEANKYQISVNKYRGTAGNALMDGASQLM  391
             |  |    ||:  ||
Db   407 -----SFTWHNGKQFTTLDRDHDVYTGN--------                         

Qy   392 GENRTMTIHNGMFFSTYDRDNDGWLTSDPRKQCSKEDGGGWWYNRCHAANPNGRYYWGGQ  451
                                 :::||||    :
Db   407 -----SFTWHNGKQFTTLDRDHDVYTGN------CAHYQKGGWWYNACAHSNLNGVWYRGGH 457

Qy   458 Y------RSRYQDGVYWAEFRGGSYSLKKVVMMIRP 487
                    :||||:||||||:||||:|||||||
Db   452 YTWDMAKHGTDDGVVWMNWKGSWYSYRKMSMKIRP  486
```

RESULT 3
FGBOB
fibrinogen beta chain - bovine
N;Contains: fibrinopeptide B
C;Species: Bos primigenius taurus (cattle)
C;Date: 29-Jul-1981 #sequence_revision 29-Jul-1981 #text_change 13-Sep-1996
C;Accession: A03122; B03117; B37507; A37513; S02443
R;Blomback, B.; Doolittle, R.F.
Acta Chem. Scand. 17, 1816-1819, 1963
A;Title: The sequence of amino acids at the N-terminal end of bovine fibrinopeptides.
A;Reference number: A03117
A;Molecule type: protein
A;Residues: 1-4 <BLO>
R;Sjoquist, J.; Blomback, B.; Wallen, P.
Ark. Kemi 16, 425-436, 1960
A;Reference number: A03122
A;Accession: A03122
A;Molecule type: protein
A;Residues: 5-21 <SJO>
R;Martinelli, R.A.; Inglis, A.S.; Rubira, M.R.; Hageman, T.C.; Hurrell, J.G.R.; Leach, S
Arch. Biochem. Biophys. 192, 27-32, 1979
A;Title: Amino acid sequences of portions of the alpha and beta chains of bovine fibrino
A;Accession: A37507; MUID:79164394; PMID:434821
A;Molecule type: protein
A;Accession: B37507
A;Residues: 22-53 <MAR>
R;Chung, D.W.; Rixon, M.W.; MacGillivray, R.T.A.; Davie, E.W.
Proc. Natl. Acad. Sci. U.S.A. 78, 1466-1470, 1981
A;Title: Characterization of a cDNA clone coding for the beta chain of bovine fibrinogen
A;Reference number: A37513; MUID:81199473; PMID:6262803
A;Accession: A37513
A;Molecule type: mRNA
A;Residues: 44-468 <CHU>
R;Medved, L.V.; Platonova, T.N.; Litvinovich, S.V.; Lukinova, N.I.
FEBS Lett. 232, 56-60, 1988
A;Title: The cleavage of beta-chain in bovine fibrinogen D(H) fragment (95 kDa) leads to
A;Reference number: S02443; MUID:88211875; PMID:2966748
A;Molecule type: protein
A;Residues: 373-374 <MED>
A;Comment: Thrombin cleaves the bond between Arg-21 and Gly-22 to release fibrinopeptide
A;Comment: Fibrinogen is a hexamer containing two sets of three nonidentical chains (alp
A;Superfamily: fibrinogen beta chain; fibrinogen beta/gamma homology; fibrinogen disulfi
C;Keywords: blood coagulation; glycoprotein; plasma; pyroglutamic acid; sulfoprotein
F;76-205/Domain: fibrinogen disulfide ring homology <FBG>
F;215-464/Domain: fibrinogen beta/gamma homology <FDR>
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;6/Binding site: sulfate (Tyr) (covalent) #status experimental
F;21-22/Cleavage site: Arg-Gly (thrombin) #status experimental
F;371/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;372-373/Cleavage site: Arg-Thr (plasmin) #status experimental

Query Match   19.5%;   Score 524.5;   DB 1;   Length 468;
Best Local Similarity   30.3%;   Pred No. 1.2e-26;
Matches 134; Conservative 69; Mismatches 126; Indels 113; Gaps 12;
```

```
Qy    92 LNNELLKQKR--------QIETLQQLIVKDGGIVSEVKLLIRKESRNMMSRVTQIYMQLLHEIR 147
            :          |     ||||
Db    89 LQDTLVRQEPIRKSIEDLRNTV----------------DSVSRTSSSTFQYITILLKNMWK    133

Qy   148 KRDNALELSQLENRILNQTADMLQLASKYDLIEHKYQHLATIAHNQSEIIAQLEHCQRV    207
            :||     :|       |                                    :
Db   134 GRQNQV--QDNENVVNEYSSHLEKHQLYID-------ETVKNN----------------    167

Qy   208 PSARPVPQPPPAAPRRVYQPPTYNRIINQISTN-------EIQSDQNLKVLPPPLFTMPTL   261
                                    ||||       ::|    ::
Db   168 -------------------IPTKLRVLRSILENLRSKIQKLESDVSTQMEYCRTPCTVT-    207

Qy   262 TSLPSSTDKPSGPWRDCLQALEDGHDTSSIYLVKPENTNRLMQVWCDQRDPGGWWYNGR    321
            |: |   ||| ||  |    :||  |       |        :  ||| | ||||||
Db   208 CNIPVVSGK-------ECEKIRNEGETSEMTLIQPEDSSKPYRVVICDMKIEKGGWTVIQN  261

Qy   322 RLDGSVNFFRNWETYKQGFGNI---------DGEYWLGLENIYWLTNQGNYKLLVTM     369
            | || :||   ||:|||||||          ||:|||| :  | |  |  ||| :|
Db   262 RQDGSLDFGRKWDPYKQGFGNIATNAEGKKYCGVPGEYWLGNDRISQLTNNGPTKLLIEM   321

Qy   370 EDWSGRKVPAEYASFRLEPESEYKLRLGRYHGNAGD------------SFTWHNGKQ      415
            ||| | ||:| ||||:   ||||:|||||||||||            |||| || 
Db   322 EDWKGDKVTALYEGFTVQNEANKYQLSVSKYRGTAGNALIEGASQLVGENRTMTIHNSMF   381

Qy   416 FTTLDRDHDVY-------TGNCAHYQKGGWWYNACAHSNLNGVWYRGGHY-----RSRYQDG   465
            | | |||:| |       ||||  |||||||| | |  |  ||| | |      |||||
Db   382 FSTYDRDNDGWKTTDPRKQCSKEDGGGWWYNRCHAANPNGRYYWGGAYTWDMAKHGTDDG   441

Qy   466 VYWAEFRGGSYSLKKVVMMIRP 487
            |:|      ||| |:   ||||
Db   442 VVWMNWQGSWYSMKRMSMKIRP 463
```

RESULT 4
D44234
fibrinogen alpha chain precursor, extended splice form - human
N;Alternate names: coagulation factor I
N;Contains: fibrinopeptide A
C;Species: Homo sapiens (man)
C;Date: 10-Jun-1993 #sequence_revision 06-Sep-1996 #text_change 19-Jan-2001
C;Accession: D44234; B44234
R;Fu, Y.; Weissbach, L.; Plant, P.W.; Oddoux, C.; Cao, Y.; Liang, T.J.; Roy, S.N.; Redma
Biochemistry 31, 11968-11972, 1992
A;Title: Carboxy-terminal-extended variant of the human fibrinogen alpha subunit: a nove
A;Reference number: A44234; MUID:93090725; PMID:1457396
A;Accession: D44234
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA; DNA
A;Residues: 1-866 <FU>
A;Cross-references: GB:M58569; NID:g182406; PID:g182407
A;Note: neither the complete nucleic acid sequence nor the complete translation are show
A;Accession: B44234
A;Molecule type: mRNA; DNA
A;Residues: 605-866 <FU2>
A;Cross-references: GB:M58569; NID:g182406; PID:g182407
A;Note: sequence extracted from NCBI backbone (NCBIP:119917)
C;Comment: The alpha chain binds by 2-4 cross-links to the amino end of fibronectin.
C;Comment: The conversion of fibrinogen to fibrin is triggered by thrombin, which cleave
C;Comment: The soft clot is converted into the hard clot by factor XIIIa (fibrin-stabili
iation sites responsible for the formation of the soft clot.
ger) and between alpha chains (weaker) of different monomers.
C;Comment: All fibrinogen chains are synthesized in the liver.
C;Comment: See PIR:FGHUA for the major splice form. It is not known whether this form is
C;Genetics:
A;Gene: GDB:FGA
A;Cross-references: GDB:119129; OMIM:134820
A;Map position: 4q28-4q28
A;Introns: 18/3; 60/3; 122/1; 171/2
A;Note: the list of introns is incomplete
C;Complex: The fibrinogen molecule is a hexamer containing two sets of three nonidentica
ntained in the core. Two three-chain coiled coils emerge from this core and connect it t
distal domain nodes.
C;Function:

A;Description: fibrinogen cleaved by thrombin yields monomers that are polymerized into
A;Pathway: blood coagulation
C;Superfamily: blood coagulation
A;Superfamily: human extended splice form fibrinogen alpha chain; fibrinogen beta/gamma
C;Keywords: alternative splicing; blood coagulation; glycoprotein; liver; phosphoprotein
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-863/Product: fibrinogen alpha chain, extended splice form #status predicted <MAT>
F;20-35/Product: fibrinopeptide A #status experimental <APT>
F;36-863/Product: fibrin alpha chain, extended splice form #status predicted <FGA>
F;57-185/Domain: fibrinogen disulfide ring homology <FDR>
F;591-593/Region: cell attachment (R-G-D) motif
F;629-863/Domain: fibrinogen beta/gamma
F;22-460/Binding site: phosphate (Ser) (covalent) #status experimental
F;35-36/Cleavage site: Arg-Gly (thrombin) #status experimental
F;47/Disulfide bonds: interchain (to alpha-47) #status experimental
F;55/Disulfide bonds: interchain (to beta-95) #status experimental
F;64/Disulfide bonds: interchain (to gamma-49) #status experimental
F;68/Disulfide bonds: interchain (to beta-106) #status experimental
F;180/Disulfide bonds: interchain (to gamma-165) #status experimental
F;184/Disulfide bonds: interchain (to beta-223) #status experimental
F;288,419/Binding site: carbohydrate (Asn) (covalent) #status absent
F;322/Cross-link: isopeptide (Lys) (interchain to Gln) (interchain to Gin-41 of alpha-2-plasmin inhibitor) #
F;347,385/Cross-link: isopeptide (Gln) (interchain to Lys N6-amino of alpha) #status exp
F;461-491/Disulfide bonds: #status experimental
F;527,558,575,581,599/Cross-link: isopeptide (Lys) (interchain to Gln of alpha) #status
F;686,831/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match   19.4%; Score 520.5; DB 2; Length 866;
Best Local Similarity   43.3%; Pred. No. 4.9e-26;
Matches 104; Conservative 40; Mismatches 69; Indels 27; Gaps 7;

Qy 272 SGPWRDC--LQALEDGHDTSSIILVKPENTNRLMQVWCDQRRDPGGWTVIQRRLDGSVN 328
Db 626 SRPVRDCDDVLQTHPSG-TQSGIFNIKLPGSSKIFSVCDQETSLGGWLILQQRMDGSLN 684

Qy 329 FFRNWETYKQGFGNI----DGEYWLGLENIYWLTNQGNYKLLIVTMEDWSGRKVFAEYASF 384
Db 685 FNRTWQDYKRGFGSLNDEGEGEFWIGNDYIHLLTQRGSV-LRVELEDWAGNEAYAEY-HF 742

Qy 385 RLFPESEYYKLRLGRYHGNAGDS-----------FTWHNGKQFTTLDRDHDVYTGNCAHY 433
Db 743 RVGSEAGYALQVSSYEGTAGDALIEGSVEEGAEYTSHNNMQFSTFDRDADQWEENCAEV 802

Qy 434 QKGGWWYNACAHSNLNGIWYWYRGGHYRSR------YQDGVYWAEFRGGSYSLKKVVMMIRP 487
Db 803 YGGGWWYNNCQAANLNGIYYPGGSYDPRNNSPYEIENGVVWVSFRGADYSLRAVRMKIRP 862

RESULT 5
A25052
fibrinogen beta chain - sea lamprey (fragments)
N;Contains: fibrinopeptide B (sea lamprey)
C;Species: Petromyzon marinus (sea lamprey)
C;Date: 25-Oct-1987 #sequence revision 19-Feb-1999 #text_change 13-Aug-1999
C;Accession: A25052; A03124; B03124
R;Bohonus, V.L.; Doolittle, R.F.; Pontes, M.; Strong, D.D.
Biochemistry 25, 6512-6516, 1986
A;Title: Complementary DNA sequence of lamprey fibrinogen beta chain.
A;Reference number: A25052; MUID:87076582; PMID:3790537
A;Accession: A25052
A;Molecule type: mRNA
A;Residues: 39-479 <BCH>
R;Cottrell, B.A.; Doolittle, R.F.
Biochim. Biophys. Acta 453, 426-438, 1976
A;Title: Amino acid sequences of lamprey fibrinopeptides A and B and characterization of
A;Accession: A25052; A03124; B03124
A;Residues: 1-36 <COT1>
A;Molecule type: protein
A;Accession: B03124
A;Residues: 37-42 <COT2>
C;Superfamily: fibrinogen beta chain; fibrinogen beta/gamma homology; fibrinogen disulfi

C;Keywords: blood coagulation; glycoprotein; sulfoprotein
F;1-36/Product: fibrinopeptide B #status experimental <FPB>
F;37-479/Product: fibrin beta chain #status experimental <MAT>
F;90-219/Domain: fibrinogen disulfide ring homology <FDR>
F;229-477/Domain: fibrinogen beta/gamma homology <FBG>
F;13/Binding site: sulfate (Tyr) (covalent) #status experimental
F;27/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match   19.1%; Score 512.5; DB 2; Length 479;
Best Local Similarity   29.2%; Pred. No. 7.2e-26;
Matches 136; Conservative 64; Mismatches 138; Indels 128; Gaps 15;

Qy 67 GALCVNSKEP-PEVLLENR------VHKQELELLNNELLKQKRQIETLLQQLVKVDGGIV 117
Db 94 GVLCPTGCQCLREELLKQRDPVRYKISMLKQNLLTYFINSFDRMASDSNTLKQ------ 144

Qy 118 SEVKLLRKESRNMNSRVTQLYMQLLHEIIRKRDNALELSQLENRLINQTADMLQLASKYK 177
Db 145 -NVQTLR---RRLNSRSS------THVNAQK------EIENR------YK 172

Qy 178 DLEHKYQH-LATLAHNQSEIIAQLEEHCQRVPSARPVPQPPPAAPPRVYQPPTYNRIRQ 236
Db 173 EVKIRIESTVAGSLRSMKSVLEHLRAKMQRVEEAIKTQKELCSAPCTV------ 220

Qy 237 ISTNEIQSDQNIKVLPPPLPTMPTLTSLPPSSTDKPSGPWRDCLQALEDGHDTSSIYLVKP 296
Db 221 -----NCRV------PVVSGM------HCEDIYRNGGRTSEAYYIQP 250

Qy 297 ENTNRLMQVWCDQRHDPGGWTVIQRRLDGSVNFFRNWETYKQGFG-- 345
Db 251 DLFSEPYXVFCDMESHGGGWTVVQNRVDGSSNFARDWNTYKAEFGNIAFGNGKSICNPG 310

Qy 346 EYWLGLENIYWLTNQGNYKLLVTMEDWSGRKVFAEYASFRLFPESEYYKLRLGRYHGNAG 405
Db 311 EVWLGTKTVHQLTKQHTCQQVLFDMSDWEGSSVYAQVASFRPENEAQGYRLWVEDYSGNAG 370

Qy 406 D-------SFTWHNGKQFTTLDRDHDVY-----TGNCAHYQKGGWWYNACAHS 446
Db 371 NALLEGATQLMGDNRTMTIHNGMQFSTFDRDNDNWNPGDPTKHCSREDAGGWWYNRCHAA 430

Qy 447 NLNGIWYWYRGGHYRSRY-----QDGVYWAEFRGGSYSLKKVVMMIRP 487
Db 431 NPNGRYYWGGIYTKEQADYGIDDGVVWMNWKGSWYSMRQWAMKLRP 476

RESULT 6
A38463
fibrinogen beta chain - chicken (fragment)
C;Species: Gallus gallus (chicken)
C;Date: 31-Jul-1991 #sequence_revision 31-Jul-1991 #text_change 13-Aug-1999
C;Accession: A38463
R;Weissbach, L.; Oddoux, C.; Procyk, R.; Grieninger, G.
Biochemistry 30, 3290-3294, 1991
A;Title: The beta chain of chicken fibrinogen contains an atypical thrombin cleavage sit
A;Reference number: A38463; MUID:91182745; PMID:2009266
A;Accession: A38463
A;Status: Preliminary
A;Molecule type: mRNA
A;Residues: 1-463 <WEI>
A;Cross-references: GB:M58514; NID:g211779; PIDN:AAA48770.1; PID:g211780
C;Superfamily: fibrinogen beta chain; fibrinogen beta/gamma homology; fibrinogen disulfide ring homology; fibrinogen beta/gamma homology <FDR>
F;73-202/Domain: fibrinogen disulfide ring homology <FDR>
F;212-460/Domain: fibrinogen beta/gamma homology <FBG>

Query Match   18.7%; Score 503; DB 2; Length 463;
Best Local Similarity   29.6%; Pred. No. 2.9e-25;
Matches 128; Conservative 63; Mismatches 146; Indels 96; Gaps 11;

Qy 92 LNNELLKQKRQIETLLQQLVKVDGGIVSEVKLLRKESRNMNSRVTQLYMQLLHEIIRKRDN 151
Db 86 LQTTLLKQEXTVKPVLRDLK-----DRVAKFSDTSTTMYQYVNMIDNXLVKTQKORKDN 139

Qy 152 ALELSQLENRLINQTADMLQLASKYKDLEHKYQHLATLAHNQSEIIAQLEEHCQRVPSAR 211

RESULT 7

FGHUG

fibrinogen gamma-A chain precursor [validated] - human

N;Alternate names: coagulation factor I

C;Species: Homo sapiens (man)

C;Date: 24-Apr-1984 #sequence revision 25-Feb-1985 #text_change 08-Dec-2000

C;Accession: A90470; C94433; B93956; B92448; I37393; A40698; H54223; A03125; C37

R;Bertagnolli, M.E.; Beckerle, M.C.

A;Cross-references: EMBL:X00086; NID:g314445; PIDN:CAA24944.1; PID:g577055

A;Molecule type: mRNA

A;Residues: 209-270 <RES>

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Reference number: I37393; MUID:84069777; PMID:6689067

A;Title: Isolation and characterisation of cDNA clones for the Aalpha- and gamma-chains o

Db   140   DIILSEYNT-----------------------------NIPSSL 169

Qy   212   PVPQPPAAPRVYQPPTYNRIINQISTNEIQSDQNLKVLPPLPIMPILTSLP--SSTD 269

Db   170   RV------LRAVIDSLH-KKIQKLEN-----AIAIQTDYCRSPCVASCN 206

Qy   270   KPSGPWRDCLQALEDGHDTSSSIYLVKPENTNRLMQVWCDQRHDPGGWTVIQRRLDGSVNF 329

R;Chung, D.W.; Chan, W.Y.; Davie, E.W.

J;Cell Biol. 121, 1329-1342, 1993

A;Title: Evidence for the selective association of a subpopulation of GPIIb-IIIa with th

A;Reference number: A40698; MUID:93286185; PMID:8509453

A;Molecule type: protein

Db   207   IPVVSGRECEDIYRKGGETSEMYIIQPDPFTTPYRVYCDMETDNGGWTLIQNRQDGSVNF 266

Qy   330   FRNWETYKQGFGNI-------------DGEYWLGLENIYWLTNQGNYKLLVTMEDWSGRKVF 378

A;Accession: A40698

A;Molecule type: protein

A;Residues: 27-33,'XX',36-41 <BER>

A;Experimental source: thrombin-activated platelets

A;Note: sequence extracted from NCBI backbone (NCBIP:133734)

R;Kunitake, S.T.; Carlill, C.T.; Lau, K.; Protter, A.A.; Naya-V.gne, J.; Kane, J.P.

Biochemistry 33, 1988-1993, 1994

A;Title: Identification of proteins associated with apolipoprotein A-I-containing lipopr

A;Reference number: A54223; MUID:94162201; PMID:8117655

A;Accession: H54223

Db   267   GRAWDEYKRGFGNIAKSGGKKYCDTPGEYWLGNDKISQLTKIGPTKVLIEMEDWNGDKVS 326

Qy   379   AEYASFRLEPESSYYKLRLGRYHHGNAGD------------SFTWWINGKQPTTLDRDHD 424

A;Accession: A90470

A;Molecule type: protein

A;Residues: 27-33,'XX',36-41 <KUN>

A;Note: identification of tryptic peptides from high-density lipoproteins

R;Henschen, A.; Lottspeich, F.; Kehl, M.; Southan, C.

Ann. N. Y. Acad. Sci. 408, 28-43, 1983

A;Title: Covalent structure of fibrinogen.

A;Reference number: A90037; MUID:83254370; PMID:6575689

A;Contents: annotation; review; disulfide bonds

Db   327   ALYGGFTIHNEGNKYQLSVSNYKGNAGNALMEGASQLYGENRTMTIHNGMFSTYDRDND 386

Qy   425   VY-------TGNCAHYQKGGWWYNACAHSNLNGVWYWRGGHY----RSRYQDGVYWAEFRGG 474

R;Doolittle, R.F.; Takagi, T.; Watt, K.; Bouma III, H.; Cottrell, B.A.; Cassman, K.G.; G

in Regulatory Proteolytic Enzymes and Their Inhibitors, Magnusson, S.; Ottesen, M.; Folt

A;Title: The structures of fibrinogen and fibrin.

A;Reference number: A94437

A;Contents: annotation; disulfide bonds

R;Blomback, B.; Hessel, B.; Hogg, D.

Thromb. Res. 8, 639-658, 1976

A;Title: Disulfide bridges in NH-2-terminal part of human fibrinogen.

A;Reference number: A94309; MUID:76225080; PMID:936108

A;Contents: annotation; disulfide bonds

R;Hoeprich, P.D.; Doolittle, R.F.

Biochemistry 22, 2049-2055, 1983

A;Title: Dimeric half-molecules of human fibrinogen are joined through disulfide bonds i

A;Reference number: A90467; MUID:83231445; PMID:6860649

A;Contents: annotation; quaternary structure; disulfide bonds

R;Doolittle, R.F.

Annu. Rev. Biochem. 53, 195-229, 1984

A;Title: Fibrinogen and fibrin.

A;Reference number: A90041; MUID:84305751; PMID:6383194

A;Contents: annotation; review; EM structure; polymerization; ligands

Db   387   GWLTTDRKQCSKEDGGGWWYNRCHAANPNGRYYWGGTYSWDMAKHGTDDGIVWMNWKGS 446

Qy   475   SYSLKKVVMMIRP 487

R;Horwitz, B.H.; Varadi, A.; Scheraga, H.A.

Proc. Natl. Acad. Sci. U.S.A. 81, 5980-5984, 1984

A;Title: Localization of a fibrin gamma-chain polymerization site within segment Thr-374

A;Reference number: A94006; MUID:85014892; PMID:6592597

A;Contents: annotation; polymerization region

R;Kloczewiak, M.; Timmons, S.; Lukas, T.J.; Hawiger, J.

Biochemistry 23, 1767-1774, 1984

A;Title: Platelet receptor recognition site on human fibrinogen. Synthesis and structure

A;Reference number: A90483; MUID:84303545; PMID:6326808

A;Contents: annotation; platelet aggregation region

R;Plow, E.F.; Srouji, A.H.; Meyer, D.; Marguerie, G.; Ginsberg, M.H.

J. Biol. Chem. 259, 5388-5391, 1984

A;Title: Evidence that three adhesive proteins interact with a common recognition site o

A;Reference number: A92477; MUID:84185664; PMID:6325435

A;Contents: annotation; platelet aggregation region

R;Dang, C.V.; Ebert, R.F.; Bell, W.R.

J. Biol. Chem. 260, 9713-9719, 1985

A;Title: Localization of a fibrinogen calcium binding site between gamma-subunit positic

A;Reference number: A92549; MUID:85261382; PMID:3160702

A;Contents: annotation; calcium binding region

R;Kirschbaum, N.E.; Budzynski, A.Z.

J. Biol. Chem. 265, 13669-13676, 1990

A;Title: A unique proteolytic fragment of human fibrinogen containing the Aalpha COOH-te

A;Reference number: A37117; MUID:90377977; PMID:2143188

Db   447   WYSMKKMSMKIKP 459

R;Rixon, M.W.; Chung, D.W.; Davie, E.W.

Biochemistry 24, 2077-2086, 1985

A;Title: Nucleotide sequence of the gene for the gamma chain of human fibrinogen.

A;Reference number: A90494; MUID:85252774; PMID:2990550

A;Accession: B90494

A;Molecule type: DNA

A;Residues: 1-113,'I',115-437 <RIX>

R;Kant, J.A.; Lord, S.T.; Crabtree, G.R.

Proc. Natl. Acad. Sci. U.S.A. 80, 3953-3957, 1983

A;Title: Partial mRNA sequences for human Aalpha, Bbeta, and gamma fibrinogen chains: ev

A;Reference number: A93956; MUID:83247396; PMID:6575389

A;Accession: B93956

A;Molecule type: mRNA

A;Residues: 276-437 <KAN>

R;Fornace Jr., A.J.; Cummings, D.E.; Comeau, C.M.; Kant, J.A.; Crabtree, G.R.

J. Biol. Chem. 259, 12826-12830, 1984

A;Title: Structure of the human gamma-fibrinogen gene. Alternate mRNA splicing near the

A;Reference number: A92448; MUID:85030379; PMID:6092246

A;Accession: B92448

A;Molecule type: DNA

A;Residues: 286-437 <FOR>

R;Imam, A.M.A.; Eaton, M.A.W.; Williamson, R.; Humphries, S.

Nucleic Acids Res. 11, 7427-7434, 1983

R;Henschen, A.; Lottspeich, F.; Kehl, M.; Southan, C.

A;Contents: annotation; hementin cleavage site
A;Note: hementin, a protease from Haementeria ghilianii, the giant South American leech,
C;Comment: The conversion of fibrinogen to fibrin is triggered by thrombin, which cleave
ization sites responsible for the formation of the soft clot.
C;Comment: The soft clot is converted into the hard clot by factor XIIIa (fibrin-stabili
ger) and between alpha chains (weaker) of different monomers.
C;Comment: All fibrinogen chains are synthesized in the liver.
C;Comment: The two forms of gamma chain, A and B (see PIR:FGHUGB), arise by alternate sp
intron, which makes this chain different from the gamma-B chain at positions 434-437 and
from the distal domain nodes.
A;Gene: GDB:FGG
A;Genetics:
A;Cross-references: GDB:119132; OMIM:134850
A;Map position: 4q28-4q28
A;Introns: 26/3; 41/3; 103/1; 134/2; 178/1; 222/3; 284/2; 377/1; 433/3
C;Superfamily: fibrinogen gamma chain; fibrinogen beta/gamma homology
A;Pathway: blood coagulation
A;Description: fibrinogen cleaved by thrombin yields monomers that are polymerized into
C;Keywords: alternative splicing; blood coagulation; calcium; coiled coil; glycoprotein;
F;1-26/Domain: signal sequence #status predicted <SIG>
F;27-437/Product: fibrinogen gamma-A chain #status experimental <MPT>
F;176-415/Domain: fibrinogen beta/gamma homology <FBG>
F;341-355/Domain: fibrinogen gamma homology <FBG>
F;400-422/Region: polymerization site, binding to the amino end of the alpha chain of an
F;423-437/Region: platelet aggregation #status predicted
F;34/Disulfide bonds: interchain (to gamma-35) #status predicted
F;35/Disulfide bonds: interchain (to gamma-34) #status experimental
F;45/Disulfide bonds: interchain (to beta-110) #status experimental
F;49/Disulfide bonds: interchain (to alpha-64) #status experimental
F;78/Binding site: carbohydrate (Asn) (covalent) #status experimental
F;161/Disulfide bonds: interchain (to beta-227) #status experimental
F;165/Disulfide bonds: interchain (to alpha-180) #status experimental
F;179-208,352-365/Disulfide bonds: #status experimental
F;424/Cross-link: isopeptide (Gln) (interchain to Lys-432 N6-amino) #status experimental
F;432/Cross-link: isopeptide (Lys) (interchain to Gln-424) #status experimental

Query Match   18.7%;   Score 501;   DB 1;   Length 437;
Best Local Similarity   29.4%;   Pred. No. 3.6e-25;
Matches 128;   Conservative 57;   Mismatches 140;   Indels 110;   Gaps 11;

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Qy   90 ELLNNELLKQKRQIETLQQLVKVDGGIVSEVKLLRK--------ESRMNNSRVTQLY 138
           : :   :          ::   ::   :
Db   53 DFLSTYQTKVDKDLQSLEDILHQVENKTSEVKQLIKAIQLTYNPDESSKPNMIDAATLKS 112

Qy  139 MQLLHEIIRKRDNALELSQLENRRIINQTADMLQLASXYKDLEHKYQHLATLAHNQSEIIA 198
           :: :  :           :::          ::
Db  113 RKMLEEIMK--------YEASILTHDSSIRYLQEIYNSNMQKIVNL------KEKVA 155

Qy  199 QLEEHCQRVPSARPVPQPPPAAPPRVYQPPTYNRIINQISTNEIQSDQNLKYLPPPLPTM 258
        :: :  :
Db  156 QLEAQCQE----------------------------------------------PCK 166

Qy  259 PTLTSLPSSTDKPSGPWRDCLQALEDGHDTSSIYLVKPENTRLMQVVCDQRHDPGGWTV 318
          :         :        :                ::    : : :      ::||
Db  167 DTV-QIHDITGK------DCQDIANKGAKQSGLYFIKPLKANQQFLVYCEIDGSGNGWTV 219

Qy  319 IQRLDGSVNFRNWETYKQGFGNID-----GEYWLGLENIYWLTNQG--NYKLLVTVMEDW 372
        :||||||| ||  :::: : :::            | :|| ||:||   : ||  |:||
Db  220 FQKRLDGSVDFKKNWIQYKEGFGHLSPTGTTEFWLGNEKIHLISTQSAIPYALRVELEBDW 279

Qy  373 SGRKVFAEYASFRLEPESEYYKLRLGRY-HGNAGDS--------FTWHGNGKQFT 417
          :   : : :   : ::  ::       :     ::         || ||  ||
Db  280 NGRSTADYAMFKVGPEADKYRLTYAYFAGGDAGDAFDGFDGGDFDSDKFFSHNGMQFS 339

Qy  418 TLDRDHDVYTGNCAHYKGXGWWWNACAHSNLNGVWYRGGHYP-----SRYQDGVYWAEFR 472
        | ::: :  |||||        ||  ||| |||| |:||||        ::|| |:| :
Db  340 TWDNDNDKFEGNCAEQDGSGWWMNKCHAGHLNGVYYQGGTYSKASTPNGYDNGIIWATWK 399

Qy  473 GGSYSLKKVVMMIRP 487
          :||  |||  | |
Db  400 TRWYSMKKTTMKIIP 414
```

Db   400 TRWYSMKKTTMKIIP 414

RESULT 8
FGHUGB
fibrinogen gamma-B chain precursor [validated] - human
N;Alternate names: coagulation factor I; fibrinogen gamma-55 chain
A;Species: Homo sapiens (man)
C;Date: 17-Mar-1987 #sequence_revision 17-Mar-1987 #text_change 08-Dec-2000
A;Accession: A90494; A92448; A90453; A28203; B28203; I37390; A03126
R;Rixon, M.W.; Chung, D.W.; Davie, E.W.
Biochemistry 24, 2077-2086, 1985
A;Title: Nucleotide sequence of the gene for the gamma chain of human fibrinogen.
A;Reference number: A90494; MUID:85252774; PMID:2990550
A;Accession: A90494
A;Molecule type: DNA
A;Residues: 1-113, 'I', 115-453 <RIX>
A;Cross-references: GB:M10014; GB:J00134; GB:J00135; GB:X00086; NID:g182438; PIDN:AAB595
R;Fornace Jr., A.J.; Cummings, D.E.; Comeau, C.M.; Kant, J.A.; Crabtree, G.R.
J. Biol. Chem. 259, 12826-12830, 1984
A;Title: Structure of the human gamma-fibrinogen gene. Alternate mRNA splicing near the
A;Reference number: A92448; MUID:85030379; PMID:6092346
A;Accession: A92448
A;Molecule type: DNA
A;Residues: 286-453 <FOR>
R;Wolfenstein-Todel, C.; Mosesson, M.W.
Biochemistry 20, 6146-6149, 1981
A;Title: Carboxy-terminal amino acid sequence of a human fibrinogen gamma-chain variant
A;Reference number: A90453; MUID:82068993; PMID:7306501
A;Accession: A90453
A;Molecule type: protein
A;Residues: 411-434,'Y',436-440,'2',442,'2',444,'B',446-447,'R',449,'ZBB','R',449 <WOL>
R;Francis, C.W.; Mueller, E.; Henschen, A.; Simpson, P.J.; Marder, V.J.
Proc. Natl. Acad. Sci. U.S.A. 85, 3358-3362, 1988
A;Title: Carboxyl-terminal amino acid sequences of two variant forms of the gamma-chain
A;Reference number: A94194; MUID:88217900; PMID:3368448
A;Accession: A28203
A;Molecule type: protein
A;Residues: 433-449 <FRA>
A;Accession: B28203
A;Molecule type: protein
A;Residues: 433-453 <FR2>
R;Marchetti, L.; Zanelli, T.; Malcovati, M.; Tenchini, M.L.
DNA Seq. 1, 419-422, 1991
A;Title: Polymorphism of the human gamma fibrinogen gene.
A;Reference number: I37390; MUID:92119334; PMID:1685103
A;Accession: I37390
A;Molecule type: mRNA
A;Residues: translated from GB/EMBL/DDBJ
A;Residues: 75-286 <RES>
A;Cross-references: EMBL:X51473; NID:g31410; PIDN:CAA35837.1; PID:g930064
C;Comment: The two forms of gamma chain, A (see PIR:FGHUG) and B, arise by alternate spl
ntron, which makes this chain different from the gamma-B chain at positions 434-437 and
C;Comment: The gamma-B chain is present in about 10% of the fibrinogen molecules in plas
from the distal domain nodes.
C;Function:
A;Description: fibrinogen cleaved by thrombin yields monomers that are polymerized into
A;Pathway: blood coagulation
A;Gene: GDB:FGG
C;Genetics:
A;Cross-references: GDB:119132; OMIM:134850
A;Map position: 4q28-4q28
A;Introns: 26/3; 41/3; 103/1; 134/2; 178/1; 222/3; 284/2; 377/1
C;Keywords: alternative splicing; blood coagulation; calcium; coiled coil; glycoprotein;
C;Complex: The fibrinogen molecule is a hexamer containing two sets of alpha (see PIR:FG
ins are contained in the core. Two three-chain coiled coils emerge from this core and co
from the distal domain nodes.
C;Superfamily: fibrinogen gamma chain; fibrinogen beta/gamma homology
F;1-26/Domain: signal sequence #status predicted <SIG>
F;27-453/Product: fibrinogen gamma-B chain #status experimental <MPT>
F;176-415/Domain: fibrinogen beta/gamma homology <FBG>
F;341-355/Domain: fibrinogen gamma homology <FBG>
F;340-422/Region: polymerization site, binding to the amino end of the alpha chain of an
F;34/Disulfide bonds: interchain (to gamma-35) #status predicted

F;35/Disulfide bonds: interchain (to gamma-34) #status predicted
F;45/Disulfide bonds: interchain (to beta-110) #status predicted
F;49/Disulfide bonds: interchain (to alpha-64) #status predicted
F;78/Disulfide bonds: interchain (to alpha-64) #status predicted
F;161/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;165/Disulfide bonds: interchain (to beta-227) #status predicted
F;179-208,352-365/Disulfide bonds: interchain (to alpha-180) #status predicted
F;424/Cross-link: isopeptide (Gln) (interchain to Lys-432 N6-amino) #status predicted
F;432/Cross-link: isopeptide (Lys) (interchain to Gln-424) #status predicted

```
Query Match                18.7%;  Score 501; DB 1; Length 453;
Best Local Similarity   29.4%;  Pred. No. 3.8e-25;
Matches 128;  Conservative 57;  Mismatches 140;  Indels 110;  Gaps 11;

Qy     90  ELLNNELLKQKRQIETLQQLVKVDGGIVSEVKLIRK---------------ESRNMNSRVTQLY 138
               ::|::| ::| |  |       |  ||    |                  : :| || :
Db     53  DFISTYQTKVDKDLQSLEDILHQVENKTSEVKQLIKAIQLITYNPDSSKPNMIDAATLKS 112

Qy    139  MQLLHEIIRKRDNALELSLQLENRILNQTADMLQLASKYKDLEHKYQHLATLAHNQSEIIA 198
               :|| |:|| |   | |: |  | : |::| |    |:| |    :||: ||| |:
Db    113  RKMLEEIMK--------YEASILTHDSSIRYLQEIYNSNNQKIVNL------KEKVA 155

Qy    199  QLEEHCQRVPSARPVPQPPPAAPPRVYQPPTYNRIINQISTNEIQSDQNLKVLPPLPTM 258
               |:|  ||   | |     | ||  || :|::  |:|| | |:|:|| |::|
Db    156  QLEAQCQE------------------------------------PCK 166

Qy    259  PTLTSLPSSTDKPSGPWRDCLQALEDGHDTSSIYLVKPENTNRLMQVWCDQRHDPGGWTV 318
               | | | | |     ||| |  |  | |  |:    :  |  :|  || || |
Db    167  DTY-QIHGTGK------DCQDIANKGAKQSGLYFIKPLKANQFLVYCEIDGSGNGWTV 219

Qy    319  IQRRLDGSVNFFRNWETYKQGFGNID--------GEYWLGLENIYWLTNQG-NYKLLVTMEDW 372
               |:| || |         |  |            |: | |   : |  :|  | |:  |
Db    220  FQKRLDGSVDFKKNWIQYKEGFGHLSPTGTTEFWLGNEKIHLISTQSAIPYALRVELEDW 279

Qy    373  SGRKVFAEYASFRLEPESEYYKLRLGRY-HGNAGDS-------------FTWHNGKQFT 417
               || | || | | |||  | | |  |  | |          |:||||| |
Db    280  NGRTSTADYAMFKVGPEADKYRLTYAYFAGGDAGDAFDGFDFGDDPSDKFFTSHNGMQFS 339

Qy    418  TLDRDHDVYTGNCAHYQKGGWWTNACAHSNLNGVYWYRGGHYR-----SRYQDGVYWAEFR 472
               || | | |       |::||||||||  |||  |: |:  || |
Db    340  TWDNDNDKFEGNCAEQDGSGWWMNKCHAGHLNGVYYQGGTYSKASTPNGYDNGIIWATWK 399

Qy    473  GGSYSLKKVVMMIRP 487
               |||||| |  | | |
Db    400  TRWYSMKKTTMKIIP 414
```

RESULT 9
A05299
fibrinogen beta chain precursor - rat (fragments)
C;Contains: fibrinopeptide B
N;Species: Rattus norvegicus (Norway rat)
C;Date: 05-Jun-1987 #sequence_revision 10-Mar-1994 #text_change 13-Aug-1999
C;Accession: A05299; PE0010
R;Fowlkes, D.M.; Mullis, N.T.; Comeau, C.M.; Crabtree, G.R.
Proc. Natl. Acad. Sci. U.S.A. 81, 2313-2316, 1984
A;Title: Potential basis for regulation of the coordinately expressed fibrinogen genes:
A;Reference number: A93989; MUID:84194000; PMID:6232608
A;Molecule type: DNA
A;Residues: 1-32 <FOW>
R;Bastman, E.M.; Gilula, N.B.
Gene 79, 151-158, 1989
A;Title: Cloning and characterization of a cDNA for the B beta chain of rat fibrinogen:
A;Reference number: PE0010; MUID:89378771; PMID:2673932
A;Molecule type: mRNA
A;Residues: 33-328 <EAS>
A;Cross-references: GB:M27220; NID:g529585; PIDN:AAA41160.1; PID:g529586
C;Superfamily: fibrinogen beta chain; fibrinogen beta/gamma homology
C;Keywords: blood coagulation; glycoprotein; liver; plasma
F;33-65/Domain: fibrinogen disulfide ring homology (fragment) <FDR>
F;75-324/Domain: fibrinogen beta/gamma homology <FBG>

F;231/Binding site: carbohydrate (Asn) (covalent) #status predicted

```
Query Match                18.8%;  Score 500; DB 2; Length 328;
Best Local Similarity   31.2%;  Pred. No. 2.8e-25;
Matches 118;  Conservative 54;  Mismatches 100;  Indels 106;  Gaps 9;

Qy    153  LELSQLENRILNQTADMLQ-------LASKYKDLEHKYQHLATLAHNQSEIIAQLEEHCQ 205
               | ::| || ::|    |        || | |:|:|| ||| |||||  |:  ||::||
Db      9  LSVSLVQTQAATTDSDKVDLLSARRVLRSILEDLRSKMQKL-------ESDISAQ-TEYC- 60

Qy    206  RVPSARPVPQPPPAAPPRVYQPPPTYNRIINQISTNEIQSDQNLKVLPPLPTMPFLTSLP 265
               :        |   | |    | ::                |: || | | |
Db     61  ------------------HTPCTVNCNIPVVSGKE------------------------ 77

Qy    266  SSTDKPSGPWRDCLQALEDGHDTSSIYLVKPENTNRLRLMQVWCDQRHDPGGWTVIQRRLDG 325
               |       || |     |    ||     :   | |   |                :||
Db     78  -----CEIIRKGGETSEMYLIQPDTSSKPYRVYCDMKTENGGWTVICNRQDG 125

Qy    326  SVNFFRNWETYKQGFGNI----------DGEYWLGLENIYWLTNQGNYKLLVTMEDWS 373
               || || |  |  || |           |: | |   : |  :|  | |:  |
Db    126  SVDFGRKWDPYKKGFGNIATNEDTKKYCGLPGEYWLGNDKISQLTRIGPTELLIEMEDWK 185

Qy    374  GRKVFAEYASFRLEPESEYYKLRLGRYHGNAGD----------SFTWHNGKQFTTL 419
               || | || | | |||  | | |  | | |         | |:||||| ::|
Db    186  GDKVKAHYGGFTVQTEANKYQVSVNKYKGTAGNALMEGASQLVGENRTMTIHNGMFFSTY 245

Qy    420  DRDHDVYT-------GNCAHYQKGGWWTNACAHSNLNGVYWYRGGHY----RSRYQDGVYWA 469
               | | | |        ||| |::|||| ||||  |||  |: | |     :|| |  ||
Db    246  DRDNDGWVTTDPRKQCSKEDGGGWWMNRCHAANPNGRYYWGGLYSWDMSKHGTDDGVVMM 305

Qy    470  EFRGGSYSLKKVVMMIRP 487
               |  |||||| |  | | |
Db    306  NWKGSWYSMRRMSMKIRP 323
```

RESULT 10
A35084
fibrinogen-related protein A precursor - sea cucumber (Parastichopus parvimensis)
C;Species: Parastichopus parvimensis
C;Date: 03-Aug-1990 #sequence_revision 03-Aug-1990 #text_change 09-Sep-1997
C;Accession: A35084
R;Xu, X.; Doolittle, R.F.
Proc. Natl. Acad. Sci. U.S.A. 87, 2097-2101, 1990
A;Title: Presence of a vertebrate fibrinogen-like sequence in an echinoderm.
A;Reference number: A35084; MUID:90192754; PMID:2315305
A;Accession: A35084
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-282 <XUX>
A;Cross-references: GB:M31326; NID:g161164; PID:g161165
C;Superfamily: fibrinogen beta/gamma homology
F;67-280/Domain: fibrinogen beta/gamma homology <FBG>

```
Query Match                18.4%;  Score 495; DB 2; Length 282;
Best Local Similarity   34.6%;  Pred. No. 4.8e-25;
Matches 104;  Conservative 45;  Mismatches 96;  Indels 56;  Gaps 6;

Qy    192  NQSEIIAQLEEHCQRVPSARPVPQPPPAAPPRVYQPPPTYNRIINQISTNEIQSDQNLKVL 251
               |:|   | || ||  | |    |     |       |  | :|:|| | |:|:|| |
Db     28  NESEITFPEEERSLADPAGRQKROSGLSCPKRISHSPEYP------------------ 67

Qy    252  PPLPTMPFLTSLPSSTDKPSGPWRDC----LQALEDGHDTSSIYLVKPENTNRLRLMQVWCD 308
               |   |    | |    |  || |     |  |   || |    | :     |  |
Db     68  ------------RDCYDILQSCSGQSPPSGQYYIQPDGGN-LIKVCD 102

Qy    309  QRHDPGGWTVIQRRLDGSVNFFRNWETYKQGFGNIDGEYWLGLENIYWLTNQGNYKLLVT 368
               |  | |||  ::|| |   |  | | |  || |  |:||||| |   : |  :|  |
Db    103  METDEGGWTVFQRRIDGTINFNRPWSYQTQFGNLNTFWLGNDNIHYLTSQDYELRVE 162

Qy    369  MEDWSGRKVFAEVASFRLEPESEYYKLRLGRYHGNAGDSFTWHNGKQFTTLDRDHDVYTG 428
               :|||  || | ||| | ||  | | |  || | |:  |:||  | |::| | | |  |
Db    163  LNNTLGNHYYAKYNKFRIGDSFSEYYILVLGAYSGTAGDSLAYAHNTMRFSTYDNDNDVYSI 222
```

```
Qy    429  NCA---HYQKGGWWYNACAHSNLNGVWYRGGHYRSRYQDGVYWAEFRGGSYSLKKVVMMI  485
                |||  || || ||||||||||||||||||||  ::||||:  ||:||| :::||  ||
Db    223  NCASHSSYGRGAWYKSCLLSNLNGQYY---DYSG--APSIYWSYLPGDNDQIFFAEMKL  277

Qy    486  R  486
           R
Db    278  R  278
```

RESULT 11
A32670

A;Accession: A32670
fibrinogen gamma chain - African clawed frog
C;Species: Xenopus laevis (African clawed frog)
C;Date: 15-Jun-1990 #sequence_revision 15-Jun-1990 #text_change 13-Aug-1999
C;Accession: A32670; I51416
R;Pastori, R.L.; Moskaitis, J.E.; Smith Jr, L.H.; Schoenberg, D.R.
Biochemistry 29, 2599-2605, 1990
A;Title: Estrogen regulation of Xenopus laevis gamma-fibrinogen gene expression.
A;Reference number: I51416; MUID:91146806; PMID:2289632
A;Accession: A32670
A;Molecule type: mRNA
A;Residues: 1-438 <PAS>
R;Bhattacharya, A.; Shepard, A.R.; Moser, D.R.; Holland, L.J.
Mol. Cell. Endocrinol. 72, 213-220, 1990
A;Title: Isolation and characterization of cDNA clones for the gamma subunit of Xenopus
A;Reference number: I51416; MUID:91146806; PMID:2289632
A;Accession: I51416
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Accession: A32670
A;Status: preliminary
A;Accession: A32670
A;Molecule type: mRNA
A;Residues: 1-58 <BHA>
C;Superfamily: fibrinogen gamma chain; fibrinogen beta/gamma homology
C;Cross-references: GB;M35548; NID:g214141; PIDN:AAA03247.1; PID:g214142
C;Keywords: blood coagulation
F;173-413/Domain: fibrinogen beta/gamma homology <FBG>

```
Query Match             18.2%;  Score 489.5;  DB 2;  Length 438;
Best Local Similarity   31.4%;  Pred. No. 2e-24;
Matches  125;  Conservative  54;  Mismatches 154;  Indels  65;  Gaps  13;

Qy    145  IIRKRDNALELSQLENRLINQTADMLQLASKYK-----DLEHKYQHLATLAINQSEIIAQ  199
                | | :|   | | | |   | :|  |  ||          |:: | |  | |||| |
Db     25  IIPNTDNCCILDGRFGEYCPTTCGISDFLNRYQENVDTDIQY-LENLLTQISNSTSGTTI  83

Qy    200  LEEHCQRVPSA-RPVPQPPPAAPPRVYQPPT----------YNRIINQISTNEIQSDQN  247
                ||  | |     |    | |                  :||| | |||||| ||
Db     84  IVEHL--IDSGKPATSPQTAIDPMTQKSKTCWMKLTDMKNYYQYEENILYLQEVYSSNQ  141

Qy    248  LKV-----LPPPLPTMPTLTSLPSSTDKPSGPWRDCLQALEDGHDTSSIYLVKP  296
                     | ||| | ||  |  | :|| || |  |:||| ||| ||||| |||
Db    142  NKIFLLKQKIANLELCQQPCRDTV-QIQEFTGK------DCQEVANKGARLSGLYYIKP  194

Qy    297  ENTNRLMCQVWCDQRHDPGGWTVIQRRLDGSVNFFRNWETYKQGFG----NIDGEYWLGLE  352
               | | |  |  | |  || |||||||||| ||   || ||       | |||  |:
Db    195  LKAKQGFLVCEIEPGGSSAWTVIQRLDGSVNFHKQWVQYEGFGVLSPNDKTEFWLGNE  254

Qy    353  NIYWLTNQGN--YKLLVTMEDWSGRKVFAEYASFRLEPESEYYKLRLGRY-HGNAGDSF-  408
               |||| |||     | | |||| | | ||||  |:|  |:|:||| ||  |||| ||
Db    255  KIHLLSTQSTIPYVMRIELEDWSNQKSTADYSTFRLGSEKDNYRFTYAYFIGGDADDAFD  314

Qy    409  ------------TWINGKQFTTLDHDVVTGNCAHYQKGGWWYNACAHSNLNGVWYRG  455
                           |:|||||||||:|:|||: |||  ||:|||||||||||||||||
Db    315  GFDFGDDPSDKFYTSHNGMQFSTFDXDNDKFDGNCAEQDGSGWWMNRCHAAHLNGKYYQG  374

Qy    456  GHYR-------SRYQDGVYWAEFRGGSYSLKKVVMMIRP  487
               ||||        ||| | | | |||||||||||||||
Db    375  GTYSEADSGPGSYDNGIIWATWRRRYSMKSVTMKIMP  412
```

RESULT 12
A45445
Janusin precursor, long form - rat

N;Alternate names: neural recognition glycoprotein J1-160/180, long form
N;Contains: neural recognition glycoprotein J1-160/180, short form
C;Species: Rattus norvegicus (Norway rat)
C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 20-Aug-1999
C;Accession: A45445; B45445; S32023
R;Fuss, B.; Wintergerst, E.S.; Bartsch, U.; Schachner, M.
J. Cell Biol. 120, 1237-1249, 1993
A;Title: Molecular characterization and in situ mRNA localization of the neural recognit
A;Reference number: A45445; MUID:93171267; PMID:7679676
A;Accession: A45445
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-1356 <FUS>
A;Cross-references: GB;Z18630; NID:g57961; PIDN:CAA79229.1; PID:957962
A;Accession: B45445
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-772, 863-1356 <FU2>
A;Cross-references: GB;Z18630
R;Fuss, B.; Wintergerst, E.J.; Bartsch, M.
submitted to the EMBL Data Library, November 1992
A;Description: Molecular characterization and in situ mRNA localization of the neural re
A;Reference number: S32023
A;Accession: S32023
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-1356 <FUS2>
C;Cross-references: EMBL;Z18630; NID:g57961; PIDN:CAA79229.1; PID:957962
C;Superfamily: restrictin; EGF homology; fibrinogen beta/gamma homology; fibronectin typ
C;Keywords: alternative splicing; duplication; extracellular matrix; glycoprotein; oligo
C;Product: janusin, long form #status experimental <MAT>
F;1-772/Product: janusin, short form #status experimental <ALT>
F;1-1356/Product: janusin
F;204-230/Domain: EGF homology <EG1>
F;235-261/Domain: EGF homology <EG2>
F;266-292/Domain: EGF homology <EG3>
F;297-323/Domain: EGF homology <EG4>
F;325-405/Domain: fibrinogen beta/gamma homology <FBG>
F;413-494/Domain: fibronectin type III repeat homology <FN1>
F;502-584/Domain: fibronectin type III repeat homology <FN2>
F;592-676/Domain: fibronectin type III repeat homology <FN3>
F;684-764/Domain: fibronectin type III repeat homology <FN4>
F;772-854/Domain: fibronectin type III repeat homology <FN5>
F;1038-1118/Domain: fibronectin type III repeat homology <FN6>
F;863-1356/Product: fibronectin type III repeat homology <FN7>
F;1133-1341/Domain: fibrinogen beta/gamma homology <FBG>

```
Query Match             18.2%;  Score 488;  DB 2;  Length 1356;
Best Local Similarity   36.2%;  Pred. No. 1.2e-23;
Matches  109;  Conservative  41;  Mismatches 103;  Indels  48;  Gaps  7;

Qy    215  QPPPAAPPRVYQPPTYNRIINQISTNEIQSDQNLKVLPPPLPTMPTLTSLPSSTDKP---  271
               | | | |  |    ::||| |  || |||  |||||||||||||||||||||||
Db   1060  QPPRAA------------IENYVLTYKSTDGSRKELIVDAEDTWIRLEGLSENTDYTVLL  1107

Qy    272  -----------------SGPWRDCLQALEDGHDTSSIYLLV--KPENTNRLMQVW  306
                              |||||||||||||||||||||  ||:| | |  |
Db   1108  QAAQEATRSSLTSTLFTTGGRVFSHP-QDCAQHLMNGDTLSGVVTFIFLNGELSHKL-QVY  1165

Qy    307  CDQRHDPGGWTVIQRRLDGSVNFRNWETYKQGFGNIDGEYWLGLENIYWLTNQGNYKLL  366
               | || || | | ||||||| |  |||| ||  ||  | || |:||| ||   | ||
Db   1166  CDMTTDGGGWTVFQRQRNCQTDFPRKWADYRVGFGNLEDEFWLGLDNVHRITAQGRYELR  1225

Qy    367  VTMEDWSGRKVFAEYASFRLEPESEYYKLRLGRYHGNAGDSFTWHNGKQFTTLDRDHDVY  426
               |||||||||||||||||||||||||||||||||||  || |||||||||||:|||||
Db   1226  VDMRD-GQEAVFAVYDKFAVEDSRSLYKLRIGGYNGTAGDSLSYHQGRPFSTEDRDNDVA  1284

Qy    427  TGNCAHYQKGGWWYNACAHSNLNGVWYRGGHYRSRYQDGVYWAEFRGGSYSLKKVVMMIR  486
               |||| || ||||| |  || ||||||||||   ||||:|| | |||||||||||||||
Db   1285  VTNCAMSYKGAWYKNCHRTNLN----GKYGESRHSQGINWHWKGHEFSIPVEMKXR  1339

Qy    487  P  487
           P
Db   1340  P  1340
```

RESULT 13
B47172
ficolin-beta - pig
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999
C;Accession: B47172
R;Ichijo, H.; Hellman, U.; Wernstedt, C.; Gomez, L.J.; Claesson-Welsh, L.; Heldin, C.H.;
J. Biol. Chem. 268, 14505-14513, 1993
A;Title: Molecular cloning and characterization of ficolin, a multimeric protein with fi
A;Reference number: A47172; MUID:93300852; PMID:7686157
A;Accession: B47172
A;Status: preliminary
A;Molecule type: mRNA; protein
A;Residues: 1-326 <ICH>
A;Cross-references: GB:L12345; NID:g294219; PIDN:AAC69641.1; PID:g1228925
A;Experimental source: uterus
A;Note: sequence extracted from NCBI backbone (NCBIN:134468, NCBIP:134470)
C;Superfamily: fibrinogen beta/gamma homology
F;115-326/Domain: fibrinogen beta/gamma homology <FBG>

Query Match   18.0%; Score 484.5; DB 2; Length 326;
Best Local Similarity   46.6%; Pred. No. 2.8e-24;
Matches 103; Conservative 35; Mismatches 68; Indels 15; Gaps 6;

Qy   272 SGPWRDCLQALEDGHDTS---SIYL-VKPENTNRLMQVWCDQRHDPGGWTVIQRRLDGS 326
          |||||||:||: ||| |: ||| |||||||||||||||||||||||||||||||:|
Db   113 TGP-RTCKELLIRGHFLSGWHTIYLPDCQP-----LTVLCDMDTDGGGWTVFQRRSDGS 165

Qy   327 VNFFRNWETYKQGFGNIDGEYWLGLENIYWLIGNQGNYKLLIVTMEDWSGRKVFAEYASFRL 386
          ||||||||||||||:|||||||||||||||| |||||||||:|||||||:|||||||||||
Db   166 VDFYRDWAAYKRGFGSQLGEFWLGNDHIHALTAQGTSELRVDLVDFEGNHQFAKYRSFQV 225

Qy   387 EEPSEYYKLRLGRY-HGNAGDSFTWHNGKQFTTLDRDHDVYTGNCAHYQKGGWWYNACAH 445
          ||:||||||:||| |||||||||||||||||||||:||:|||||:|||:|||||||||||
Db   226 AGEAEKYKLVLGGFLEGNAGDSLSSHRDQFFSTKDQDNDHSGNCAEQYHGAWWYNACHS 285

Db   446 SNLNGVWYRGGHYRSRYQDGVYWAEFRGGSYSLKKVVMMIR 486
          |||||||:|||||:||||||||||||||||||||||||||:
Db   286 SNLNGRYLRGLH--TSYANGVNWRSGRGYNYSYCVSEMKVR 324

RESULT 14
S61517
ficolin-1 precursor - human
N;Alternate names: 36K HLA-cross-reactive plasma protein; hucolin, 35K
C;Species: Homo sapiens (man)
C;Date: 27-Apr-1996 #sequence_revision 13-Mar-1997 #text_change 18-Feb-2000
C;Accession: S61517; JC4942
R;Lu, J.; Tay, P.N.; Kon, O.L.; Reid, K.B.M.
Biochem. J. 313, 473-478, 1996
A;Title: Human ficolin: cDNA cloning, demonstration of peripheral blood leucocytes as th
A;Reference number: S61517; MUID:96152529; PMID:8573080
A;Accession: S61517
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-326 <LUJ>
A;Cross-references: GB:S80990; NID:g1911529; PIDN:AAB50706.1; PID:g1911530
A;Harumiya, S.; Takeda, K.; Sugiura, T.; Fukumoto, Y.; Tachikawa, H.; Miyazono, K.; Fuji
J. Biochem. 120, 745-751, 1996
A;Title: Characterization of ficolins as novel elastin-binding proteins and molecular cl
A;Reference number: JC4942; MUID:97103465; PMID:8947836
A;Accession: JC4942
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 8-132,'T',134-286,'N',288-326 <HAR>
A;Cross-references: DDBJ:D83926; NID:g1510126; PIDN:BAA12120.1; PID:d1012794; PID:g15101
A;Experimental source: uterus
C;Comment: This is an elastin-binding plasma protein.
C;Superfamily: fibrinogen beta/gamma homology
C;Keywords: glycoprotein; plasma
F;1-22/Domain: signal sequence #status predicted <SIG>
F;52-108/Region: collagen-like

F;115-326/Domain: fibrinogen beta/gamma homology <FBG>
F;305/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match   18.0%; Score 483.5; DB 2; Length 326;
Best Local Similarity   45.9%; Pred. No. 3.3e-24;
Matches 101; Conservative 39; Mismatches 69; Indels 11; Gaps 6;

Qy   272 SGPWRDCLQALEDGHDTS---SIYL-VKPENTNRLMQVWCDQRHDPGGWTVIQRRLDGSVN 328
          |||||||:||: ||| |: ||| |||||||||||||||||||||||||||||||:|
Db   113 TGP-RNCKDLLDRGYFLSGWHNIYL--PD--CRPLTVLCDMDTDGGGWTVFQRRMDGSVD 167

Qy   329 FFRNWETYKQGFGNIDGEYWLGLENIYWLIGNQGNYKLLIVTMEDWSGRKVFAEYASFRLEP 388
          ||||||||||||||:|||||||||||||||| |||||||||:|||||||:|||||||||:|
Db   168 FYRDWAAYKQGFGSQLGEFWLGNDNIHALTAQGSSELRVDLVDFEGNHQFAKYRSFKVAD 227

Qy   389 ESEYYKLRLGRY-HGNAGDSFTWHNGKQFTTLDRDHDVYTGNCAHYQKGGWWYNACHSN 447
          |:||||||:||| ||||||||||||||||||||||:|||||:|||:|||||||||||||
Db   228 EAEKYKLVLGAFVGGSGAGNSLTGHHNNFFSTKDQDNDVSSSNCAEKFQGAWWYADCHASS 287

Qy.   448 LNGVWYRGGHYRSRYQDGVYWAEFRGGSYSLKKVVMMIRP 487
          ||||:||||||:||||| ||||||||||||||||||||:
Db   288 LNGLYLMGPH--ESYANGINWSAAKGYKSYSVVSEMKVRP 325

RESULT 15
A27447
cytotoxic T-lymphocyte-specific protein precursor (clone p749) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 03-Dec-1999
C;Accession: A27447
R;Koyama, T.; Hall, L.R.; Haser, W.G.; Tonegawa, S.; Saito, H.
Proc. Natl. Acad. Sci. U.S.A. 84, 1609-1613, 1987
A;Title: Structure of a cytotoxic T-lymphocyte-specific gene shows a strong homology to
A;Reference number: A27447; MUID:87175527; PMID:3550794
A;Accession: A27447
A;Molecule type: mRNA
A;Residues: 1-432 <KOY>
A;Cross-references: GB:M16238; NID:g193304; PIDN:AAA37624.1; PID:g387156
C;Superfamily: fibrinogen gamma chain; fibrinogen beta/gamma homology
F;203-428/Domain: fibrinogen beta/gamma homology <FBG>

Query Match   18.0%; Score 483.5; DB 2; Length 432;
Best Local Similarity   26.3%; Pred. No. 4.8e-24;
Matches 136; Conservative 84; Mismatches 164; Indels 133; Gaps 17;

Qy   9 W-WL--GILLAMGAVAQGEDGEEGTEEGSSPREFIYLNRYKRAGESQ-DKCTYTFIVPQR 64
          : |:   :|| |:| | |:|::|::||:| :|| || : |
Db   6 WLMLSSAVLAACRAVE-EHNLTEGLEDASAQAACPA-RLEGGSCRCEGSQCPFQLITLPTLT 63

Qy   65 VTGAICVNSKEPEVLLENRVHKQELELINNELLKQKROIB--------------- 105
          : | : |||||:|| |:|:|| | |||||||:|
Db   9 LQQLVKVDGGIVSEVKLLRKESRNMNSRVTQLYMQLLHEIIRKRDNALELSQLENRINQ 122

Qy   106 LQQLVKVDGGIVSEVKLLRKESRNMNSRVTQLYMQLLHEIIRKRDNALELSQLENRINQ 165
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   64 IQLPRQLGSME-EVLKEVRTLKEAVDSLKKSCQDCKLQADDHRDPGGNGNGAETAEDSR 122

Qy   166 TADMLQLASKYDLEHKYQHLATLAHNQSEITAQLEEHCQRVPSARPVPQPPPAAPRVY 225
          : | :   :|: |:   :::::
Db   123 VQELESQVNKLSSELKNAKDIQGIQGRLETLHL---------VNMNIENYVDNK 169

Qy   226 QPPYNRIINQISTNEIGSDQNLKVLPPPLPMTPLTTSLPSSTDKPSGPWRDCLQALEDG 285
                           :QHJ:
Db   170 VA-----------------------NLTVVNSLDGKCSKCPSQEHMQSOPV------ 198

Qy   286 HDTISSIYLVKPENTNRLMQVWCDQRHDPGGWTVIQRRLDGSVNFFRNWETYKQGFGNID 345
          :|:|:|:|:||||||||||||||||||||||||||:|||||||||||||||||||||||
Db   214 RRSSGAYRVTPDHRNSSFEVYCDMETMGGGWTVLQARLDGSTNFTREWKDYKAGFGNLER 273

Qy   346 EYWLGLENIYWLIGNQGNYKLLIVTMEDWSGRKVFAEYASFRLEPBSEYYKLRLGRYHGNAG 405
          |||||||||||| |||||||||:|||||||:|||||||||| ||::|||||:||||||||||
Db   274 EFWLGNDKIHLLTKSKEMIIRIDLEDFNGLTLYALYDQFYVANEFLKYRLHIGNYNGTAG 333

```
Qy   406  DSFTW-----HNGKQFTTLDRDHDVY-TGNCAHYQKGGWWYNACAHSNLNGVWYRGGHYR  459
               :  : |.|.|.||||.||:..|| .|||:|||: .||.|||.||.:.|.:
Db   334  DALRFSRHYNHDLRFFTTPDRDNDRYPSGNCGLYYSSGWWFDSCLSANLNGKYY---HQK  390

Qy   460  SR-YQDGVYWAEFRG-------GSY--SLKKVVMIRP  487
               :.:|.:|.|        |.:  |||||||
Db   391  YKGVRNGIFWGTWPGINQAQPGGYKSSFKQARMMIRP  427
```

Search completed: July 30, 2004, 12:38:01
Job time : 19 secs

OM protein - protein search, using sw model

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GenCore version 5.1.6

Run on: July 30, 2004, 12:19:33 ; Search time 13 Seconds
               (without alignments)
               1974.660 Million cell updates/sec

Title: US-10-018-386-2
Perfect score: 2686
Sequence: 1 MRPLCVTCWWLGLLAAMGAV.........GSYSLKKVVMMIRPNNTFH 493

Scoring table: BLOSUM62
               Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2682	99.9	493	1	ANL2_HUMAN	Q9uku9 homo sapien
2	2550	94.9	493	1	ANL2_MOUSE	Q9r045 mus musculu
3	577	21.5	497	1	AGP1_RAT	O35460 rattus norv
4	575.5	21.4	498	1	AGP1_MOUSE	O08538 mus musculu
5	574	21.4	496	1	AGP2_HUMAN	O15123 homo sapien
6	572.5	21.3	498	1	AGP1_HUMAN	O15389 homo sapien
7	558	20.8	509	1	AGP4_MOUSE	Q9wvh6 mus musculu
8	541	20.1	503	1	AGP4_HUMAN	Q9y264 homo sapien
9	537	20.0	312	1	FGL1_HUMAN	O08830 homo sapien
10	537	20.0	496	1	AGP2_HUMAN	Q9bdy7 homo sapien
11	535.5	20.0	496	1	AGP2_PIG	O18920 sus scrofa
12	535.5	19.9	496	1	AGP2_MOUSE	O35608 mus musculu
13	527.5	19.6	468	1	FIBB_BOVIN	P02676 bos taurus
14	526.5	19.6	491	1	FIBB_HUMAN	P02675 homo sapien
15	524	19.5	741	1	FIBA_CHICK	P14448 gallus gall
16	522.5	19.5	479	1	FIBA_RAT	P14480 rattus norv
17	520.5	19.4	866	1	FIBA_HUMAN	P02671 homo sapien
18	512.5	19.1	477	1	FIBB_PETMA	P02678 petromyzon
19	506.5	18.9	299	1	FCN3_HUMAN	O75636 homo sapien
20	505	18.8	782	1	FIBA_RAT	P06399 rattus norv
21	504.5	18.8	375	1	AGP2_BOVIN	O77802 bos taurus
22	503.5	18.7	306	1	FCN2_MOUSE	Q15485 mus musculu
23	503.5	18.7	313	1	FCN2_HUMAN	Q15485 homo sapien
24	503	18.7	463	1	FIBB_CHICK	Q02020 gallus gall
25	501	18.7	453	1	FIBB_HUMAN	P02679 homo sapien
26	495	18.4	438	1	FIBA_PARPA	P17634 xenopus lae
27	489.5	18.2	326	1	FCN1_HUMAN	O00602 homo sapien
28	488.5	18.1	255	1	MFA4_HUMAN	P55083 homo sapien
29	486.5	18.1	432	1	FGL2_MOUSE	P12804 mus musculu
30	483.5	18.0	432	1	FGL2_HUMAN	Q14314 homo sapien
31	482.5	18.0	334	1	FCN1_MOUSE	O70165 mus musculu
32	480.5	17.9	439	1	FGL2_HUMAN	Q14314 homo sapien
33	479.5	17.9	319	1	FCN2_RAT	P57756 rattus norv
34	476.5	17.7	444	1	FIBG_BOVIN	P12799 bos taurus
35	473	17.6	335	1	FCN1_RAT	Q9wt88 rattus norv
36	471	17.5	445	1	FIBG_RAT	P02680 rattus norv
37	465.5	17.3	641	1	FIB2_PETMA	P33573 petromyzon
38	463.5	17.3	432	1	FIBG_PETMA	P04415 petromyzon
39	450.5	16.8	1808	1	TENA_CHICK	P10039 gallus gall
40	450	16.8	4289	1	TENA_HUMAN	P22105 homo sapien
41	434.5	16.2	1746	1	TENX_HUMAN	Q29116 sus scrofa
42	430.5	16.0	1294	1	TENN_PIG	Q9ucp3 homo sapien
43	424.5	15.8	1560	1	TENN_MOUSE	Q80271 mus musculu
44	423	15.7	406	1	ANL4_HUMAN	Q9by76 homo sapien
45	421.5	15.7	2201	1	TENA_HUMAN	P24821 homo sapien

ALIGNMENTS

RESULT 1
ANL2_HUMAN

ID   ANL2_HUMAN   STANDARD;   PRT;   493 AA.
AC   Q9UKU9;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   Angiopoietin-related protein 2 precursor (Angiopoietin-like 2)
DE   (UNQ170/PRO196).
GN   ANGPTL2 OR ARP2.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Heart;
RX   MEDLINE=99403103; PubMed=10473614;
RA   Kim I., Moon S.-O., Koh K.N., Kim H., Uhm C.-S., Kwak H.J., Kim N.-G.,
RA   Koh G.Y.;
RT   "Molecular cloning, expression, and characterization of angiopoietin-
RT   related protein, angiopoietin-related protein induces endothelial cell
RT   sprouting.";
RL   J. Biol. Chem. 274:26523-26528(1999).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=22887296; PubMed=12975309;
RA   Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
RA   Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA   Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,
RA   Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA   Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,
RA   Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
RA   Vandlen R., Watanabe C., Wieand D., Woods K., Xie M.-H., Yansura D.,
RA   Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
RA   Godowski P.;
RT   "The secreted protein discovery initiative (SPDI), a large-scale
RT   effort to identify novel human secreted and transmembrane proteins: a
RT   bioinformatics assessment.";
RL   Genome Res. 13:2265-2270(2003).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Ovary;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Left column

```
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RL   "Generation and initial analysis of more than 15,000 full-length
RL   human and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC   -!- FUNCTION: Induces sprouting in endothelial cells through an
CC       autocrine and paracrine action.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- TISSUE SPECIFICITY: Widely expressed in heart, small intestine,
CC       spleen and stomach. Also found in lower levels in colon, ovary,
CC       adrenal gland, skeletal muscle and in prostate.
CC   -!- PTM: N-glycosylated.
CC   -!- SIMILARITY: Contains 1 fibrinogen C-terminal domain.
CC   --------------------------------------------------------------------------
```

```
DR   EMBL; AF125175; AAD55557.1; -.
DR   EMBL; AY358274; AAQ88641.1; -.
DR   EMBL; BC012368; AAH12368.1; -.
DR   HSSP; P02671; 1FZD.
     Genew; HGNC:490; ANGPTL2.
     MIM; 605001; -.
DR   GO; GO:0005615; C:extracellular space; TAS.
DR   GO; GO:0005102; F:receptor binding; TAS.
DR   GO; GO:0007275; P:development; TAS.
     SMART; SM00186; FBG; 1.
     Pfam; PF00147; fibrinogen_C.
     InterPro; IPR002181; Fibrinogen_C.
     PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1.
KW   Signal; Coiled coil; Glycoprotein.
FT   SIGNAL        1     22       POTENTIAL.
FT   CHAIN        23    493       ANGIOPOIETIN-RELATED PROTEIN 2.
FT   DOMAIN       76    115       COILED COIL (POTENTIAL).
FT   DOMAIN      152    206       COILED COIL (POTENTIAL).
FT   DOMAIN      438    450       COILED COIL (POTENTIAL).
FT   DOMAIN      278    307       FIBRINOGEN C-TERMINAL.
FT   DISULFID    430    443       BY SIMILARITY.
FT   DISULFID                     BY SIMILARITY.
FT   CARBOHYD    164    164       N-LINKED (GlcNAc...) (POTENTIAL).
FT   CARBOHYD    192    192       N-LINKED (GlcNAc...) (POTENTIAL).
SQ   SEQUENCE   493 AA;  57104 MW;  0F2ADECE53D185CA CRC64;

Query Match            99.8%;  Score 2682;  DB 1;  Length 493;
Best Local Similarity  99.8%;  Pred. No.1.3e-159;
Matches  492;  Conservative   1;  Mismatches   0;  Indels   0;  Gaps   0;

Qy        1  MRPLCVTCWWLGLLAAMGAVAGQEDGFEGTEEGSPREFIYLNRYKRAGESGQDKCTYTFIV  60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1  MRPLCVTCWWLGLLAAMGAVAGQEDGFEGTEEGSPREFIYLNRYKRAGESGQDKCTYTFIV  60

Qy       61  PQQRVTGAICVNSKEPEVLLENRVHKQELELLNNELLKQKRQIETLQQLVKVDGGIVSEV  120
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       61  PQQRVTGAICVNSKEPEVLLENRVHKQELELLNNELLKQKRQIETLQQLVKVDGGIVSEV  120

Qy      121  KLLRKESRNMNSRVTQLYMQLLHEIIRKRDNALELSQLENRILNQTADMLQLASKYKDLE  180
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      121  KLLRKESRNMNSRVTQLYMQLLHEIIRKRDNALELSQLENRILNQTADMLQLASKYKDLE  180

Qy      181  HKYQHLATLAHNQSEIIAQLEEHCQRVPSARPVPQPPPAAPPRRVQPPPTYNRIINQISTN  240
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      181  HKYQHLATLAHNQSEIIAQLEEHCQRVPSARPVPQPPPAAPPRRVQPPPTYNRIINQISTN  240

Qy      241  EIQSDQNLKVLPPPLPFMPTLTSLPSSTDKPSGPWRDCLQALEDGHDTSSIYLVKPENTN  300
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      241  EIQSDQNLKVLPPPLPFMPTLTSLPSSTDKPSGPWRDCLQALEDGHDTSSIYLVKPENTN  300
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Right column

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RESULT 2
ID   ANL2_MOUSE     STANDARD;      PRT;   493 AA.
AC   Q9R045;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Angiopoietin-related protein 2 precursor (Angiopoietin-like 2).
GN   ANGPTL2 OR ARP2.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Heart;
RX   MEDLINE=9940 3103; PubMed=10473614;
RA   Kim I., Moon S.-O., Koh K.N., Kim H., Uhm C.-S., Kwak H.J., Kim N.-G.,
RA   Koh G.Y.;
RT   "Molecular cloning, expression, and characterization of angiopoietin-
RT   related protein. Angiopoietin-related protein induces endothelial cell
RT   sprouting.";
RL   J. Biol. Chem. 274:26523-26528(1999).
CC   -!- FUNCTION: Induces sprouting in endothelial cells through an
CC       autocrine and paracrine action (By similarity).
CC   -!- SUBCELLULAR LOCATION: Secreted (By similarity).
CC   -!- TISSUE SPECIFICITY: WIDELY EXPRESSED IN HEART, TONGUE, LUNG AND
CC       SKELETAL MUSCLE. ALSO FOUND IN LOWER LEVELS IN KIDNEY, EPIDIDYMUS
CC       AND TESTIS.
CC   -!- SIMILARITY: Contains 1 fibrinogen C-terminal domain.
CC   --------------------------------------------------------------------------
```

```
DR   EMBL; AF125176; AAD55358.1; -.
DR   HSSP; P02671; 1FZD.
DR   MGD; MGI:1347002; Angptl2.
DR   InterPro; IPR002181; Fibrinogen_C.
DR   Pfam; PF00147; fibrinogen_C; 1.
     SMART; SM00186; FBG; 1.
     PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1.
KW   Signal; Coiled coil; Glycoprotein.
FT   SIGNAL        1     19       POTENTIAL.
FT   CHAIN        20    493       ANGIOPOIETIN-RELATED PROTEIN 2.
FT   DOMAIN       77    115       COILED COIL (POTENTIAL).
FT   DOMAIN      152    202       COILED COIL (POTENTIAL).
FT   DOMAIN      438    450       COILED COIL (POTENTIAL).
FT   DOMAIN      278    307       FIBRINOGEN C-TERMINAL.
FT   DISULFID    430    443       BY SIMILARITY.
FT   DISULFID                     BY SIMILARITY.
FT   CARBOHYD    164    164       N-LINKED (GlcNAc...) (POTENTIAL).

Qy      301  RLMQVWCDQRHDPGGWMTVIQRRLDGSVNFFRNWETYKQGFGNIDGEYWLGLENIYWLTNQ  360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      301  RLMQVWCDQRHDPGGWMTVIQRRLDGSVNFFRNWETYKQGFGNIDGEYWLGLENIYWLTNQ  360

Qy      361  GNYKLLVTMEDWSGRKVPAEYASFRLEPESEYYKLRLGRYHGNAGDSFTWHNGKQFTTLD  420
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      361  GNYKLLVTMEDWSGRKVPAEYASFRLEPESEYYKLRLGRYHGNAGDSFTWHNGKQFTTLD  420

Qy      421  RDHDVYTGNCAHYQKGGWWYNACAHSNLNGVWYRGGHYRSRYQDGVYWAEFRGGSYSLKK  480
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      421  RDHDVYTGNCAHYQKGGWWYNACAHSNLNGVWYRGGHYRSRYQDGVYWAEFRGGSYSLKK  480

Qy      481  VVNMIRPNPNTFH  493
             |||||||||||||
Db      481  VVNMIRPNPNTFH  493
```

FT   CARBOHYD   192   192   N-LINKED (GlcNAc. .) (POTENTIAL).
SQ   SEQUENCE   493 AA;   57118 MW; 22885ABEF0746BF2 CRC64;

     Query Match   94.9%; Score 2550; DB 1; Length 493;
     Best Local Similarity   94.7%; Pred. No. 2.1e-151;
     Matches 467; Conservative 10; Mismatches 16; Indels 0; Gaps 0;

Qy   1 MRPLCVTCWWLLLAAMAVAGAQEDGFEGTEEGSPREFIYLNRYKRAGESQDKCTYTFIV   60
           |:| |:||: | |||| | | ||| | || ||| ||| |||||||||||||||
Db   1 MRPLCMTYWWLGLLATVGAATGPEADVEGTEDGSQREYIYLNRYKRAGESPDKCTYTFIV   60

Qy   61 PQQRVTGAICVNSKEPEVLLENRVHKQELELLNNELLKQKRQIETLQQLVKVDGGIVSEV 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 PQQRVTGAICVNSKEPEVHLENRVHKQELELLNNELLKQKRQIETLQQLVEVDGGIVSEV 120

Qy   121 KLLRKESRNMNSRVTQLYMQLLHEIIRKRDNALELSQLENRIINQTADMLQLASKYKDLE 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 KLLRKESRNMNSRVTQLYMQLLHEIIRKRDNALELSQLENRIINQTADMLQLASKYKDLE 180

Qy   181 HKYQHLATLLAHNQSEIIAQLEEHCQRVPSARPVPQPPPAAPPRVYQPPTYNRIINQISTN 240
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 HKFQHLAMLAHNQSEVIAQLEEHCQRVPAARPMPQPPPAAPPRVYQPPTYNRIINQISTN 240

Qy   241 EIQSDQNLKVLPPPLPTMPTLITSLPSSTDKPSGPWRDCLQALEDGHDTSSIYLVKPENTN 300
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 EIQSDQNLKVLPPSLPTMPALTSLPSSTDKPSGPWRDCLQALEDGHSTSSIYLVKPENTN 300

Qy   301 RLMQVWCDQRHDPGGWTVIQRRLDGSVNFFRNWETYKQGFGNIDGEYWLGLENIYWLTNQ 360
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 RLMQVWCDQRHDPGGWTVIQRRLDGSVNFFRNWETYKQGFGNIDGEYWLGLENIYWLTNQ 360

Qy   361 GNYKLLVTMEDWSGRKVFAEYASFRLEPESEYYKLRLGRYHGNAGDSFTWHNGKQFTTLD 420
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 GNYKLLVTMEDWSGRKVFAEYASFRLEPESEYYKLRLGRYHGNAGDSFTWHNGKQFTTLD 420

Qy   421 RDHDVYTGNCAHYQKGGWWYNACAHSNLNGVWYRGGHYRSRYQDGVYWAEFRGGSYSLKK 480
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 RDHDVYTGNCAHYQKGGWWYNACAHSNLNGVWYRGGHYRSRYQDGVYWAEFRGGSYSLKK 480

Qy   481 VVMMIRPNPNTEH 493
           ||||||||||||||
Db   481 VVMMIRPNPDIFH 493

RESULT 3
AGP1_RAT
ID   AGP1_RAT   STANDARD;   PRT;   497 AA.
AC   O35460; Q8K4Q4;
DT   16-OCT-2001 (Rel. 40, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Angiopoietin-1 precursor (ANG-1).
GN   ANGPT1.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Wistar; TISSUE=Placenta;
RX   MEDLINE=22346496; PubMed=12458684;
RA   Iizasa H., Bae S.H., Asashima T., Kitano T., Matsunaga N.,
RA   Terasaki T., Kang Y.S., Nakashima E.;
RT   "Augmented expression of the tight junction protein occludin in brain
RT   endothelial cell line TR-bBB by rat angiopoietin-1 expressed in
RT   baculovirus-infected sf plus insect cells.";
RL   Pharm. Res. 19:1757-1760(2002).
RN   [2]
RP   SEQUENCE OF 91-200 FROM N.A.
RC   STRAIN=Sprague-Dawley; TISSUE=Placenta;
RX   MEDLINE=98451564; PubMed=9776732;
RA   Mandriota S.J., Pepper M.S.;
RT   "Regulation of angiopoietin-2 mRNA levels in bovine microvascular

RT   endothelial cells by cytokines and hypoxia.";
RL   Circ. Res. 83:852-859(1998).
-!- FUNCTION: BINDS AND ACTIVATES TIE2 RECEPTOR BY INDUCING ITS
     TYROSINE PHOSPHORYLATION. IMPLICATED IN ENDOTHELIAL DEVELOPMENTAL
     PROCESSES LATER AND DISTINCT FROM THAT OF VEGF. APPEARS TO PLAY A
     CRUCIAL ROLE IN MEDIATING RECIPROCAL INTERACTIONS BETWEEN THE
     ENDOTHELIUM AND SURROUNDING MATRIX AND MESENCHYME. MEDIATES BLOOD
     VESSEL MATURATION/STABILITY. IT MAY PLAY AN IMPORTANT ROLE IN THE
     HEART EARLY DEVELOPMENT.
-!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: Contains 1 fibrinogen C-terminal domain.

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     between the Swiss Institute of Bioinformatics and the EMBL outstation -
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     use by non-profit institutions as long as its content is in no way
     modified and this statement is not removed. Usage by and for commercial
     entities requires a license agreement (See http://www.isb-sib.ch/announce/
     or send an email to license@isb-sib.ch).

DR   EMBL; AB080023; BAC10290.1; -.
DR   EMBL; AF003376; AAC78246.1; -.
DR   InterPro; IPR002181; Fibrinogen_C.
DR   Pfam; PF00147; Fibrinogen_C; 1.
DR   SMART; SM00186; FBG; 1.
DR   PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1.
KW   Angiogenesis; Glycoprotein; Coiled coil; Signal.
FT   SIGNAL   1   19   POTENTIAL.
FT   CHAIN   20   497   ANGIOPOIETIN-1.
FT   DOMAIN   81   119   COILED COIL (POTENTIAL).
FT   DOMAIN   153   261   COILED COIL (POTENTIAL).
FT   DOMAIN   283   497   FIBRINOGEN C-TERMINAL.
FT   DISULFID   285   314   BY SIMILARITY.
FT   DISULFID   438   451   BY SIMILARITY.
FT   CARBOHYD   92   92   N-LINKED (GlcNAc. .) (POTENTIAL).
FT   CARBOHYD   122   122   N-LINKED (GlcNAc. .) (POTENTIAL).
FT   CARBOHYD   154   154   N-LINKED (GlcNAc. .) (POTENTIAL).
FT   CARBOHYD   243   243   N-LINKED (GlcNAc. .) (POTENTIAL).
FT   CARBOHYD   294   294   N-LINKED (GlcNAc. .) (POTENTIAL).
FT   CONFLICT   98   98   Q -> E (IN REF. 2).
FT   CONFLICT   172   172   E -> K (IN REF. 2).
FT   CONFLICT   189   189   E -> K (IN REF. 2).
SQ   SEQUENCE   497 AA;   57461 MW; 08E66AEBEFD868AE CRC64;

     Query Match   21.5%; Score 577; DB 1; Length 497;
     Best Local Similarity   29.5%; Pred. No. 8.7e-29;
     Matches 149; Conservative 84; Mismatches 170; Indels 102; Gaps 14;

Qy   43 RYKRAGESQDKCTYTFIVP--------------------QQRVTGAICVNSKEPEV-------L   79
           |::||| || |::|::|:| : :|||||||||||||| |
Db   32 RYNRIQHGQ--CAYTFLPEHDGNCRESATEQYNTNALQRDAPHVETDFSSQKLQHEHV   89

Qy   80 LENRVHKQELELLNNELLK-QKRQIETLQQ-------------LVKVDGGIVSEVKLLRKESRN 129
           :|| | :| |:| |: |||:|:|| |:|:|| | :::| ||
Db   90 MEN--YIQWLQELENYIVENMKSEMAQIQQNAVQNHFATMLEIGTSLLSQT---AEQTRK 144

Qy   130 MNSRVTQLYMQLLHEIIRKRDNALELSQLENRIINQTADMLQLASKYKDLEHKY------ 183
           |:|| :| ||:|:: : |:| |:| |:|::|| |:| |::||| :
Db   145 LTDVETQVLNQTSRLEIQLLENSLSTVELEKQLLQQTNEILKIQEKNSLLEHKILEMEGK 204

Qy   184 --------QHLATLLAHNQSEIIAQLEEHCQRVPSARPVPQPPPAAPPRVYQPPTYN 231
                   :| || ||: : :| | :|:| | :|
Db   205 HKEELDLKEEKNLQGLVTRQTFIIQELEKQLSRA----------------------- 240

Qy   232 RIINQISTNEIQSDQNLKVLPPPLPTMPTLITSLPSSTDKPSG-----------PWRDCLQALED 284
           :| :|:| | :|::| |||||| | | | :|:|| |: | |: | |
Db   241 -----TSNNSVLQKQQIEL----MDTVHNLVSLCTKEVLLKGKREEEKPFRDCADVVQA 291

Qy   285 GHDTSSIYLVKPENTNRLMQVWCDQRHDPGGWTVIQRRLDGSVNFFRNWETYKQGFGNID 344
           | |::||:|:||: ::|:| | |:|| |||:|:|::|::|::::::::| |: |:
Db   292 GFNKSGIYTIYFNNMPEFKVFCNMDVNEGGWTVIQHREDGSLDFQRGWKEYKMGFGNPS 351

Qy   345 GEYWLGLENIYWLTNQGNYKLLVTMEDWSGRKVFAEYASFRLEPESEYYKLRLGRYHGNA 404

```
RESULT 4
AGP1_MOUSE
ID   AGP1_MOUSE     STANDARD;      PRT;   498 AA.
AC   O08538;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Angiopoietin-1 precursor (ANG-1).
GN   ANGPT1 OR AGP1.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=97134663; PubMed=8980223;
RA   Davis S., Aldrich T.H., Jones P.F., Acheson A., Compton D.L., Jain V.,
RA   Ryan T.E., Bruno J., Radziejewski C., Maisonpierre P.C.,
RA   Yancopoulos G.D.;
RT   "Isolation of angiopoietin-1, a ligand for the TIE2 receptor, by
RT   secretion-trap expression cloning.";
RL   Cell 87:1161-1169(1996).
CC   -!- FUNCTION: BINDS AND ACTIVATES TIE2 RECEPTOR BY INDUCING ITS
CC       TYROSINE PHOSPHORYLATION. IMPLICATED IN ENDOTHELIAL DEVELOPMENTAL
CC       PROCESSES LATER AND DISTINCT FROM THAT OF VEGF. APPEARS TO PLAY A
CC       CRUCIAL ROLE IN MEDIATING RECIPROCAL INTERACTIONS BETWEEN THE
CC       ENDOTHELIUM AND SURROUNDING MATRIX AND MESENCHYME. MEDIATES BLOOD
CC       VESSEL MATURATION/STABILITY. IT MAY PLAY AN IMPORTANT ROLE IN THE
CC       HEART EARLY DEVELOPMENT.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- DEVELOPMENTAL STAGE: EARLY IN DEVELOPMENT, AT E9 TO E11, IT IS
CC       FOUND MOST PROMINENTLY IN THE HEART MYOCARDIUM SURROUNDING THE
CC       ENDOCARDIUM. LATER, IT BECOMES MORE WIDELY DISTRIBUTED, MOST OFTEN
CC       IN THE MESENCHYME SURROUNDING DEVELOPING VESSELS, IN CLOSE
CC       ASSOCIATION WITH ENDOTHELIAL CELLS.
CC   -!- SIMILARITY: Contains 1 fibrinogen C-terminal domain.
CC   -------------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   -------------------------------------------------------------------------
DR   EMBL; U83509; AAB50558.1; -.
DR   HSSP; P02671; 1FZD.
DR   MGD; MGI:108448; Angpt.
DR   GO; GO:0007169; P:transmembrane receptor protein tyrosine kin...; IDA.
DR   InterPro; IPR002181; Fibrinogen_C.
DR   Pfam; PF00147; fibrinogen_C; 1.
DR   SMART; SM00186; FBG; 1.
DR   PROSITE; PS00514; FIBRINOGEN_C_1; 1.
KW   Angiogenesis; Glycoprotein; Coiled coil; Signal.
FT   SIGNAL        1     19
FT   CHAIN        20    498       ANGIOPOIETIN-1.
FT   DOMAIN       81    119       COILED COIL (POTENTIAL).
FT   DOMAIN      153    261       COILED COIL (POTENTIAL).
FT   DOMAIN      284    498       FIBRINOGEN C-TERMINAL.
FT   DISULFID    286    315       BY SIMILARITY.
FT   DISULFID    439    452       BY SIMILARITY.
FT   CARBOHYD     92     92       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD    122    122       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD    154    154       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD    243    243       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD    295    295       N-LINKED (GLCNAC...) (POTENTIAL).
SQ   SEQUENCE   498 AA;  57505 MW;  2B5B4FDE2260D800 CRC64;

Query Match
Best Local Similarity  29.8%;   Pred. No. 1.1e-28;  DB 1;  Length 498;
Matches 151;  Conservative 83;  Mismatches 169;  Indels 103;  Gaps 15;

Qy   43  RYKRAGESQQDKCTYTFIVP--------QQRVTGAICVNSK--EP--------EVL  79
         :  :.  . :  ::|||.|.|        :    ||.:||.|   :.         .:.
Db   32  RVNRIQHGQ--CAYTILPEHDGNCRESATEQYNTNALQRDAPHVEPDFSSQKLQHLEHV  89

Qy   80  LENRVHKQELELLNNELLK-QKRQIETLQQ------------LVKVDGGIVSEVLLRKESRN 129
Db   90  MEN--YTQWLQKLENYIVENMKSEMAQIQNAVQNHTATMLBIGTSLISQT---AEQTRK  144

Qy  130  MNSRVTQLYMQLLHEIIRKRDNALELSQLENRILNQTADMLQLASKYKDLEHKY----- 183
Db  145  LTDVETQVLNQTSRLEIIQLLENSLSTYKLEKQLLQQTNEILKIHEKSLLEHKILEMEGK 204

Qy  184  --------QHLATLAHHQSEIIAQLEEHCQRVPSARVPQPPPAAAPPRVQPPTYN 231
Db  205  HKEELDTLKEEKENLQGLVSRQTFIIQELEKQLSRA--                240

Qy  232  RIINQISTNEIQSDQNLKVLPPPLPTMPTLTS-----------LPSSTDKPSGFPWRDCLQALE 283
Db  241  ----TNNNSILQKQQLEL---MDTVHNLVSLCTKEGVLLKGGKREEEKFPRDCADVQ 291

Qy  284  DGHDTSSIYLIVKPENTNRLMQVWCDQRHDPGGWTVIQRRLDGSVNFRRNWETYKQGFGNI 343
Db  292  AGFNKSGIYTIYFNNMPEPKKVFCNMDVNGGGWTVIQHREDGSLDFQRGWKEYKQGFGNP 351

Qy  344  DGEYWLGLENIYWLTNQGNYKLLVTMEDWSGRKVFAEYASFRLEPESEYYKLRLGRYHGN 403
Db  352  SGEYWLGNEFIFAITSQRQYMLRIELMDWEGNRAYSQYDRFHIGNEKQNYRLYLKGHTGT 411

Qy  404  AG---DSFTWHNGKQFTTLDRDHDVYTGNCAHYQKGGWWYNACAHSNLNGVYWYRGGHYRSR 461
Db  412  AGKQSSLILH-GADFSTKDADNDNCMCKCALMLTGGWWFPDACGPSNLNGMFYTAGQNHGK 470

Qy  462  YQDGVTWAEFRGGSYSLKKVVMMIRP 487
Db  471  L-NGIKWHYFKGPSYSLRSTTMMIRP 495
```

```
RESULT 5
AGP2_HUMAN
ID   AGP2_HUMAN     STANDARD;      PRT;   496 AA.
AC   O15123; Q9NRR7; Q9P2Y7;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Angiopoietin-2 precursor (ANG-2).
GN   ANGPT2.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORM 1).
RC   TISSUE=Lung;
RX   MEDLINE=97349327; PubMed=9204896;
RA   Maisonpierre P.C., Suri C., Jones P.F., Bartunkova S., Wiegand S.J.,
RA   Radziejewski C., Compton D., McClain J., Aldrich T.H.,
RA   Papadopoulos N., Daly T.J., Davis S., Sato T.N., Yancopoulos G.D.;
RT   "Angiopoietin-2, a natural antagonist for Tie2 that disrupts in vivo
RT   angiogenesis.";
RL   Science 277:55-60(1997).
RN   [2]
RP   SEQUENCE FROM N.A. (ISOFORM 1).
```

RX   MEDLINE=99126459; PubMed=9927494;
RA   Tanaka S., Mori M., Sakamoto Y., Makuuchi M., Sugimachi K.,
RA   Wands J.R.;
RT   "Biologic significance of angiopoietin-2 expression in human
RT   hepatocellular carcinoma.";
RL   J. Clin. Invest. 103:341-345(1999).
RN   [3]
RP   SEQUENCE FROM N.A. (ISOFORM 2);
RC   TISSUE=Umbilical vein endothelial cells;
RX   MEDLINE=20309811; PubMed=10766762;
RA   Kim I., Kim J.-H., Ryu Y.S., Jung S.H., Nah J.J., Koh G.Y.;
RT   "Characterization and expression of a novel alternatively spliced
RT   human angiopoietin-2.";
RL   J. Biol. Chem. 275:18550-18556(2000).
CC   -!- FUNCTION: BINDS TO TIE2 RECEPTOR AND COUNTERACTS BLOOD VESSEL
CC   MATURATION/STABILITY MEDIATED BY ANGIOPOIETIN-1. ITS FUNCTION MAY
CC   BE CONTEXT-DEPENDENT. IN THE ABSENCE OF ANGIOGENIC INDUCERS, SUCH
CC   AS VEGF, ANG2-MEDIATED LOOSENING OF CELL-MATRIX CONTACTS MAY
CC   INDUCE ENDOTHELIAL CELL APOPTOSIS WITH CONSEQUENT VASCULAR
CC   REGRESSION. IN CONCERT WITH VEGF, IT MAY FACILITATE ENDOTHELIAL
CC   CELL MIGRATION AND PROLIFERATION, THUS SERVING AS A PERMISSIVE
CC   ANGIOGENIC SIGNAL.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- ALTERNATIVE PRODUCTS:
CC   Event=Alternative splicing; Named isoforms=2;
CC   Name=1;
CC   IsoId=O15123-1; Sequence=Displayed;
CC   Name=2;
CC   IsoId=O15123-2; Sequence=VSP_001540;
CC   -!- SIMILARITY: Contains 1 fibrinogen C-terminal domain.
CC   ---
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---
DR   EMBL; AF004327; AAB63190.1; -.
DR   EMBL; AB009865; BAA95950.1; -.
DR   EMBL; AF187858; AAF76526.1; -.
HSSP; P02671; 1F2D.
DR   Genew; HGNC;485; ANGPT2.
DR   MIM; 601922; -.
DR   GO; GO:0005615; C:extracellular space; TAS.
DR   GO; GO:0005102; F:receptor binding; TAS.
DR   GO; GO:0008151; P:cell growth and/or maintenance; TAS.
DR   GO; GO:0007165; P:signal transduction; TAS.
DR   InterPro; IPR002181; Fibrinogen_C.
DR   Pfam; PF00147; fibrinogen_C; 1.
DR   SMART; SM00186; FBG; 1.
DR   PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1.
KW   Angiogenesis; Glycoprotein; Coiled coil; Signal; Alternative splicing.
SIGNAL   1   16
FT   CHAIN   17   496   ANGIOPOIETIN-2.
FT   DOMAIN   130   256   COILED COIL (POTENTIAL).
FT   DOMAIN   284   496   FIBRINOGEN C-TERMINAL.
FT   DISULFID   313   450   BY SIMILARITY.
FT   DISULFID   437   450   BY SIMILARITY.
FT   CARBOHYD   89   89   N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD   119   119   N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD   133   133   N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD   151   151   N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD   240   240   N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD   304   304   N-LINKED (GLCNAC...) (POTENTIAL).
FT   VARSPLIC   97   148   Missing (in isoform 2).
FT   /FTId=VSP_001540.
FT   CONFLICT   268   268   MISSING (IN REF. 2).
SQ   SEQUENCE   496 AA; 56919 MW; 5642A5847A7385C CRC64;

Query Match   21.4%; Score 574; DB 1; Length 496;
Best Local Similarity   28.5%; Pred. No. 1.3e-28;

Matches 149; Conservative   86; Mismatches 163; Indels 124; Gaps   15;

Qy   42 NRYKRAGESQDK-------------CTYTFIVPQRVTGAICVNSKEPEVLLENRVHK------ 86
Db   20 NNFRKSMDSIGKKQYQVQHGSCSYTFLLPEM----DNCRSSSSPYV--SNAVQRDAPLEY 73

Qy   87 --QELELLNN--------ELLK-------QKRQIETLQQLVKVDGGIVSEV----- 120
Db   74 DDSVQRLQVLENIMENNTQWLMKLENYIQDNMKKEMVEIQQNAVQNQTAVMIEIGTNLLN 133

Qy   121 -------KLLRKESRNMNNSRVTQLLYMQLLHEIIRKRDNALEI.SQLENRILNQTADMLQA 173
Db   134 QTAEQTRKLITDVEAQVLN-QTTRLELQLL------EHSLSTNKLEKQILDQTSEINKLQ 185

Qy   174 SKYKDLEHKY--------------QHLATLAHNQSEIIAQLEEHCQRVPSARPVPQ 215
Db   186 DKNSFLEKKVLAMEDKHIIQLQSIKEEKDLQVLVSKQNSIIEELEK------------- 232

Qy   216 PPPAAPPRVYQPPTNRIINQISTNEIQSDQNLKVLPPPLPTMPFLISLPSSTDKPSGP- 274
Db   233 -------------KIVTATVNNSVLQKQQHDL----MSTVNNLLTMMSTSNSAKCPT 272

Qy   275 ------WRDCLQALEDGHDTSSIYLVKPENTNRILMQVWCDQRHDPGGWTVIQRRLDGS 326
Db   273 VAKEEQISFRDCAEVFKSGHTTNGIYTLTFPNSTEEIKAYCDMEAGGGGWTIIQRREDGS 332

Qy   327 VNFFRNWETYKQGFGNIDGEYWLGLENIYWLTINQGNYKLLLVTMEDWSGRKVFAEYASFRL 386
Db   333 VDFQRTWKEYKVGFGNPSGEYWLGNEFVSQLTNQQRYVLKIHLKDWEGNEAYSLYEHFYL 392

Qy   387 EPESEYYKLRLGRYHGNAGD-SFTWHNGKQFTTLDRDHDVYTGNCAHYQKGGWWYNACAH 445
Db   393 SSEELNYRIHLKGLTGTAGKISSISQPGNDFSTKDGNDKCICKCSQMLTGGWWFDACGP 452

Qy   446 SNLNGVWYRGGHYRSRYQDGVYWAEFRGGSYSLKKVVMMIRP 487
Db   453 SNLNGMYYPQRQNTNKF-NGIKWYYWKGSGYSLKATTMWIRP 493

RESULT 6
AGP1_HUMAN
ID   AGP1_HUMAN   STANDARD;   PRT;   498 AA.
AC   Q15389;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Angiopoietin-1 precursor (ANG-1).
GN   ANGPT1 OR KIAA0003.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A., AND VARIANT GLY-269 DEL.
RC   TISSUE=Fetal lung;
RX   MEDLINE=97134663; PubMed=8980223;
RA   Davis S., Aldrich T.H., Jones P.F., Acheson A., Compton D.L., Jain V.,
RA   Ryan T.E., Bruno J., Radziejewski C., Maisonpierre P.C.,
RA   Yancopoulos G.D.;
RT   "Isolation of angiopoietin-1, a ligand for the TIE2 receptor, by
RT   secretion-trap expression cloning.";
RL   Cell 87:1161-1169(1996).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=22158633; PubMed=12168954;
RA   Nakajima D., Okazaki N., Yamakawa H., Kikuno R., Ohara O., Nagase T.;
RT   "Construction of expression-ready cDNA clones for KIAA cDNA clones:
RT   curation of 330 KIAA cDNA clones for KIAA genes: manual
RT   curation of 330 KIAA cDNA clones.";
RL   DNA Res. 9:99-106(2002).
RN   [3]
RP   SEQUENCE OF 307-498 FROM N.A.
RC   TISSUE=Bone marrow;
RX   MEDLINE=96051387; PubMed=7584026;

RA   Nomura N., Miyajima N., Sazuka T., Tanaka A., Kawarabayashi Y.,
RA   Sato S., Nagase T., Seki N., Ishikawa K.-I., Tabata S.;
RT   "Prediction of the coding sequences of unidentified human genes. I.
RT   The coding sequences of 40 new genes (KIAA0001-KIAA0040) deduced by
RT   analysis of randomly sampled cDNA clones from human immature myeloid
RT   cell line KG-1.";
RL   DNA Res. 1:27-35(1994).
RN   [4]
RP   SEQUENCE FROM N.A., AND VARIANT GLY-269 DEL.
RA   Nakatsukasa M., Komai K., Shiozawa S.;
RT   "Human angiopoietin-1 mRNA variant form.";
RL   Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
RN   [5]
RP   SEQUENCE FROM N.A. AND VARIANT GLY-269 DEL.
RA   Shan Z.X., Yu X.Y., Lin Q.Y., Fu Y.H., Tan H.H., Zheng M., Lin S.G.;
RT   "Human angiopoietin-1 mRNA variant forms.";
RL   Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: BINDS AND ACTIVATES TIE2 RECEPTOR BY INDUCING ITS
CC   TYROSINE PHOSPHORYLATION. IMPLICATED IN ENDOTHELIAL DEVELOPMENTAL
CC   PROCESSES LATER AND DISTINCT FROM THAT OF VEGF. APPEARS TO PLAY A
CC   CRUCIAL ROLE IN MEDIATING RECIPROCAL INTERACTIONS BETWEEN THE
CC   ENDOTHELIUM AND SURROUNDING MATRIX AND MESENCHYME. MEDIATES BLOOD
CC   VESSEL MATURATION/STABILITY. IT MAY PLAY AN IMPORTANT ROLE IN THE
CC   HEART EARLY DEVELOPMENT.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- PTM: Glycosylated.
CC   -!- MISCELLANEOUS: IT MAY HAVE A POTENTIAL THERAPEUTIC UTILITY SINCE
CC   IT CAN BE USED FOR SPECIFICALLY TARGETING TUMOR VASCULATURE OR FOR
CC   PROMOTING ANGIOGENIC PROCESSES IN CERTAIN ORGANS SUCH AS AN
CC   ISCHEMIC HEART.
CC   -!- SIMILARITY: Contains 1 fibrinogen C-terminal domain.
CC   --
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   the European Bioinformatics Institute. There are no restrictions on its
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   --
DR   EMBL; U83508; AAB50557.1; -.
DR   EMBL; D13628; BAA02793.2; ALT_INIT.
DR   EMBL; AB084554; BAB91325.1; -.
DR   EMBL; AY121504; AAM81745.1; -.
DR   EMBL; AY124380; AAM92271.1; -.
DR   HSSP; P02671; 1FZD.
DR   Genew; HGNC:484; ANGPT1.
DR   MIM; 601667; -.
DR   GO; GO:0005102; F:receptor binding; TAS.
DR   GO; GO:0007165; P:signal transduction; TAS.
DR   InterPro; IPR002181; Fibrinogen_C.
DR   Pfam; PF00147; fibrinogen_C; 1.
DR   SMART; SM00186; FBG; 1.
DR   PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1.
KW   Angiogenesis; Glycoprotein; Coiled coil; Signal; Polymorphism.
FT   SIGNAL   1   15   POTENTIAL.
FT   CHAIN   16   498   ANGIOPOIETIN-1.
FT   DOMAIN   81   119   COILED COIL (POTENTIAL).
FT   DOMAIN   153   261   COILED COIL (POTENTIAL).
FT   DOMAIN   284   498   FIBRINOGEN C-TERMINAL.
FT   DISULFID   286   315   BY SIMILARITY.
FT   DISULFID   439   452   BY SIMILARITY.
FT   CARBOHYD   92   92   N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD   122   122   N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD   154   154   N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD   243   243   N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD   295   295   N-LINKED (GLCNAC...) (POTENTIAL).
FT   VARIANT   269   269   Missing (in cell line T98G; may be due to
FT   exon slippage).
FT   /FTId=VAR_009940.
SQ   SEQUENCE   498 AA; 57513 MW; 5D5FA63AEF6BE920 CRC64;

Query Match   21.3%; Score 572.5; DB 1; Length 498;

Best Local Similarity   29.4%;
Matches 149; Conservative 85; Mismatches 169; Indels 103; Gaps 15;
Pred. No. 1.7e-28;

Qy   43 RYKRAGESQDKCTYTFIVPQ-------------QRVTGAICVNSK--EP---------EVL 79
         |||: ::|| ||: : |:| : | |: || | | |||
Db   32 RYNRIQHGQ--CAYTFLPEHDGNCRESTTDQYNTNAIQRDAPHVEPDFSSQKLQHLEHV 89

Qy   80 LENRVHKQELELLNNELLK-QKRQIETLQQ---------LVRVDGGIVSEVKLLRKESRN 129
         |: : || ||| : |||| ||:||| ||| |||| : ||| | ||| | |
Db   90 MEN--YTQWLQKLENYIVENMKSEMAQIQQNAVQNHTATMLEIGTSLLSQI---AEQTRK 144

Qy 130 MNSRVTLQLYMQLLHEIIRKRDNALELSQLENRILNQTADMLQLASKYKDLEHKY----- 183
         |:||||| ||||| :|: |: |||: | ||:|||: : :||| |:|||| |||:
Db 145 LTDVETQVLNQTSRLEIQLLENSLSTYKLEKQLLQQTNEILKIHEKNSLLEEKILEMEGK 204

Qy 184 ------QHLATLAHNQSEIIAQLEEHCQRVPSARPVQPQPPAAPRVQPPTYN 231
               |||||||||||:|||| ||:|||||:| | :::: |:|| || |
Db 205 HKEELDTLKEEKENLQGLVTRQTYIIQELEKQLNRA------------------- 240

Qy 232 RIINQISTNEIQSDQNLKVLPPPLPIMPTLTIS-------LPSSTDKPSGPWRDCLQALE 283
          ::| ::| : | ::|:|| | | ||| |:| |||:|||||||||| ||||
Db 241 -TTNNSVLQKQQLEL---MDIVHNLVNLCTKEGVLLKGGKEEEKPFRDCADVYQ 291

Qy 284 DGHDTSSIYLVKPENTINRLMQVWCDQRHDPGGWTVIQRRLDGSVNFRNWETYKQGFGNI 343
         |||: ||||| ||:|:| ||| | |: | ||||||| | ||: ||:| |: |:||||:
Db 292 AGFNKSGIYTIYINNMEPRKVFCNMDVNGGGWTVIQHREDGSLDFQRGWKEYKMGFGNP 351

Qy 344 DGEYWLGLENIYWLTNQGNYKLLVTMEDWSGRKVFAEYASFRLEPESEYYKLRLGRYHGN 403
         |||||||:|| | ||:|:||:|: |: | ||:|:|| || || | :|||| |:||||||
Db 352 SGEYWLGNEFIFAITSQRQYMLRIELMDWEGNRAYSQYDRFHIGNEKQNYRLYLKGHTGT 411

Qy 404 AG---DSFTWHNGKQFTTLDRDHDVYTGNCAHYQKGGWWYNACAHSNLNGLWYWRGGHYRSR 461
         || |: | || |:| ||:|||:||||||: |:|||| |:| |:||||:| |||||| |
Db 412 AGKQSSLILH-GADFSTKDADNDNCMCKCALMLTGGWWFDACGPSLNGMYYTAGQNHGK 470

Qy 462 YQDGVTVWAEFRGGSYSLRKVVMMIRP 487
         | ||| ||||| ||||| | ||||||
Db 471 L-NGIKHYFKGPSYSLRSTTMMIRP 495

RESULT 7
AGP4_MOUSE
ID   AGP4_MOUSE   STANDARD;   PRT;   509 AA.
AC   Q9WVH6;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Angiopoietin-4 precursor (ANG-4) (ANG-3).
GN   ANGPT4 OR AGPT4 OR ANG3.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxId=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Myoblasts, and Uterus;
RX   MEDLINE=99162530; PubMed=10051567;
RA   Valenzuela D.M., Griffiths J.A., Rojas J., Aldrich T.H., Jones P.F.,
RA   Zhou H., McClain J., Copeland N.G., Gilbert D.J., Jenkins N.A.,
RA   Huang T., Papadopoulos N., Maisonpierre P.C., Davis S.,
RA   Yancopoulos G.D.;
RT   "Angiopoietins 3 and 4: diverging gene counterparts in mice and
RT   humans.";
RL   Proc. Natl. Acad. Sci. U.S.A. 96:1904-1909(1999).
CC   -!- FUNCTION: BINDS TO TYROSINE-PROTEIN KINASE RECEPTOR TIE2 AND MAY
CC   ACT AS AN ANTAGONIST.
CC   -!- SUBCELLULAR LOCATION: Secreted (Probable).
CC   -!- TISSUE SPECIFICITY: Widely expressed.
CC   -!- SIMILARITY: Contains 1 fibrinogen C-terminal domain.
CC   -!- CAUTION: Was originally (Ref.1) called angiopoietin-3.
CC   --
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CC   or send an email to license@isb-sib.ch).
CC
CC
DR   EMBL; AF113707; AAD21586.1; -.
DR   HSSP; P02671; 1FZD.
DR   MGD; MGI:1336887; Agpt4.
DR   Interpro; IPR002181; Fibrinogen_C.
DR   Pfam; PF00147; fibrinogen_C; 1.
DR   SMART; SM00186; FBG; 1.
DR   PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1.
KW   Coiled coil; Signal.
FT   SIGNAL        1     21       POTENTIAL.
FT   CHAIN        22    509       ANGIOPOIETIN-4.
FT   DOMAIN      181    269       COILED COIL (POTENTIAL).
FT   DOMAIN      294    480       FIBRINOGEN-LIKE.
FT   DISULFID    297    326       BY SIMILARITY.
FT   DISULFID    450    463       BY SIMILARITY.
SQ   SEQUENCE   509 AA;  57805 MW;  9B5A74A20A6664F6 CRC64;

Query Match    20.8%;  Score 558;  DB 1;  Length 509;
Best Local Similarity   29.1%;  Pred. No. 1.4e-27;
Matches  154;  Conservative  90;  Mismatches  195;  Indels  90;  Gaps  16;

Qy    13 LLAAMGAVAGQEDGDFBGTEEGSPREFIYLNRYKRAGESQDKCYTFIVPQQSVTGAIC--  70
            :||.:         ::|:               .|: .:|||:||::.    :||
Db    14 ----------HRGPEAGGHRQIHQVRR---------GQCSYTFVVPEP----DICQL  56

Qy    71 VNSKEPEVL--------------------LENRVHKQELELLNNE--LLKQKRQ 102
                                        :|:|:.::||.|:||||  .|::::.
Db    57 APTAAPEALGGSNSLQRDLPASRLHLTDWRAQRAQRVSQLEKILENNTQWLLKLBQS 116

Qy   103 I-------------ETLLQQ------LVKVDGGIVSBVKLLRKESRNMNSRVTQLYMQLLHEI 145
           :            ::||||      .:|.:.|:.  :::|.:.:.|:.|:||||:|:|
Db   117 IKVNLRSHLVQAQODI-ONQTTTMLALGANLMNQTK---AQTHKLTAVBAQVLNQTLHMK 173

Qy   146 IRXRDNALELSQLENRILNQTADMLQSLASKYKDLEHKYQHLATLAHNQSEIIAQLEEHCQ 205
            :.:.|.|.:.|:|:||:::.:|.|:.:       .:::|.||.||:||.:|:.||:|:
Db   174 TQMLENSLSTNKLERQMLMQSRELQRLQGRNRALETRLQALE--AQHQAQ-LNSLQEKRE 230

Qy   206 RVPSARVPQPPPAAPRVYQPPTYNRL----INQISTNEI---QSDQNLKVLPPPLPTMP 259
                          .:.|:     :|   :.|.:.|:   |.:..|.:|.    |
Db   231 QLHSLLG----------HQTGTLANLKHNLHALSSNSSSLQQQOQQLTEFVQRLVRIV 278

Qy   260 TLTSLPSSTDKPSGPWRDCLQALEDGHDTSSIYLVKPENTNRLMQVWCDQRDHPGGWTVI 319
              :|.   |.|: .||.|  :|:.:|...:::.|.:....:|.||.|:|:.|.|||.|::|
Db   279 AQDQHPVSLKTPKPVFVQDCAEIKRSGVNTSGVTIYETNMTKPLKVFCDMETDGGGWTLI 338

Qy   320 QRRLDGSVNFRNWETYKQGFGNIDGEYWLGLENIVWILTNQGNYKLLVTMEDWSGRKVFA 379
           |:|.||||||:.||.||:||||:.:|:|||:|.:. |:|.:.:|:||:|:|||.||::.
Db   339 QHREDGSVNFQRTWEEYKEGFGNVAREHWLGNEAVHRLTSRTAYLLRVELHDWEGRQTSI 398

Qy   380 EYASFRLEPESEYYKLRLGRYHGNAG--DSFTWHNGKQFTTLDRDHDVYTGNCAHYQKGGW 438
           :|..|.|..:.: ::|.:.:.. ..:  :.||:.::: ||.:|.||:..:|||| :.|||
Db   399 QYENFQLGSERQRYSLSVNDSSSAGRKNSIAPQGTKFSTKDMDNDNCMCKCAQMLSGGW 458

Qy   439 WYNACAHSNLNGWYRGGHYRSRYQDGVYWAEFRGGSYSLKKVVMMIRP 487
           |::||..||||.:|  :|:.::|.:|:.|.::||.|||||:.:|:||
Db   459 WFDACGLSNLNGIYY-SVHQHLHKINGIRWHYFRGPSYSLHGTRMMLRP 506

RESULT 8
ID   AGP4_HUMAN    STANDARD;      PRT;   503 AA.
AC   Q9Y264; Q9H424;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Angiopoietin-4 precursor (ANG-4) (ANG-3).
GN   ANGPT4 OR ANG4 OR ANG3.
OS   Homo sapiens (Human).
```

Right column:

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OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Aorta;
RX   MEDLINE=99232854; PubMed=10218486;
RA   Nishimura M., Miki T., Yashima R., Yokoi N., Yano H., Sato Y.,
RA   Seino S.;
RT   "Angiopoietin-3, a novel member of the angiopoietin family.";
RL   FEBS Lett. 448:254-256(1999).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Ovary;
RX   MEDLINE=99162530; PubMed=10051567;
RA   Valenzuela D.M., Griffiths J.A., Rojas J., Aldrich T.H., Jones P.F.,
RA   Zhou H., McClain J., Copeland N.G., Gilbert D.J., Jenkins N.A.,
RA   Huang T., Papadopoulos N., Maisonpierre P.C., Davis S.,
RA   Yancopoulos G.D.;
RT   "Angiopoietins 3 and 4: diverging gene counterparts in mice and
RT   humans.";
RL   Proc. Natl. Acad. Sci. U.S.A. 96:1904-1909(1999).
RN   [3]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21638749; PubMed=11780052;
RA   Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,
RA   Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagguley C.L.,
RA   Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,
RA   Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
RA   Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,
RA   Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
RA   Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
RA   Coulson A., Coville G.J., Deadman R., Dhami P.D., Dunn M.,
RA   Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
RA   Grafham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,
RA   Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
RA   Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
RA   Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
RA   Lehvaeslaiho M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
RA   Marsh V.L., Martin S.L., McConnachie L.J., McLay K., McMurray A.A.,
RA   Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
RA   Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
RA   Phillimore B.J.C.T., Prathalingham S.R., Plumb R.W., Ramsay H.,
RA   Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Shownkeen R., Sims S.,
RA   Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,
RA   Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
RA   Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,
RA   Whitehead S.L., Whittaker P., Willey D.L., Williams S.A.,
RA   Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
RA   Rogers J.;
RT   "The DNA sequence and comparative analysis of human chromosome 20.";
RL   Nature 414:865-871(2001).
CC   -!- FUNCTION: BINDS TO TYROSINE-PROTEIN KINASE RECEPTOR TIE2 AND
CC       ACTIVATES IT.
CC   -!- SUBCELLULAR LOCATION: Secreted (Probable).
CC   -!- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN THE LUNG WITH MUCH LOWER
CC       LEVELS FOUND IN OTHER TISSUES.
CC   -!- SIMILARITY: Contains 1 fibrinogen C-terminal domain.
CC   -!- CAUTION: Was originally (Ref.1) called angiopoietin-3.
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```
DR   EMBL; AF074332; AAD31728.1; -.
DR   EMBL; AF113708; AAD21587.1; -.
DR   EMBL; AL161939; CAC09933.1; -.
DR   HSSP; P02671; 1FZD.
DR   Genew; HGNC:487; ANGPT4.
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DR   MIM; 603705; -.
DR   GO; GO:0030297; F:transmembrane receptor protein tyrosine kin...; NAS.
DR   InterPro; IPR002181; Fibrinogen_C.
DR   Pfam; PF00147; fibrinogen_C; 1.
DR   SMART; SM00186; FBG; 1.
DR   PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1.
KW   Coiled coil; Signal.
FT   SIGNAL        1     24       POTENTIAL.
FT   CHAIN        25    503       ANGIOPOIETIN-4.
FT   DOMAIN       84    238       COILED COIL (POTENTIAL).
FT   DOMAIN      287    474       FIBRINOGEN C-TERMINAL.
FT   DISULFID    291    320       BY SIMILARITY.
FT   DISULFID    444    457       BY SIMILARITY.
SQ   SEQUENCE   503 AA;  56848 MW;  79CE52F66B532340 CRC64;

Query Match             20.1%;  Score 541; DB 1;  Length 503;
Best Local Similarity   31.7%;  Pred. No. 1.5e-26;
Matches  148;  Conservative  83;  Mismatches 194;  Indels  42;  Gaps  13;

Qy     54 CTYTFIVPQQRVTGAICVNSKEPEVL------------KQ-ELELLNNE--LL  97
          ||:|||:|               |::|                  |:||
Db     43 CSYTFLLPKSEPCPGPGEVSRDSNTLQRESLANPLHLGKLPTQQVKQLEQALQNNT-QWLK 102

Qy     98 KQKRQIETL--------QQLVKVDGGIVSEV--KLLREKESRNMNSRVTQLYMQLLHEII 146
          :|:||            ||                |::|    |:| :||::||::|
Db    103 KLERAIKITLLRSKLEQVQQMAQNQTAPMLELGTSLLNQTTAQIR-KLTDMEAQLLNQTS 161

Qy    147 R---KRDNALELSQLENRILNQTADYLMQLASRYKDLEHKYQHLATLAHNGSEIIAQLEE 202
          |                :|::|  :|    |:
Db    162 RMDAQMPETFLSTNKLENQLLLQORQKLQOLQGQNSALEKRLQALET--KQQELASILSK 219

Qy    203 HCQRVPSARPVPQPPPRAPPRVYQPPTNYRIINQISTNEIQSDQNLKVLPPPLPTMPTLT 262
          |:|||                    |:|
Db    220 KAKLLNTL---SRQSAALTNIERGLRGVRHNSSLLQDQOHSLRQLLVLLRHLVQERANA 275

Qy    263 SLPSSTDKPSGPWRDCLQALEDGHDTSSIYLVKPENTNRLMQVWCDQHPDPGGWTVIQRR 322
          ::|      |   :|                  |:|
Db    276 SAPAPIMAGEQVFQDCAEIQRSGASASGVTIQVSNATKPRKVFCDLQSSGGRWTLIQRR 335

Qy    323 LDGSVNFPRNWETYKQGFGNIDGEYWLGLENIYWLTNQGNYKLLVTMEDWSGRKVFAEYA 382
          ||:|||:               |::|        ||   |:|      :|| |
Db    336 ENGTVNFQRNWKDYKQGFGDPAGEHWLGNEVVHQLIRRAAYSLRVELLQDWEGHEAYAQYE 395

Qy    383 SFRLEPESEYYKLRLGRYHGNAG--DSFTWHNGKQFTTLDRDHDVYTGNCAHYQKGGWWY 440
          :||   |       ||:|       |  |:||   |||  |:|  | |     ||:|||
Db    396 HFHLGSENQLYRLSVSGYSGSAGRQSSLVLQN-TSFSTLDSDNDHCLCKCAQVMSGGWWF 454

Qy    441 NACAHSNLNGVWYRGGHYRSRYQDGVYWAEFRGGSYSLKKVVMMIRP 487
          ::|         |:  |        ||         |
Db    455 DAGLSNLNGVYYHAPDNKYK-MDGIRWHYFKGPSYSLRASRMMIRP 500
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RT   fibrinogen-related gene, HFREP-1.";
RL   Biochem. Biophys. Res. Commun. 193:681-687(1993).
RN   [2]
RP   SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC   TISSUE=Liver;
RX   MEDLINE=21363035; PubMed=11470158;
RA   Hara H., Yoshimura H., Uchida S., Toyoda Y., Aoki M., Sakai Y.,
RA   Morimoto S., Shiokawa K.;
RT   "Molecular cloning and functional expression analysis of a cDNA for
RT   human hepassocin, a liver-specific protein with hepatocyte mitogenic
RT   activity.";
RL   Biochim. Biophys. Acta 1520:45-53(2001).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Liver;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length
RT   human and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC   -!- FUNCTION: Has hepatocyte mitogenic activity.
CC   -!- SUBUNIT: Homodimer (Probable).
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- TISSUE SPECIFICITY: Liver specific.
CC   -!- SIMILARITY: Contains 1 fibrinogen C-terminal domain.
CC   --------------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   or send an email to license@isb-sib.ch).
CC   --------------------------------------------------------------------------
DR   EMBL; D14446; BAA03336.1; -.
DR   EMBL; D87342; BAB70690.1; -.
DR   EMBL; BC007047; AAH07047.1; -.
DR   PIR; JN0596; JN0596.
DR   Genew; HGNC:3695; FGL1.
DR   HSSP; P02671; 1FZD.
DR   MIM; 605776; -.
DR   GO; GO:0005577; C:fibrinogen complex; TAS.
DR   InterPro; IPR002181; Fibrinogen_C.
DR   Pfam; PF00147; fibrinogen_C; 1.
DR   SMART; SM00186; FBG; 1.
DR   PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1.
KW   Signal.
FT   SIGNAL        1     22
FT   CHAIN        23    312       FIBRINOGEN-LIKE PROTEIN 1.
FT   DOMAIN       78    305       FIBRINOGEN C-TERMINAL.
FT   DOMAIN       26     26       INTERCHAIN
FT   DISULFID     26     26       INTERCHAIN (POTENTIAL).
FT   DISULFID     83    112       BY SIMILARITY.
FT   DISULFID    248    261       BY SIMILARITY.
FT   CONFLICT     15     15       I -> T (IN REF. 3).
FT   CONFLICT     15     15       I -> T (IN REF. 3).
FT   CONFLICT     69     69       N -> D (IN REF. 1).
FT   CONFLICT     72     72       V -> V (IN REF. 1).
FT   CONFLICT    105    105       P -> L (IN REF. 2).
```

```
RESULT 9
FGL1_HUMAN
ID   FGL1_HUMAN             STANDARD;      PRT;   312 AA.
AC   Q08830; Q96KW6; Q96QM6;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Fibrinogen-like protein 1 precursor (Hepatocyte-derived fibrinogen-
DE   related protein 1) (HFREP-1) (Hepassocin) (HP-041).
GN   FGL1 OR HFREP1.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Liver;
RX   MEDLINE=93209661; PubMed=8390249;
RA   Yamamoto T., Gotoh M., Sasaki H., Terada M., Kitajima M.,
RA   Hirohashi S.;
RT   "Molecular cloning and initial characterization of a novel
```

RESULT 10

```
ID   AGP2_PIG   STANDARD;   PRT;   496 AA.
AC   Q9BDY7;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Angiopoietin-2 precursor (ANG-2).
GN   ANGPT2.
OS   Sus scrofa (Pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX   NCBI_TaxID=9823;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21153163; PubMed=11230987;
RA   Kim I., Moon S.O., Han C.Y., Pak Y.K., Moon S.K., Kim J.J., Koh G.Y.;
RT   "The angiopoietin-tie2 system in coronary artery endothelium prevents
RT   oxidized low-density lipoprotein-induced apoptosis.";
RL   Cardiovasc. Res. 49:872-881(2001).
-!-  FUNCTION: BINDS TO TIE2 RECEPTOR AND COUNTERACTS BLOOD VESSEL
CC   MATURATION/STABILITY MEDIATED BY ANGIOPOIETIN-1. ITS FUNCTION MAY
CC   BE CONTEXT-DEPENDENT. IN THE ABSENCE OF ANGIOGENIC INDUCERS, SUCH
CC   AS VEGF, ANG2-MEDIATED LOOSENING OF CELL-MATRIX CONTACTS MAY
CC   INDUCE ENDOTHELIAL CELL APOPTOSIS WITH CONSEQUENT VASCULAR
CC   REGRESSION. IN CONCERT WITH VEGF, IT MAY FACILITATE ENDOTHELIAL
CC   CELL MIGRATION AND PROLIFERATION, THUS SERVING AS A PERMISSIVE
CC   ANGIOGENIC SIGNAL (By similarity).
-!-  SUBCELLULAR LOCATION: Secreted.
-!-  SIMILARITY: Contains 1 fibrinogen C-terminal domain.
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DR   EMBL; AF233228; AAK14993.1; -.
DR   HSSP; P02671; 1FZD.
DR   InterPro; IPR002181; Fibrinogen_C.
DR   Pfam; PF00147; fibrinogen_C; 1.
DR   SMART; SM00186; FBG; 1.
DR   PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1.
KW   Angiogenesis; Glycoprotein; Coiled coil; Signal.
FT   SIGNAL       1     18       POTENTIAL.
FT   CHAIN       19    496       ANGIOPOIETIN-2.
FT   DOMAIN     130    255       COILED COIL (POTENTIAL).
FT   DOMAIN     280    496       FIBRINOGEN C-TERMINAL.
FT   DISULFID   284    313       BY SIMILARITY.
FT   DISULFID   437    450       BY SIMILARITY.
FT   CARBOHYD    89     89       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD   119    119       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD   133    133       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD   151    151       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD   240    240       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD   304    304       N-LINKED (GLCNAC...) (POTENTIAL).
SQ   SEQUENCE   496 AA;  56911 MW;  33B02BE224FE6B9D CRC64;
```

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Query Match             20.0%;  Score 537;  DB 1;  Length 496;
Best Local Similarity   28.1%;  Pred. No. 2.6e-26;
  Matches  141;  Conservative  95;  Mismatches  182;  Indels  84;  Gaps  12;

Qy   42 NRYKRAGESQDK----------------CTYTFIVPQ---QRVTGAICVNSKEPEVLLENRVHKQE 88
         :::::                                      :::::       :::       :
Db   20 NNFRKSMDSTGKRQVQVQHGPCSYTFLLPETDNCRSPSSSSVSNAVQRDAPLDYDSVRR 79

Qy   89 LELLNN------------ELLK--------QKRQIETLLQQLVKDGGIVSEV--------- 120
         :::::             ::::         ::::
Db   80 LQVLENIMENNTQWLMKLESYIQDNMKKEMVEIQQNAVQNQTAVMLEIGTNLLNQTAEQT 139

Qy  121 -KLLRKESRSRNMNSRVTQLYMQLLHEIIRKRDNALELSQLENRILNQTADMIQLASKYKDL 179
          ::::                 :::::
Db  140 RKLTDVEAQVLN-QTTRLELQLL------EHSLSTNKLEKQILDQTSEINKLQDKNSFL 191

Qy  180 EHKYQHLLATLLAHNQSEIIAQLEEHCQRVPSARPVPQPPPAAPPRVVQPPPTYNRIINQIST 239
         ::                      :::::
Db  192 EKKVLDMEDKHIVQLQSIKEEKDQLQVLVSKQ-----------NSIIEELEK 232

Qy  240 NEIQSDQNLKVLPPP---LPTMPTLTSLPSSTDKPSGP----------------WRDCLQALEDGH 287
         :::::                ::::::::::::::                     ::::::::::
Db  233 QLVTATVNNSVLQKQQHDLMETVHNLLTMISTSNSAKHSLVAKEEQIIFRDCAEAFKSGL 292

Qy  288 DTSSIYLVKPENTNRLMQVWCDQRHDPGGWTVIQRRLDGSVNFFRNWETYKQGFGNIDGE 347
         ::::::::::::::::::::::::::::::::::::::::::::::::::
Db  293 TTSGTYTILTFPNSTEETKAYCDMETGGGGWTVIQRREDGSVDFQRTWKEYKQGFGPSGE 352

Qy  347 YWLGLENIYWLTNQGNYKLLVTMEDWSGRKVFAEYASFRLEPESEYYKLRLGRYHGNAGD 406
         ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db  353 HWLGNEFVSQVTNQKRYVLKIHLRDWEGNEAYSLYEHFYLSSSEFNYRIHLKGLTGTAGK 412

Qy  407 -SFTWHNGKQFTTLDRDHDVYTGNCAHYQKGGWWYNACAHSNLNGVWYRGGHYRSRYQDG 465
          ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db  413 ISSISQPGNDFSTCDADNDKCICKCCSQMLTGGWWFDACGPSNLNGMYYPQRQNTNKF-NG 471

Qy  466 VYWAEFRGGSYSLKKVVMMIRP 487
         :::::::::::::::::::::
Db  472 IKWYYWKGSGYSLKATTMMMIRP 493
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RESULT 11

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ID   AGP1_BOVIN   STANDARD;   PRT;   481 AA.
AC   O18920;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   28-FEB-2003 (Rel. 40, Last annotation update)
DE   Angiopoietin-1 precursor (ANG-1) (Fragment).
GN   ANGPT1 OR ANGI.
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Ovary;
RX   MEDLINE=99054348; PubMed=9840613;
```

Left-column alignment detail for RESULT 10 (query vs Db):

```
SQ   SEQUENCE   312 AA;  36391 MW;  26BC82124E6660C2 CRC64;

Query Match             20.0%;  Score 537;  DB 1;  Length 312;
Best Local Similarity   39.6%;  Pred. No. 1.5e-26;
  Matches  111;  Conservative  40;  Mismatches  89;  Indels  40;  Gaps  9;

Qy  232 RIINQISTNEIQ---------SDONLKVLPPLPTMPTLTSLPSSTDKPSGPFWRDCLQALEDGHD 287
         ||||                                        |||||||||||||||||
Db   50 KIKQLLOENEVQFLDKGDEN-----TVIDLGSKRQ-----YADCSEIFNDGYK 92

Qy  288 TSSIYLVKPENTNRLMQVWCDQRHDPGGWTVIQRRLDGSVNFFRNWETYKQGFGNI---D 344
         |:|||||||||||||||||||||| ||||||||||| ||||||| | ||||||
Db   93 LSGFYKIKPLQSPAEFSVYCDM-SDGGGWTVLQRRSDGSENFNRGWKDYENGFGNFVQKH 151

Qy  345 GEYWLGLENIYWLTNQGNYKLLVTMEDWSGRKVFAEYASFRLEPESEYYKLRLGRYHGNA 404
         |||||| :|| :|:|| |||:|: :  | :|: || || :    ||| | :|| :|
Db  152 GEYWLGNKNLHFITTQEDYTLKIDLADFEKNSRYAQYKNFKVGDEKNFYELNIGEYSGTA 211

Qy  405 GDSFT-------W-HNGKQFTTLDRDHDVYTGNCAHYQKGGWWYNACAHSNLNGVWY 453
         |||                 |||||||:|  ||| :   |||:| || ||||||| |
Db  212 GDSLAGNFHPEVQWWASHQRMKFSTWDRDHDNYEGNCAEEDQSGWWFNRCHSANLNGVYY 271

Qy  454 RGGHYRSRYQDGVYWAEFRGGSYSLKKVVMMIRPN---PN 490
          ||  |:    |:|| : :| | ||| ::| :|||
Db  272 -SGPYTAKTDNGIVWYHGWWYSLKSVVMKIRPNDFIPN 310
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RA   Goede V., Schmidt T., Kimmina S., Kozian D., Augustin H.G.;
RT   "Analysis of blood vessel maturation processes during cyclic ovarian
RT   angiogenesis.";
RL   Lab. Invest. 78:1385-1394(1998).
RN   [2]
RP   SEQUENCE OF 91-200 FROM N.A.
RC   TISSUE=Liver;
RX   MEDLINE=99451564; PubMed=9776732;
RA   Mandriota S.J., Pepper M.S.;
RT   "Regulation of angiopoietin-2 mRNA levels in bovine microvascular
RT   endothelial cells by cytokines and hypoxia.";
RL   Circ. Res. 83:852-859(1998).
CC   -!- FUNCTION: BINDS AND ACTIVATES TIE2 RECEPTOR BY INDUCING ITS
CC   TYROSINE PHOSPHORYLATION. IMPLICATED IN ENDOTHELIAL DEVELOPMENTAL
CC   PROCESSES LATER AND DISTINCT FROM THAT OF VEGF. APPEARS TO PLAY A
CC   CRUCIAL ROLE IN MEDIATING RECIPROCAL INTERACTIONS BETWEEN THE
CC   ENDOTHELIUM AND SURROUNDING MATRIX AND MESENCHYME. MEDIATES BLOOD
CC   VESSEL MATURATION/STABILITY. IT MAY PLAY AN IMPORTANT ROLE IN THE
CC   HEART EARLY DEVELOPMENT (BY SIMILARITY).
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- DEVELOPMENTAL STAGE: Found to be expressed throughout the ovarian
CC   cycle.
CC   -!- SIMILARITY: Contains 1 fibrinogen C-terminal domain.
CC
DR   EMBL; AF093573; AAC61872.1; -.
DR   EMBL; AF032223; AAC78845.1; -.
DR   HSSP; P02671; 1FZD.
DR   InterPro; IPR002181; Fibrinogen_C.
DR   Pfam; PF00147; fibrinogen_C; 1.
DR   SMART; SM00186; FBG; 1.
DR   PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1.
KW   Angiogenesis; Glycoprotein; Coiled coil; Signal.
FT   SIGNAL   1   15   POTENTIAL.
FT   CHAIN   16   >481   ANGIOPOIETIN-1.
FT   DOMAIN   153   261   COILED COIL (POTENTIAL).
FT   DOMAIN   283   >481   FIBRINOGEN C-TERMINAL.
FT   DISULFID   285   314   BY SIMILARITY.
FT   DISULFID   438   451   BY SIMILARITY.
FT   CARBOHYD   92   92   N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD   122   122   N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD   154   154   N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD   243   243   N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD   294   294   N-LINKED (GLCNAC...) (POTENTIAL).
FT   NON_TER   481   481
SQ   SEQUENCE   481 AA; 55556 MW; 8EEC9ED84FC2BB50 CRC64;

Query Match   20.0%; Score 536.5; DB 1; Length 481;
Best Local Similarity   28.5%;
Matches 146; Conservative   86; Mismatches 186; Indels   95; Gaps   16;

Qy   14 LAAMGAVAGQEDGFEGTEEGSPREFIYLNRYKRAGESQDKCIYTEIVPQ-----QRVTG 67
Db   10 LAAILTHIGCSNQRSPENGG------RRYNRIQHGQ--CAYTFLPEHDGNCRESTTD 60

Qy   68 AICVNSKE------PEV------LLENRVHKQELELLNNELIK-QKRQIETLQQ- 108
Db   61 QYNTNALQRDAPHVEQDFSSQKLQHLEHVMEN--YTQWLQKIENYIVENMKSEMAQIQQN 118

Qy   109 ------LVKVDGGIVSEVKLLRKESRNMNSRVTQLYMQLLHEIIRKRDNALELSQLEN 160
Db   119 AVQNHTATMLEIGTSLLSQT--AEQTKLIDVETQVLNQTSRLEIQLLENSLSTYKLEK 175

Qy   161 RIINQTADMLQLASKYKDLEHKY-----------QHLATLAHNQSEIIAQLEE 202
Db   176 QLLQQTNEILKIHEKNSLLEHKIFEMEGKHKEELDTLKEEKENLQGIVTRQTYIIQELEK 235

RESULT 12
AGP2_MOUSE

ID   AGP2_MOUSE   STANDARD;   PRT;   496 AA.
AC   O35608;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Angiopoietin-2 precursor (ANG-2).
GN   ANGPT2 OR AGPT2.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Uterus;
RX   MEDLINE=97349327; PubMed=9204896;
RA   Maisonpierre P.C., Suri C., Jones P.F., Bartunkova S., Wiegand S.J.,
RA   Radziejewski C., Compton D.L., McClain J., Aldrich T.H.,
RA   Papadopoulos N., Daly T.J., Davis S., Sato T.N., Yancopoulos G.D.;
RT   "Angiopoietin-2, a natural antagonist for Tie2 that disrupts in vivo
RT   angiogenesis.";
RL   Science 277:55-60(1997).
CC   -!- FUNCTION: BINDS TO TIE2 RECEPTOR AND COUNTERACTS BLOOD VESSEL
CC   MATURATION/STABILITY MEDIATED BY ANGIOPOIETIN-1. ITS FUNCTION MAY
CC   BE CONTEXT-DEPENDENT. IN THE ABSENCE OF ANGIOGENIC INDUCERS, SUCH
CC   AS VEGF, ANG2-MEDIATED LOOSENING OF CELL-MATRIX CONTACTS MAY
CC   INDUCE ENDOTHELIAL CELL APOPTOSIS WITH CONSEQUENT VASCULAR
CC   REGRESSION. IN CONCERT WITH VEGF, IT MAY FACILITATE ENDOTHELIAL
CC   CELL MIGRATION AND PROLIFERATION, THUS SERVING AS A PERMISSIVE
CC   ANGIOGENIC SIGNAL.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- TISSUE SPECIFICITY: Expressed only at sites of vascular
CC   remodeling.
CC   -!- SIMILARITY: Contains 1 fibrinogen C-terminal domain.
CC
DR   EMBL; AF004326; AAB63189.1; -.
DR   HSSP; P02671; 1FZD.
DR   MGD; MGI:1202890; Agpt2.
DR   InterPro; IPR002181; Fibrinogen_C.
DR   Pfam; PF00147; fibrinogen_C; 1.
DR   SMART; SM00186; FBG; 1.
DR   PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1.

Qy   203 HCQRVPSAAPVPQPPPAAPPRVSQPPTYNRIINQISTNEIQSDQNLKVLPPLPTMPPLIT 262
Db   236 QLNRATTNNSVLQ-----KQQLELMDTVHNLVN-LCTKEV----- 269

Qy   263 SLPSSTDKPSGPWRDCLQALEGCHDTSSIYLVKPENINRLMQVWCDQRHDPGGWTVIQRR 322
Db   270 LLKGGKRKEEKPFRDCADVYQAGFNKSGIYTIYINNMPEPKKVFCDMDLNGGGWTVIQHR 329

Qy   323 LDGSVNFRNWETYKQGFGNIDGEYWLGLENIYWLTNQGNYKLLVTIMEDWSGRKVFAEYA 382
Db   330 EDGSLDFQRGWKEYKMGFGNPSGEYWLGNEFIFAITSQRQYTLRIELLDWEGNRAYSQYD 389

Qy   383 SFRLEPESSEYYKLRLGRYHGNAG--DSFTWHNGKQFTTLDRDHDVYTGNCAHYQKGGWWY 440
Db   390 RFHIGNEKQNYRLYLKGHTGTAGKQSSLIH-GADFSTKDADNDNCMCKCALMLTGGWWF 448

Qy   441 NACAHSNLNGVWYRGGHYRSRYQDGVTWAERG 473
Db   449 DACGPSNLNGMFYTAGQNHGKL-NGIKWHYFKG 480

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KW   Angiogenesis; Glycoprotein; Coiled coil; Signal.
FT   SIGNAL        1     18
FT   CHAIN        19    496       ANGIOPOIETIN-2.
FT   DOMAIN      159    256       COILED COIL (POTENTIAL).
FT   DOMAIN      280    496       FIBRINOGEN C-TERMINAL.
FT   DISULFID    284    313       BY SIMILARITY.
FT   DISULFID    437    450       BY SIMILARITY.
FT   CARBOHYD     89     89       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD    119    119       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD    133    133       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD    151    151       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD    240    240       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD    304    304       N-LINKED (GLCNAC...) (POTENTIAL).
SQ   SEQUENCE   496 AA;  56616 MW;  FA3021PE4E01C410 CRC64;
```

```
Query Match    19.8%;  Score 535.5;  DB 1;  Length 496;
Best Local Similarity   28.9%;
Matches  144;  Conservative  82;  Mismatches  163;  Indels  109;  Gaps  15;
Pred. No. 3.3e-26;
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Qy   54  CYTFIVPQQRVTGAICVNSKEEVLLENRVHK-------QELELLNN------EL  96
             |||||:::|                             ||:||:|
Db   41  CSYTFLLPET-----DSCRSSSSP--YMSNAVQRDAPLDYDDSVQRLQVLENILENNTQWL  94

Qy   97  LK------------QKRQIETLQQLVKVDGGIVSEV------------KLLRKESRNMNSRV 134
            ::               ::|:|:||:    |:|               ::|:|:
Db   95  MKLENYIQDNMKKEMVEIQQNVVQNQTAVMIEIGTSLLNQTAAQTRKLTDVERQVLN-QT  153

Qy  135  TQLYMQLLHEIIRKRDNALELSQLENRILNQTADMLQLASKYKDLEHKY----------  183
            ||:||::::|:| ||:||:|:|||||:|||:|::|:||:|:::|||
Db  154  TRLELQLL-------QHSISTNKLEKQILDQISEINKLQNKNSFLEQKVLDMEGKHSSBOL 206

Qy  184  ------QHLATLAHNQSEIIAQLEEHCQRVPSARPVPQPPPAAPPRVYQPPTYNRIINQ  236
                :::|:||      ::|:|||:                   :|::|
Db  207  QSMKEQKDELQVIVSKQSSVIDELE---KKLVTA--------------TVNNSLLQ     245

Qy  237  ISTNEIQSDQNLKVLPPPLPTMPTLTSLPSSTD------KPSGPWRDCLQALEDGHDTSS  290
Db  246  KQOHDLMETVN------------SLLTMMSSPNSKSSVAIRKEBEQTTFRDCAEIFKSGLTTSG 296

Qy  291  IYIVKPENTNRLMQVWCDQRDHDPGGWTVIQRRLDGSVNFFRNWETYKQGFGNIDGEYWLG  350
Db  297  IYTLTFPNSTEIKAYCDMDVGGGGWTVIQHREDGSVDFQRTWKEYKEGFGNPLGEYWLG   356

Qy  351  LENIYWLTNQGNYKLLVIVMEDWSGRKVFAEYASFRLEPESEYYKLRLGRYHGNAGD-SFT  409
Db  357  NEFVSQLTGQHRVLKIQLKDWEGNEAHSLYDHFYLAGEESNYRIHLTGLTGTAAKISSI   416

Qy  410  WHNGKQFTTLDRDHDVYTGNCAHYQKGGWWYNACAHSNLNGVWYRGGHYRSRYQDGGYVWA  469
Db  417  SQPGSDFSTKDSDNDKCICKCSQMLSGGWWFDACGPSNLNGQYYPQKQNTNKE-NGIKWY   475

Qy  470  EFRGGSYSLKKVVMMIRP 487
Db  476  YWKGSGYSLKATIMMIRP 493
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RESULT 13
FIBB_BOVIN
ID   FIBB_BOVIN     STANDARD;      PRT;   468 AA.
AC   P02676;
DT   21-JUL-1986 (Rel. 01, Created)
DT   01-FEB-1996 (Rel. 33, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Fibrinogen beta chain precursor [Contains: Fibrinopeptide B].
GN   FGB.
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   SEQUENCE OF 1-4.
RA   Blomback B., Doolittle R.F.;
RT   "The sequence of amino acids at the N-terminal end of bovine
RT   fibrinopeptide B.";
RL   Acta. Chem. Scand. 17:1816-1819(1963).
RN   [2]
RP   SEQUENCE OF 5-21.
RA   Sjoquist J., Blomback B., Wallen P.;
RT   "Amino acid sequence of bovine fibrinopeptides.";
RL   Ark. Kemi 16:425-436(1960).
RN   [3]
RP   SEQUENCE OF 22-53.
RX   MEDLINE=79164394; PubMed=434821;
RA   Martinelli R.A., Inglis A.S., Rubira M.R., Hageman T.C.,
RA   Hurrell J.G.R., Leach S.J., Scheraga H.A.;
RT   "Amino acid sequences of portions of the alpha and beta chains of
RT   bovine fibrinogen.";
RL   Arch. Biochem. Biophys. 192:27-32(1979).
RN   [4]
RP   SEQUENCE OF 44-468 FROM N.A.
RX   MEDLINE=81199473; PubMed=6262803;
RA   Chung D.W., Rixon M.W., McGillivray R.T.A., Davie E.W.;
RT   "Characterization of a cDNA clone coding for the beta chain of bovine
RT   fibrinogen.";
RL   Proc. Natl. Acad. Sci. U.S.A. 78:1466-1470(1981).
-!-  FUNCTION: Fibrinogen has a double function: yielding monomers that
     polymerize into fibrin and acting as a cofactor in platelet
     aggregation.
-!-  SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
     (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
-!-  PTM: Conversion of fibrinogen to fibrin is triggered by thrombin,
     which cleaves fibrinopeptides A and B from alpha and beta chains,
     and thus exposes the N-terminal polymerization sites responsible
     for the formation of the soft clot. The soft clot is converted
     into the hard clot by factor XIIIA which catalyzes the epsilon-
     (gamma-glutamyl)lysine cross-linking between gamma chains
     (stronger) and between alpha chains (weaker) of different
     monomers.
-!-  SIMILARITY: Contains 1 fibrinogen C-terminal domain.
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DR   EMBL; V00110; CAA23444.1; -.
DR   PDB; 1JY2; 22-MAY-02.
DR   PDB; 1JY3; 22-MAY-02.
DR   InterPro; IPR002181; Fibrinogen_C.
DR   Pfam; PF00147; fibrinogen_C; 1.
DR   SMART; SM00186; FBG; 1.
DR   PROSITE; PS00514; FIBRINOGEN_C_DOMAIN; 1.
DR   PROSITE; PS00515; FIBRINOGEN_C; 1.
KW   Blood coagulation; Plasma; Platelet; Glycoprotein; Sulfation;
KW   Pyrrolidone carboxylic acid; 3D-structure.
FT   PEPTIDE       1     21       FIBRINOPEPTIDE B.
FT   CHAIN        22    468       FIBRINOGEN BETA CHAIN.
FT   MOD_RES       1      1       PYROLIDONE CARBOXYLIC ACID.
FT   MOD_RES       6      6       SULFATION.
FT   SITE         21     22       CLEAVAGE (BY THROMBIN; RELEASE
FT                                FIBRINOPEPTIDE B).
FT   DISULFID     72     72       INTERCHAIN (WITH ALPHA).
FT   DISULFID     83     83       INTERCHAIN (WITH ALPHA).
FT   DISULFID     87     87       INTERCHAIN (WITH GAMMA).
FT   DISULFID    200    200       INTERCHAIN (WITH GAMMA).
FT   DISULFID    204    204       INTERCHAIN (WITH ALPHA).
FT   DISULFID    208    208       INTERCHAIN (WITH GAMMA).
FT   DISULFID    218    293       BY SIMILARITY.
FT   DISULFID    247    247       BY SIMILARITY.
FT   DISULFID    401    414       BY SIMILARITY.
FT   CARBOHYD    371    371       N-LINKED (GLCNAC...) (PROBABLE).
SQ   SEQUENCE   468 AA;  53340 MW;  2DED42F443AAA4B37 CRC64;

Query Match   19.6%;  Score 527.5;  DB 1;  Length 468;
```

Best Local Similarity 30.5%; Pred. No 9.6e-26;
Matches 135; Conservative 68; Mismatches 126; Indels 113; Gaps 12;

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Qy    92 LNNELLKQXR-----QIETLQQLVKVDGGIVSEVKLLRKESRNNNSRVTQLYMQLLHEIIR 147
                          |:|:            :||  |   | :   : | ::: |  |: 
Db    89 LQDTLVRQERPIRKSIEDLRNTV------DSVSRTSSSTFQYITLLRNMWK            133

Qy   148 KRDNALELSQLENRILNQTADMLQLASRYKYKDLEHKYQHLATLAHNQSEIIAQLEEHCQRV 207
                                                                           
Db   134 GRQNQV---QDNENVVNEYSSHLEKHQLYID------ETVKNN------               167

Qy   208 PSARPVPDQPPPAAPPRVTQPPTYNRIINQISTN------EIQSDQNLKVLPPLPTMPTL   261
            :|:                           |:||: 
Db   168 IPTKLRVLRSILENLRSKIQKLESDVSTQMEYCRTPCTVT-                      207

Qy   262 TSLPSSTDKPSGPWRDCLQALEDGHDTSSIYLVKPENTNRLMQVWCDQRHDPGGWTVIQR   321
              |      |      |:     :  :| ||| :  |  ||  |||||| |||||||||  
Db   208 CNIPVVSGK-----ECEKIIRNEGETSEMYLIQPEDSSKPYRVYCDMKTEKGGWTVIQN    261

Qy   322 RLDGSVNFRNWETYKQGFGNI----------DGEYWLGLENIYWLTNQGNYKLLVTM      369
         |:|||| | |  :|||| |||          :||||||:: | ||:| :  ||| 
Db   262 RQDGSVDFGRGRKWDPYKQGPGNIATNAEGKKYCGVPGEYWLGNDRISQLTNMGPTKLLEM 321

Qy   370 EDWGGRKVFAEYASFRLEPESEYYKLRLGRYHGNAGD-----------SFTWHNGKQ      415
         ||| | || | |     | : | || |  | ::|:              |||||  
Db   322 EDWKGDKVTALYEGFTVQNEANKYQLSVSKYKGTAGNALIEGASQLVGENRTWTIHNSMF   381

Qy   416 FTTLDRDHDVY------TGNCAHYQKGGWWYNACAHSNLNGVWYRGGHY-----RSRYQDG  465
          :| ||| |        | |  :  |||||| |  ::|||| | || |      | :  ||
Db   382 FSTYDRDNDGWKTDPRKQCSKEDGGGWWYNRCHAANPNGRYYWGGAYTWDMAKHGTDDG   441

Qy   466 VYWAEFRGGSYSLKKVVMMIRP 487
          |||   |||||::||  |||
Db   442 VVWMNWQGSWYSMKKMSMKIRP 463
```

RESULT 14
FIBB_HUMAN

```
ID   FIBB_HUMAN    STANDARD;    PRT;    491 AA.
AC   P02675;
DT   21-JUL-1986 (Rel. 01, Created)
DT   01-JUL-1993 (Rel. 26, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Fibrinogen beta chain precursor [Contains: Fibrinopeptide B].
GN   FGB.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
```

RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=91344740; PubMed=2102623;
RA   Chung D.W., Harris J.E., Davie E.W.;
RT   "Nucleotide sequences of the three genes coding for human
RT   fibrinogen.";
RL   (In) Liu C.Y., Chien S. (eds.);
RL   Fibrinogen, thrombosis, coagulation and fibrinolysis, pp.39-48,
RL   Plenum Press, New York (1991).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Chung D.W., Que B.G., Rixon M.W., Mace M. Jr., Davie E.W.;
RT   "Characterization of complementary deoxyribonucleic acid and genomic
RT   deoxyribonucleic acid for the beta chain of human fibrinogen.";
RL   Biochemistry 22:3244-3250(1983).
RN   [3]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=83283433; PubMed=6688356;
RA   Chung D.W., Que B.G., Rixon M.W., Mace M. Jr., Davie E.W.;
RN   [4]
RP   SEQUENCE FROM N.A., AND VARIANTS SER-100; HIS-170; LEU-265 AND
RP   LYS-478.
RA   Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Poel C.L., Yi Q.,
RA   Nickerson D.A.;
RL   Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
RN   [5]
RP   SEQUENCE OF 31-491, AND CARBOHYDRATE-LINKAGE SITE.
RA   Henschen A., Lottspeich F., Southan C., Topfer-Petersen E.;
RT   "Human fibrinogen: sequence, sulfur bridges, glycosylation and some
RT   structural variants.";
RL   (In) Peeters H. (eds.);
RL   Protides of the biological fluids, Proc. 28th colloquium, pp.51-56,
RL   Pergamon Press, Oxford (1980).
RN   [6]
RP   SEQUENCE OF 31-491.
RX   MEDLINE=79124640; PubMed=420779;
RA   Watt K.W.K., Takagi T., Doolittle R.F.;
RT   "Amino acid sequence of the beta chain of human fibrinogen.";
RL   Biochemistry 18:68-76(1979).
RN   [7]
RP   SEQUENCE OF 31-148, AND DISULFIDE BONDS.
RX   MEDLINE=76225080; PubMed=936108;
RA   Blombaeck B., Hessel B., Hogg D.;
RT   "Disulfide bridges in NH2-terminal part of human fibrinogen.";
RL   Thromb. Res. 8:639-658(1976).
RN   [8]
RP   SEQUENCE OF 1-38 FROM N.A.
RX   MEDLINE=87146483; PubMed=3029722;
RA   Huber P., Dalmon J., Courtois G., Laurent M., Assouline Z.,
RA   Marguerie G.;
RT   "Characterization of the 5'-flanking region for the human fibrinogen
RT   beta gene.";
RL   Nucleic Acids Res. 15:1615-1625(1987).
RN   [9]
RP   SEQUENCE OF 31-44.
RA   Blombaeck B., Grondahl N.J., Guthrie C., Hinton M.;
RT   "Studies on fibrinopeptides from primates.";
RL   Acta Chem. Scand. 19:1788-1789(1965).
RN   [10]
RP   REVIEW, AND DISULFIDE BONDS.
RX   MEDLINE=82254370; PubMed=6575689;
RA   Henschen A., Lottspeich F., Kehl M., Southan C.;
RT   "Covalent structure of fibrinogen.";
RL   Ann. N.Y. Acad. Sci. 408:28-43(1983).
RN   [11]
RP   DISULFIDE BONDS.
RX   MEDLINE=77245999; PubMed=891553;
RA   Gaardlund B., Hessel B., Marguerie G., Murano G., Blombaeck B.;
RT   "Primary structure of human fibrinogen. Characterization of
RT   disulfide-containing cyanogen-bromide fragments.";
RL   Eur. J. Biochem. 77:595-610(1977).
RN   [12]
RP   DISULFIDE BONDS.
RA   Doolittle R.F., Takagi T., Watt K.W.K., Bouma H. III, Cottrell B.A.,
RA   Cassman K.G., Goldbaum D.M., Doolittle L.R., Friezner S.J.;
RT   "The structures of fibrinogen and fibrin.";
RL   (In) Magnusson S., Ottesen M., Foltmann B., Dano K.,
RL   Neurath H. (eds.);
RL   Regulatory proteolytic enzymes and their inhibitors, pp.163-172,
RL   Pergamon Press, New York (1978).
RN   [13]
RP   REVIEW, EM STRUCTURE, POLYMERIZATION, AND LIGANDS.
RX   MEDLINE=84305751; PubMed=6383194;
RA   Doolittle R.F.;
RT   "Fibrinogen and fibrin.";
RL   Annu. Rev. Biochem. 53:195-229(1984).
RN   [14]
RP   X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS) OF 164-491.
RX   MEDLINE=97424408; PubMed=333233;
RA   Spraggon G., Everse S.J., Doolittle R.F.;
RT   "Crystal structures of fragment D from human fibrinogen and its
RT   crosslinked counterpart from fibrin.";
RL   Nature 389:455-462(1997).
RN   [15]

RP   X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 164-491.
RX   MEDLINE=98293395; PubMed=9628725;
RA   Everse S.J., Spraggon G., Veerapandian L., Riley M., Doolittle R.F.;
RT   "Crystal structure of fragment double-D from human fibrin with two
RT   different bound ligands.";
RL   Biochemistry 37:8637-8642(1998).
RN   [16]
RP   X-RAY CRYSTALLOGRAPHY.
RX   MEDLINE=99175089; PubMed=10074346;
RA   Everse S.J., Spraggon G., Veerapandian L., Doolittle R.F.;
RT   "Conformational changes in fragments D and double-D from human
RT   fibrin(ogen) upon binding the peptide ligand Gly-His-Arg-Pro-amide.";
RL   Biochemistry 38:2941-2946(1999).
RN   [17]
RP   INTERACTION WITH FBLN1.
RX   MEDLINE=95370284; PubMed=7642629;
RA   Tran H., Tanaka A., Litvinovich S.V., Medved L.V., Haudenschild C.C.,
RA   Argraves W.S.;
RT   "The interaction of fibulin-1 with fibrinogen. A potential role in
RT   hemostasis and thrombosis.";
RL   J. Biol. Chem. 270:19458-19464(1995).
RN   [18]
RP   VARIANT BALTIMORE-2 LYS-478.
RX   MEDLINE=89058942; PubMed=3194892;
RA   Schmelzer C.H., Ebert R.F., Bell W.R.;
RT   "A polymorphism at B beta 448 of fibrinogen identified during
RT   structural studies of fibrinogen Baltimore II.";
RL   Thromb. Res. 52:173-177(1988).
RN   [19]
RP   VARIANT ISE ARG-45.
RX   MEDLINE=91208409; PubMed=2018836;
RA   Yoshida N., Wada H., Morita K., Hirata H., Matsuda M., Yamazumi K.,
RA   Asakura S., Shirakawa S.;
RT   "A new congenital abnormal fibrinogen Ise characterized by the
RT   replacement of B beta glycine-15 by cysteine.";
RL   Blood 77:1958-1963(1991).
RN   [20]
RP   VARIANT NAPLES THR-98.
RX   MEDLINE=92340664; PubMed=1634610;
RA   Koopman J., Haverkate F., Lord S.T., Grimbergen J., Mannucci P.M.;
RT   "Molecular basis of fibrinogen Naples associated with defective
RT   thrombin binding and thrombophilia. Homozygous substitution of B beta
RT   68 Ala-->Thr.";
RL   J. Clin. Invest. 90:238-244(1992).
RN   [21]
RP   VARIANTS IJMUIDEN CYS-44 AND NIJMEGEN CYS-74.
RX   MEDLINE=92228809; PubMed=1565641;
RA   Koopman J., Haverkate F., Grimbergen J., Engesser L., Novakova I.,
RA   Kerst A.F.J.A., Lord S.T.;
RT   "Abnormal fibrinogens IJmuiden (B beta Arg14-->Cys) and Nijmegen (B
RT   beta Arg44-->Cys) form disulfide-linked fibrinogen-albumin
RT   complexes.";
RL   Proc. Natl. Acad. Sci. U.S.A. 89:3478-3482(1992).
RN   [22]
RP   VARIANT NEW YORK-1 39-GLY--LEU-102 DEL.
RX   MEDLINE=85157605; PubMed=3156856;
RA   Liu C.Y., Koehn J.A., Morgan F.J.;
RT   "Characterization of fibrinogen New York 1. A dysfunctional
RT   fibrinogen with a deletion of B beta(9-72) corresponding exactly to
RT   exon 2 of the gene.";
RL   J. Biol. Chem. 260:4390-4396(1985).
RN   [23]
RP   VARIANTS GLU-2, LEU-265 AND LYS-478.
RX   MEDLINE=99318093; PubMed=10091209;
RA   Cargill M., Altshuler D., Ireland J., Sklar P., Ardlie K., Patil N.,
RA   Shaw N., Lane C.R., Lim E.P., Kalyanaraman N., Nemesh J., Ziaugra L.,
RA   Friedland L., Rolfe A., Warrington J., Lipshutz R., Daley G.Q.,
RA   Lander E.S.;
RT   "Characterization of single-nucleotide polymorphisms in coding regions
RT   of human genes.";
RL   Nat. Genet. 22:231-238(1999).
RN   [24]
RP   ERRATUM.

RA   Cargill M., Altshuler D., Ireland J., Sklar P., Ardlie K., Patil N.,
RA   Shaw N., Lane C.R., Lim E.P., Kalyanaraman N., Nemesh J., Ziaugra L.,
RA   Friedland L., Rolfe A., Warrington J., Lipshutz R., Daley G.Q.,
RA   Lander E.S.;
RL   Nat. Genet. 23:373-373(1999).
RN   [25]
RP   VARIANTS CONGENITAL AFIBRINOGENEMIA ARG-383 AND ASP-430.
RX   MEDLINE=20129589; PubMed=10666208;
RA   Duga S., Asselta R., Santagostino E., Zeinali S., Simonic T.,
RA   Malcovati M., Mannucci P.M., Tenchini M.L.;
RT   "Missense mutations in the human beta fibrinogen gene cause
RT   congenital afibrinogenemia by impairing fibrinogen secretion.";
RL   Blood 95:1336-1341(2000).
RN   [26]
RP   VARIANT CONGENITAL AFIBRINOGENEMIA CYS-196.
RX   MEDLINE=21361164; PubMed=11461164;
RA   Lounes K.C., Lefkowitz J.B., Henschen-Edman A.H., Coates A.I.,
RA   Hantgan R.R., Lord S.T.;
RT   "The impaired polymerization of fibrinogen Longmont

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Query Match             19.6%;   Score 526.5;  DB 1;   Length 491;
Best Local Similarity   30.3%;   Pred. No. 1.2e-25;
Matches  138;  Conservative  64;  Mismatches  114;  Indels  139;  Gaps  16;

Qy   92 LNNELLKQKRQIETLLQQLVKVDGGIVSEVKLLRKESRNMNSRVTQL------YMQLLHEI 145

Db  112 LQEALLQQERPIRN-----SVD-----------------ELNNNVEAVSQTSSSSFQYMYLLKDL 154

Qy  146 IRKRDNALE-------LSQLENRIL-------NQTADMLQLASKYKDLLEHKYQHIAT 188

Db  155 WQXRQKQVRDNENVVNEYSSELEKHQLYIDETVNSNIPTNLRVLRSTLENLRSKIQKL-- 212

Qy  189 LAHNQSIIAQLEEHCQRVPSARPVPQPPAAPPRVYQPPTYNRIINQISTNEIQSDQNL 248

Db  213 ----ESDVSAQM-EYC-RTPCT----------------------VSCN------- 232

Qy  249 KVLPPPLPTMPLILTSLPSSTDKPSGPWRDCLQALEDGHDTSSIYLVKPENTNRLMQVWCD 308

Db  233 ------IPVV-----SG--KECEEIIRKGGETSEMYLLQPDSSVKPYRYVCD 271

Qy  309 QRHDPGGGWTVIQERLDGSVNFFRNWETYKQGFGNI------DGEYWLGLENIYW 356

Db  272 MNTENGGWTVIQNRQDGSVDFGRKWDYKQGFGNVAINTDGKNYCGLPGEYWIGNDKISQ 331

Qy  357 LTNQGNYXLLLVTMEDWSGRKVFAEYASFRLEPESEYYKLRLGRYHGNAGD---------- 406

Db  332 LTRMGPYELLIEMEDWKGDKVKAHYGGFTVQNEANKYQISVNKYRGTAGNALMDGASQLM 391

Qy  407 ----SFTWHNGKQFTTLDRDHDVYTGN------CAHYQKGGWWYNACAHSNLNGVWYRGGH 457

Db  392 GENRTMTIHNGMFFSTYDRDNDGWLTSDPRKQCSKEDGGGWWYNRCHAANPNGRYTWGGQ 451

Qy  458 Y-----RSRYQDGVYWAEFRGGSYSLKKVVMIRP 487

Db  452 YTWDMAKHGTDDGVVWMNWKGSWYSMRKMSMKIRP 486
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RESULT 15
FIBA_CHICK
ID   FIBA_CHICK   STANDARD;   PRT;   741 AA.
AC   P14448;
DT   01-JAN-1990 (Rel. 13, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Fibrinogen alpha/alpha-E chain precursor [Contains: Fibrinopeptide A].
GN   FGA.
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   SEQUENCE OF 1-4 FROM N.A.

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RA   Greininger G.;
RL   Submitted (FEB-1995) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE OF 5-741 FROM N.A.
RX   MEDLINE=90311369; PubMed=2367530;
RA   Weissbach L., Greininger G.;
RT   "Bipartite mRNA for chicken alpha-fibrinogen potentially encodes an
RT   amino acid sequence homologous to beta- and gamma-fibrinogens.";
RL   Proc. Natl. Acad. Sci. U.S.A. 87:5198-5202(1990).
RN   [3]
RP   SEQUENCE OF 19-33.
RX   MEDLINE=78187470; PubMed=655462;
RA   Takagi T., Finlayson J.S., Iwanaga S.;
RT   "Amino acid sequence of chicken fibrinopeptide A.";
RL   Biochim. Biophys. Acta 534:161-164(1978).
CC   -!- FUNCTION: Fibrinogen has a double function; yielding monomers that
CC       polymerize into fibrin and acting as a cofactor in platelet
CC       aggregation.
CC   -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
CC       (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=2;
CC       Name=Alpha-E;
CC         IsoId=P14448-1; Sequence=Displayed;
CC       Name=Alpha;
CC         IsoId=P14448-2; Sequence=VSP_001535, VSP_001536;
CC   -!- PTM: Conversion of fibrinogen to fibrin is triggered by thrombin,
CC       which cleaves fibrinopeptides A and B from alpha and beta chains,
CC       and thus exposes the N-terminal polymerization sites responsible
CC       for the formation of the soft clot.
CC   -!- SIMILARITY: Contains 1 fibrinogen C-terminal domain.
CC   ----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; U20803; AAB60686.1; -.
DR   EMBL; U20799; AAB60686.1; JOINED.
DR   EMBL; U20800; AAB60686.1; JOINED.
DR   EMBL; U20801; AAB60686.1; JOINED.
DR   EMBL; U20802; AAB60686.1; JOINED.
DR   EMBL; U20803; AAB60685.1; JOINED.
DR   EMBL; U20799; AAB60685.1; JOINED.
DR   EMBL; U20800; AAB60685.1; JOINED.
DR   EMBL; U20801; AAB60685.1; JOINED.
DR   EMBL; U20802; AAB60685.1; JOINED.
DR   EMBL; M34096; AAA99306.1; -.
DR   EMBL; M34096; AAA99307.1; -.
DR   PDB; 1EI3; 10-MAY-00.
DR   InterPro; IPR002181; Fibrinogen_C.
DR   Pfam; PF00147; fibrinogen_C; 1.
DR   PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1.
DR   SMART; SM00186; FBG; 1.
KW   Blood coagulation; Plasma; Signal; Alternative splicing;
KW   Pyrrolidone carboxylic acid; 3D-structure.
FT   SIGNAL        1     18
FT   PEPTIDE      19     33       FIBRINOPEPTIDE A.
FT   CHAIN        34    741       FIBRINOGEN ALPHA-E CHAIN.
FT   MOD_RES     741    741       PYRROLIDONE CARBOXYLIC ACID.
FT   DISULFID     46     46       INTERCHAIN (WITH ALPHA CHAIN)
FT                                (BY SIMILARITY).
FT   DISULFID     55     55       INTERCHAIN (WITH BETA CHAIN)
FT                                (BY SIMILARITY).
FT   DISULFID     64     64       INTERCHAIN (WITH GAMMA CHAIN)
FT                                (BY SIMILARITY).
FT   DISULFID     68     68       INTERCHAIN (WITH BETA CHAIN)
FT                                (BY SIMILARITY).
FT   DISULFID    180    180       INTERCHAIN (WITH GAMMA CHAIN)
FT                                (BY SIMILARITY).
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FT   DISULFID    184    184       INTERCHAIN (WITH BETA CHAIN)
FT                                (BY SIMILARITY).
FT   DISULFID    310    341       BY SIMILARITY.
FT   SITE         33     34       CLEAVAGE (BY THROMBIN).
FT   VARSPLIC    506    509       DCDD -> GTQK (in isoform Alpha).
FT                                /FTId=VSP_001535.
FT   VARSPLIC    510    741       Missing (in isoform Alpha).
FT                                /FTId=VSP_001536.
SQ   SEQUENCE   741 AA;  82438 MW;  A09F5F4F186DE3A6 CRC64;

Query Match            19.5%;  Score 524;  DB 1;  Length 741;
Best Local Similarity  40.6%;  Pred. No. 2.8e-25;
Matches  110;  Conservative  45;  Mismatches  84;  Indels  32;  Gaps  9;

Qy   242  IQSDQNLKVLPPPLPIPTMPTLITSLPSS-TDKPSGPWRDCLQALEDGHDT---SSIIVKPE  297
               ||  |    :      |:  |:  :         |  |||    |  | |:    |:||||
Db   474  VQHDQSAE-----DTPDFKARSFRPAAMSTRRSYNGKDC-DDIRQKHTSGAKSGIFKIKPE  528

Qy   298  NTNRLMQVWCDQRHDPGGWTVIQRRLDGSVNFFRNWETYKQGFGNID----GEYWLGLEN  353
          : |  ::|||          ||||||| | ||| :| || |:  |||    |||| |||
Db   529  GSNKVLSVYCDQETTLGGWLIQQRMDGSVNFNRTWQDYRRGFGSVDGKQGELWLGNEN  588

Qy   354  IYWLTNQGNYKLLVTMEDWSGRKVFAEYASFRLEPESEYYKLRLGRYHGNAGDS------  407
          | || ||  | |:|  |||||  |  |  |  ||  || |||  || ||  ||
Db   589  IHLLT-QNDTLLRVELEDWDGNAAAYAEYI-VQVGTEAEGYALTVSSYEGTAGDALVAGWL  646

Qy   408  ------FTWHNGKQFTTLDRDHDVYTGNCAHYQKGGWWYNACAHSNLNGVWYRGGHYRSRY  462
                |||||| ||: :||||| :|| || |  |||||| ||: ||||||| || ||| |
Db   647  EEGSEYTSHAQMQFSTFDRDQDHWEESCAEVYGGGWWYNSCQAANLNGIYYPGGHYDPRY  706

Qy   463  ------QDGVYWAEFRGGSYSLKKVVMMIRP  487
                | || | |:|   ||||| |:|| |
Db   707  NVPYEIENGVVWIPFRASDYSLKVVRMKIRP  737
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```
OM protein - protein search, using sw model

                                GenCore version 5.1.6
                                Copyright (c) 1993 - 2004 Compugen Ltd.

Run on:         July 30, 2004, 12:30:59 ; Search time 44 Seconds
                                (without alignments)
                                3535.238 Million cell updates/sec

Title:          US-10-018-386-2
Perfect score:  2686
Sequence:       1 MRPLCVTCWMLGLLAAMGAV..........GSYSLKKVVMMIRPNPNTFH 493

Scoring table:  BLOSUM62
                Gapop 10.0 , Gapext 0.5

Searched:       1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters:      1017041

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :      SPTREMBL_25:*
                1:  sp_archea:*
                2:  sp_bacteria:*
                3:  sp_fungi:*
                4:  sp_human:*
                5:  sp_invertebrate:*
                6:  sp_mammal:*
                7:  sp_mhc:*
                8:  sp_organelle:*
                9:  sp_phage:*
                10: sp_plant:*
                11: sp_rodent:*
                12: sp_virus:*
                13: sp_vertebrate:*
                14: sp_unclassified:*
                15: sp_rvirus:*
                16: sp_bacteriap:*
                17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2561	95.3	493	11	Q8BM09	Q8bm09 mus musculu
2	2546	94.8	493	11	Q9JT03	Q9jt03 rattus norv
3	1507.5	56.1	491	11	O95841	O95841 homo sapien
4	1333	50.4	236	4	Q8N2J9	Q8n2j9 homo sapien
5	1296	48.3	332	11	Q9CZZ8	Q9czz8 mus musculu
6	1245.5	46.4	484	13	Q7SXV7	Q7sxv7 brachydanio
7	1110	41.3	191	4	Q8NCH7	Q8nch7 homo sapien
8	1094.5	40.7	470	4	Q8NI99	Q8ni99 homo sapien
9	1090.5	40.6	470	4	Q9BZZ0	Q9bzz0 homo sapien
10	987	36.7	457	11	Q8R026	Q8r026 mus musculu
11	929	34.6	200	11	Q8BMV1	Q8bmv1 mus musculu
12	906.5	33.7	197	13	Q98UE9	Q98ue9 xenopus lae
13	588.5	21.9	513	13	Q90ZI9	Q90zi9 brachydanio
14	571.5	21.3	498	11	Q8C2K6	Q8c2k6 mus musculu
15	565	21.0	498	6	Q9BDY8	Q9bdy8 sus scrofa
16	558	20.8	461	4	Q8N539	Q8n539 homo sapien

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17  552    20.6   269  11  Q8BJE7   Q8bje7 mus musculu
18  550    20.5   269  11  Q8BL54   Q8bl54 mus musculu
19  549.5  20.5   431   6  Q95LU3   Q95lu3 macaca fasc
20  539.5  20.1   493  13  Q9DER2   Q9der2 gallus gall
21  538    20.0   312   4  Q8NG32   Q8ng32 homo sapien
22  536.5  20.0   337  11  Q8R1Q3   Q8r1q3 mus musculu
23  536.5  20.0   496  11  Q9D2D2   Q9d2d2 mus musculu
24  535    19.9   314  11  Q9U8W7   Q9u8w7 tachypleus
25  534.5  19.9   308   5  Q9VC25   Q9vc25 mus musculu
26  530.5  19.8   308  11  Q9U8W6   Q9u8w6 tachypleus
27  530.5  19.8   481  11  Q8K0E8   Q8k0e8 mus musculu
28  523.5  19.5   346   4  O43827   O43827 homo sapien
29  523.5  19.5   488  13  Q91589   Q91589 xenopus lae
30  522.5  19.5   441  13  Q9DER0   Q9der0 gallus gall
31  518    19.3   343  13  Q7ZXL3   Q7zxl3 xenopus lae
32  518    19.3   760  11  Q7ZTR1   Q7ztr1 xenopus lae
33  513.5  19.1   489  13  Q90ZI8   Q90zi8 brachydanio
34  511.5  19.0   407  13  Q9DER1   Q9der1 gallus gall
35  510    19.0   235   6  Q28763   Q28763 papio cynoc
36  510    19.0   782  11  Q7TQ70   Q7tq70 rattus norv
37  509.5  19.0   435  13  O93568   O93568 gallus gall
38  501.5  18.7   399   4  Q7Z664   Q7z664 homo sapien
39  499.5  18.6   407  13  Q9PU54   Q9pu54 gallus gall
40  499    18.6   439  13  Q7SZ13   Q7sz13 xenopus lae
41  498    18.5   321  11  Q7SYN8   Q7syn8 xenopus lae
42  497.5  18.5   431  13  Q7ZVG7   Q7zvg7 brachydanio
43  494    18.4   503  11  Q7TME5   Q7tme5 rattus norv
44  494    18.4   1358  4  Q92752   Q92752 homo sapien
45  494    18.4   1358  4  Q15568   Q15568 homo sapien
```

ALIGNMENTS

```
RESULT 1
Q8BM09
ID   Q8BM09           PRELIMINARY;       PRT;    493 AA.
AC   Q8BM09;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Angiopoietin-related protein 2 precursor.
GN   ANGPTL2.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Thymus;
RX   MEDLINE=22354681; PubMed=12466651;
RA   The FANTOM Consortium;
RA   the RIKEN Genome Exploration Research Group Phase I & II Team;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573(2002).
DR   EMBL; AK037265; BAC29780.1; -.
DR   MGD; MGI:1347002; Angptl2.
DR   InterPro; IPR002181; Fibrinogen_C.
DR   Pfam; PF00147; Fibrinogen_C; 1.
DR   SMART; SM00186; FBG; 1.
DR   PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1.
SQ   SEQUENCE   493 AA;   57105 MW;  2288AB4010746BF2 CRC64;

Query Match             95.3%;  Score 2561;  DB 11;  Length 493;
Best Local Similarity   95.1%;
Matches  469;  Conservative  9;  Mismatches  15;  Indels  0;  Gaps  0;

Qy    1  MRPLCVTCWMLGLLAAMGAVAGGEDGFGTEGCSPREFIYLNRYKRAGESQDKCTYTFIV  60
            |||||:|||||||||||||||:||||||||||  |||||:||||||||||||||||||
Db    1  MRPLCMTYWWLGLLATVGAATGPEADVEGTEDGSQRYIYLNRYKRAGESPDKCTYTFIV  60

Qy   61  PQQRVTGAICVNSKEPEVLLENRVHKQELELLNNELLKQKRQIETLQQLVKDGGIVSEV  120
```

```
Db     61 PQQRVTGAICVNSKEPEVHLENRVHKQELELLNNELLKQKRQIETLLQQLVEVDGGIVSEV 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     61 PQQRVTGAICVNSKEPEVHLENRVHKQELELLNNELLKQKRQIETLLQQLVEVDGGIVSEV 120

Db    121 KLLRKESRNMNSRVTQLYMQLLHEIIRKRDNALELSQLENRIINQTADMLQLASKYKDLE 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    121 KLLRKESRNMNSRVTQLYMQLLHEIIRKRDNALELSQLENRIINQTADMLQLASKYKDLE 180

Db    181 HKYQHLATLAHNQSEIIAQLEEHCQRVPSARPVPQPPPAAPPRVYQPPTYNRIINQISTN 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    181 HKYQHLATLAHNQSEIIAQLEEHCQRVPSARPVPQPPPAAPPRVYQPPTYNRIINQISTN 240

Db    241 EIQSDQNLKVLPPPLPTMPTLTSLPSSTDKPSGPWRDCLQALEDGHDTSSIYLVKPENTN 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    241 EIQSDQNLKVLPPPLPTMPTLTSLPSSTDKPSGPWRDCLQALEDGHDTSSIYLVKPENTN 300

Db    301 RLMQVWCDQRHDPGGWTVIQRRLDGSVNFFRNWETYKQGFGNIDGEYWLGLENIYWLTNQ 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    301 RLMQVWCDQRHDPGGWTVIQRRLDGSVNFFRNWETYKQGFGNIDGEYWLGLENIYWLTNQ 360

Db    361 GNYKLLVTMEDWSGRKVFAEYASFRLEPESEYYKLRLGRYHGNAGDSFTWHNGKQFTTLD 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    361 GNYKLLVTMEDWSGRKVFAEYASFRLEPESEYYKLRLGRYHGNAGDSFTWHNGKQFTTLD 420

Db    421 RDHDVYTGNCAHYQKGGWWYNACAHSNLNGVWYRGGHYRSRYQDGVYWAEFRGGSYSLKK 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    421 RDHDVYTGNCAHYQKGGWWYNACAHSNLNGVWYRGGHYRSRYQDGVYWAEFRGGSYSLKK 480

Db    481 VVMMIRPNPNTFH 493
          |||||||||||||
Qy    481 VVMMIRPNPNTFH 493
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RESULT 2
Q9JJ03

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ID   Q9JJ03;        PRELIMINARY;      PRT;    493 AA.
AC   Q9JJ03;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Angiotensin II type 1A receptor associated protein.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Wistar-Kyoto; TISSUE=Vascular smooth muscle;
RA   Guo D.F., Baranes D., Ono Y., Porter J.P., Abi-Jaoude E., Orlov S.N.,
RA   Inagami T.;
RT   "ARAP1 is required for recycling and resensitization of angiotensin II
RT   type 1A receptor.";
RL   Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF159049; AAF80364.1; -.
DR   HSSP; P02671; 1FZD.
DR   GO; GO:0004872; F:receptor activity; IEA.
DR   InterPro; IPR002181; Fibrinogen_C.
DR   Pfam; PF00147; Fibrinogen_C; 1.
DR   SMART; SM00186; FBG; 1.
DR   PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1.
KW   Receptor.
SQ   SEQUENCE   493 AA;  57159 MW;  7C37652C472B2341 CRC64;
```

Query Match   94.8%;   Score 2546; DB 11;   Length 493;
Best Local Similarity   94.5%;   Pred. No. 6e-170;
Matches 466; Conservative   9; Mismatches 18; Indels   0; Gaps   0;

```
Qy      1 MRPLCVTCVTCWLGLLAAMGAVAGQGDGFEGTEEGSPREFIYLNRYKRAGESQDKCTYFIV 60
          ||:||  ||| ||:||||||:|| |  ||| | |||||||:|||||||||||:||||||||
Db      1 MRPLCMTYWWLGLLATVGAVTGPEADVEGAEDGSQREIYLNRYKRAGESPDKCTYFIV 60

Qy     61 PQQRVTGAICVNSKEPEVHLENRVHKQELELLNNELLKQKRQIETLLQQLVEVDGGIVSEV 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 PQQRVTGAICVNSKEPEVHLENRVHKQELELLNNELLKQKRQIETLLQQLVEVDGGIVSEV 120
```

```
Qy    121 KLLRKESRNMNSRVTQLYMQLLHEIIRKRDNALELSQLENRIINQTADMLQLASKYKDLE 180
          |||||:|||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 KLVRKESRNMNSRVTQLYMQLLHEIIRKRDNALELSQLENRIINQTADMLQLVSKYKDLE 180

Qy    181 HKYQHLATLAHNQSEIIAQLEEHCQRVPSARPVPQPPPAAPPRVYQPPTYNRIINQISTN 240
          |||||||:||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 HKFQHLDMLAHNQSEVIAQLEEHCQRVPAARPVPQPPPAATPPRVYQPPTYNRIINQISTN 240

Qy    241 EIQSDQNLKVLPPPLPTMPTLTSLPSSTDKPSGPWRDCLQALEDGHDTSSIYLVKPENTN 300
          ||||||||:|||||:||||||||||||||||||||||||||||||||:||||||||||||
Db    241 EIQSDQNLKVLPPPLPTMPALTSLPSSTDKPSGPWRDCLQALEDGHGTSSIYLVKPENTN 300

Qy    301 RLMQVWCDQRHDPGGWTVIQRRLDGSVNFFRNWETYKQGFGNIDGEYWLGLENIYWLTNQ 360
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 RLMQVWCDQRHDPGGWTVIQRRLDGSVNFFRNWETYKQGFGNIDGEYWLGLENIYWLTNQ 360

Qy    361 GNYKLLVTMEDWSGRKVFAEYASFRLEPESEYYKLRLGRYHGNAGDSFTWHNGKQFTTLD 420
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 GNYKLLVTMEDWSGRKVFAEYASFRLEPESEYYKLRLGRYHGNAGDSFTWHNGKQFTTLD 420

Qy    421 RDHDVYTGNCAHYQKGGWWYNACAHSNLNGVWYRGGHYRSRYQDGVYWAEFRGGSYSLKK 480
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 RDHDVYTGNCAHYQKGGWWYNACAHSNLNGVWYRGGHYRSRYQDGVYWAEFRGGSYSLKK 480

Qy    481 VVMMIRPNPNTFH 493
          |||||||||||||
Db    481 VVMMIRPNPNTFH 493
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RESULT 3
O95841

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ID   O95841;        PRELIMINARY;      PRT;    491 AA.
AC   O95841;
DT   01-MAY-1999 (TrEMBLrel. 10, Created)
DT   01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Angiopoietin Y1 (DJ595C2.2) (Angiopoietin-related protein 1 precursor)
DE   (Angiopoietin-like 1).
GN   DJ595C2.2 OR ARP1.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Heart;
RX   MEDLINE=99148829; PubMed=10025962;
RA   Kim I., Kwak H.J., Ahn J.E., So J.N., Liu M., Koh K.N., Koh G.Y.;
RT   "Molecular cloning and characterization of a novel angiopoietin family
RT   protein, angiopoietin-3.";
RL   FEBS Lett. 443:353-356(1999).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Cobley V.;
RL   Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Placenta;
RA   Ota T., Nishikawa T., Kawai Y., Suzuki Y., Ishii S., Saito K.,
RA   Yamamoto J., Sugano S., Isogai T.;
RL   "HRI human cDNA sequencing project.";
RL   Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Placenta;
RA   Ito Y., Oike Y., Yasunaga K., Matsumoto S., Ota T., Nishikawa T.,
RA   Kawai Y., Isogai T., Hamada K., Saito Y., Miyata K., Masuho Y.,
RA   Suda T.;
RT   "Molecular cloning and characterization of novel angiopoietin-related
RT   protein (ARP4).";
RL   Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
RN   [5]
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RP   SEQUENCE FROM N.A.
RC   TISSUE=Ovary;
RA   Strausberg R.;
RL   Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF107253; AAD19608.1; -.
DR   EMBL; AL355520; CAC13169.1; -.
DR   EMBL; BC050476; AAH50476.1; -.
DR   EMBL; BC050640; AAH50640.1; -.
DR   HSSP; P02671; IFD.
DR   GO; GO:0005102; F:receptor binding; TAS.
DR   InterPro; IPR002181; Fibrinogen_C.
DR   Pfam; PF00147; fibrinogen_C; 1.
DR   SMART; SM00186; FBG; 1.
DR   PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1.
KW   Signal.
FT   SIGNAL   1   23   POTENTIAL.
FT   CHAIN   24   491   POTENTIAL.
SQ   SEQUENCE   491 AA; 56719 MW; 3C4DB9DEF6CF7E99 CRC64;

Query Match   56.1%; Score 1507.5; DB 4; Length 491;
Best Local Similarity   58.6%; Pred. No. 2.8e-97;
Matches 290; Conservative   69; Mismatches 109; Indels   27; Gaps   9;

Qy   9 WWLGLLAAMGAVAGQEDGFEGIEEGSPREF----IYLNRYKRAGESQD--KCTYTPIVP 61
Db   6 WTLGVLPFLLVDFGHCRG--------GQFKIKINQRYPRATDGKEBAAKCAYTFLVP 56

Qy   62 QQRVTGAICVNSKEPEV-LLENRVHKQELELINNELLKKQRQIETLQQLVKVDGGIVSEV 120
Db   57 EQRITGPICVNIKGQDASTIKDMITRMDLENLKDVLSRQKREIDVLQLVVDVDGNIVNEV 116

Qy 121 KLLRKESRNMNSRVTQLYMQLLHEIIIRKDNALELSQLENRIINQTADMLQLASKYKDLE 180
Db 117 KLLRKESRNMNSRVTQLYMQLLHEIIIRKRDNSLELSQLENKILNVTEMLKMATRYRPLE 176

Qy 181 HKYQHLAFILAHNQSEIIAQLEEHCQRVPSARPVPQPPP---AAPPRVYQPPYTNRIINQI 237
Db 177 VKYASLTDLVNNQSVMILLEEQCLRIFSRQDTHVSPPLVQVVPQHI--PNSQQYTPGLL 234

Qy 238 STNEIQSDQNL--KVLPPP-LPTMPTLT--SLPSSTDKPSGPWRDCLQALEDGHDTSSIY 292
Db 235 GGNEIQRDPGYPRDLMPPDLATSPTKSPFKIPPVTFINEGPFKDCQQAKEAGHSVSGIY 294

Qy 293 LVKPENTNRLMQVWCDQRHDPGGWTVIQCRRLDGSVNFFRNWETYKQGFGNIDGEYWLGLE 352
Db 295 MKPENSNGPMQLMCENSLDPGGWTVIQKRTDGSVNFFRNWENYKKGFGNIDGEYWLGLE 354

Qy 353 NIYWLTNQCNYKLLVTMEDWSGRKVFPAEYASSRLEPESEYYKLRLGRYHGNAGDSFTWHN 412
Db 355 NIYMLSNQDNYKLIIELEDWSDKKVVAEYSSFRLEPESEFYRLRLGTYQGNAGDSMWWHN 414

Qy 413 GKGQFTTLDRDHDVYTGNCAHYQKGGWWYNACAHSNLNGVWYRGGHYRSRYQDGVYWAEFR 472
Db 415 GKQFTTLDRDKDVYAGNCAHFHKGGWWYNACAHSNLNGVWYRGGHYRSKHQDGIFWAEYR 474

Qy 473 GGSYSLKKVVMMIRP 487
Db 475 GGSYSLRAVQMMIKP 489

RESULT 4
ID   Q8N2J9
AC   Q8N2J9;
DT   01-OCT-2002 (TrEMBLrel. 22, Created)
DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Hypothetical protein FLJ90545.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   TISSUE=Ovary;

RP   SEQUENCE FROM N.A.
RC   TISSUE=Ovarian carcinoma;
RA   Isogai T., Ota T., Nishikawa T., Hayashi K., Otsuki T., Sugiyama T.,
RA   Suzuki Y., Nagai K., Sugano S., Ishii S., Kawai-Hio Y., Saito K.,
RA   Yamamoto J., Wakamatsu A., Nakamura Y., Kojima S., Nagahari K.,
RA   Masuho Y., Ono T., Okano K., Yoshikawa Y., Aotsuka S., Sasaki N.,
RA   Hattori A., Okumura K., Iwayanagi T., Ninomiya K.;
RT   "NEDO human cDNA sequencing project.";
RL   Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AK075026; BAC11358.1; -.
DR   InterPro; IPR002181; Fibrinogen_C.
DR   Pfam; PF00147; fibrinogen_C; 1.
DR   SMART; SM00186; FBG; 1.
DR   PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1.
KW   Hypothetical protein.
SQ   SEQUENCE   236 AA; 27672 MW; CEB3AFA26CA12575 CRC64;

Query Match   50.4%; Score 1353; DB 4; Length 236;
Best Local Similarity 100.0%; Pred. No. 6.9e-87;
Matches 236; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy 258 MFTLTSLPSSTDKPSGPWRDCLQALEDGHDTSSIYLVKPENTNRLMQVWCDQRHDPGGWT 317
Db   1 MFTLTSLPSSTDKPSGPWRDCLQALEDGHDTSSIYLVKPENTNRLMQVWCDQRHDPGGWT 60

Qy 318 VIQCRRLDGSVNFFRNWETYKQGFGNIDGEYWLGLENIYWLTNQGNYKLLVTMEDWSGRKV 377
Db   61 VIQCRRLDGSVNFFRNWETYKQGFGNIDGEYWLGLENIYWLTNQGNYKLLVTMEDWSGRKV 120

Qy 378 FAEYASSRLEPESEYYKLRLGRYHGNAGDSFTWHNGKQFTTLDRDHDVYTGNCAHYQKGG 437
Db 121 FAEYASSRLEPESEYYKLRLGRYHGNAGDSFTWHNGKQFTTLDRDHDVYTGNCAHYQKGG 180

Qy 438 WWYNACAHSNLNGVWYRGGHYRSRYQDGVYWAEFRGGSYSLKKVVMMIRPNPNTFH 493
Db 181 WWYNACAHSNLNGVWYRGGHYRSRYQDGVYWAEFRGGSYSLKKVVMMIRPNPNTFH 236

RESULT 5
ID   Q9CZZ8
AC   Q9CZZ8;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   10 days embryo cDNA, RIKEN full-length enriched library,
DE   clone:2610304B20, full insert sequence.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Embryo;
RX   MEDLINE=21085660; PubMed=11217851;
RA   Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA   Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA   Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA   Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA   Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA   Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA   Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA   Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA   Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA   Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA   Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA   Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA   Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA   Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA   Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA   Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C.A., Wilming L.,
RA   Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA   Hayashizaki Y.;

Left column

RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL; AK011976; BAB27951.1; -.
SQ SEQUENCE 332 AA; 37221 MW; 9A6B464FCA613038 CRC64;

Query Match
Best Local Similarity 48.3%;
91.6%;
Matches 250; Conservative 9;

Score 1296; DB 11; Length 332;
Pred. No. 1.1e-82;
Mismatches 14; Indels 0; Gaps 0;

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Qy   1 MRPLCVTCWMLGLLAAMGAVAGQOEDGFEGGTEEBGSPREFIYLNRYXRAGESBSQDKCTYTFIV  60
Db   1 MRPLCMTYWWLGLLATVGBAATGPEADVEGTBDDGSQREVIYLNRYXRAGESPDKCTYTFIV     60

Qy  61 PQORVTGAICVNSKEPEVLLENRVHXQELELLNNELLKQKRQIETLQQLVKDGGIVSEV      120
Db  61 PQORVTGAICVNSKEPEVHLENRVHXQELELLNNELLKQKRQIETLQQLVEVDGGIVSEV     120

Qy 121 KLIRKESRNMNSRVTQLYMQLLIHEIIIRKRDNALELSQLENRILNQTADMLQLASKYKDLE   180
Db 121 KLIRKESRNMNSRVTQLYMQLLIHEIIIRKRDNALELSQLENRILNQTADMLQLASKYKDLE   180

Qy 181 HKYQHLATLAHNQSEIIAQLEEHCQRVPSARPVPQPPPAAPPRVYQPPTYNRIINQISTN    240
Db 181 HKFQHLAMLAHNQSEVIAQLEEHCQRVPAARPMPQPPPAAPPRVVQPPTYNRIINQISTN    240

Qy 241 EIQSDQNLKVLPPPLPMPTLTSLPSSTDKPSG  273
Db 241 EIQSDQNLKVLPPSLPTMPALTSLPSSTDKPSG 273
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RESULT 6
Q78XV7

ID Q78XV7 PRELIMINARY; PRT; 484 AA.
AC Q78XV7;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein (Fragment).
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AB; TISSUE=Body;
RX MEDLINE=22388257; PubMed=12477932;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=AB; TISSUE=Body;
RA Strausberg R.;
RL Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.
DR EMBL; BC055229; AAH55229.1; -.

Right column

KW Hypothetical protein.
FT NON_TER 1 1
SQ SEQUENCE 484 AA; 55444 MW; FDC3397A6B741768 CRC64;

Query Match
Best Local Similarity 46.4%;
49.0%;
Matches 236; Conservative 85;

Score 1245.5; DB 13; Length 484;
Pred. No. 6e-79;
Mismatches 138; Indels 23; Gaps 5;

```
Qy   8 CWWLGLLAAMGAVAGQOEDGFEGGTEEBGSPREFIYLNRYXRAGESQDKCTYTFIVPQQRVTG  67
Db  22 CWFLCVLWCVRISSSSRQRQMEAPDP-----------QRQQCSYTFLIPEQKITG          68

Qy  68 AICVNSKEPEVLLENRVHXQELELLNNELLKQKRQIETLQQLVKVDGGIVSEVKLLRKES    127
Db  69 PICA-SRGPSLEDPERVTRTDMSELRQTLSRQRREMETLRMMVDVDGDMVQEMKLLRKES    127

Qy 128 RNMNSRVTQLYMQLLHEIIIRKRDNALELSQLENRILNQTADMLQLASKYKDLEHKYQHLA   187
Db 128 RNMNSRVTQLYMQLLHEVLRKRDSSLELAALQNRLNGSAAALRLSAGYRELQQRVSVLA    187

Qy 188 TLAHNQSEIIAQLEEHCQRV--PSARPVPQPPPAAPPRVYQPPTYNRIINQISTNEIQSD   245
Db 188 ERVNSCQAELLALLEERCVRVYGRQSRDPPSLPQVLPENI--PVFVPRVSNEIQSNSWTEE  245

Qy 246 QNLKVLPPPLPMPTLTSLPSSTDKPSGPWRDCLQALEDGHDTSSIYLVKPENTNRLMQV    305
Db 246 QR-----PGAAAADTGERPAQNNSSLKGPFRDCYAALQAGHSVSGAILLQPDDTLTPVQA   300

Qy 306 WCDQRHDPGGWTVIQRLDGSVNFFRNWETYKQGFGNIDGEYWLGLENIYWLTNQGNYKL    365
Db 301 WCEHDVDRGGWTLIQRRKDGAVNFSRDWDSYXLGFGDVDGEHWLGLDTIYSLGRQEEYKL   360

Qy 366 LVTMEDWSGRKVFAEYASFRLEPESSYYKLRLGRYHGNAGDSFTWNGKQFTTLDRDHDV   425
Db 361 LVEMEDWMEKKVYAAYSSFHLEPESQSYRLRLGLYQGNAGDSLTSHNGRQFTTLDRDHDA   420

Qy 426 YTGNCAHYQKGGWWYNACAHSNLNGWYRGGHYRSRYQDGVYWABFRGGSYSLKKVVMMI   485
Db 421 FSGNCAHFQKGGWWYNACGQTNLNGWYSGGVYRSRFQDGIFWADYGGGFYSMKSVRMMI   480

Qy 486 RP 487
Db 481 RP 482
```

RESULT 7
Q8NCH7

ID Q8NCH7 PRELIMINARY; PRT; 191 AA.
AC Q8NCH7;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein FLJ90245.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.

RA Isogai T., Ota T., Nishikawa T., Hayashi K., Otsuki T., Sugiyama T.,
RA Suzuki Y., Nagai K., Sugano S., Ishii S., Kawai-Hio Y., Saito K.,
RA Yamamoto J., Wakamatsu A., Nakamura Y., Kojima S., Nagahari K.,
RA Masuho Y., Ono T., Okano K., Yoshikawa Y., Aotsuka S., Sasaki N.,
RA Hattori A., Okamura K., Iwayanagi T., Ninomiya K.;
RT "NEDO human cDNA sequencing project.";
RL Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AK074726; BAC11164.1; -.
DR InterPro; IPR002181; Fibrinogen_C.
DR Pfam; PF00147; Fibrinogen_C; 1.
DR SMART; SM00186; FBG; 1.
DR PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1.
KW Hypothetical protein.
SQ SEQUENCE 191 AA; 22717 MW; D050F4E25A57LF6A CRC64;

Query Match 41.3%; Score 1110; DB 4; Length 191;
Best Local Similarity 100.0%; Pred. No. 5,3e-70;
Matches 191; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy  303 MQVWCDQRHDPGGWTVIQRRLDGSVNFRNWETYKQGFGNIDGEYWLGLENIYWLTNQGN 362
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 MQVWCDQRHDPGGWTVIQRRLDGSVNFRNWETYKQGFGNIDGEYWLGLENIYWLTNQGN 60

Qy  363 YKLLVTMEDWSGRKVFAEYASFRLEPESSEYYKLRLGRYHGNAGDSFTWHNGKQFTTLDRD 422
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 YKLLVTMEDWSGRKVFAEYASFRLEPESSEYYKLRLGRYHGNAGDSFTWHNGKQFTTLDRD 120

Qy  423 HDVYTGNCAHYQKGGWWYNACAHSNLNGVWYRGGHYRSRYQDGVYWAEFRGGSYSLKKVV 482
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 HDVYTGNCAHYQKGGWWYNACAHSNLNGVWYRGGHYRSRYQDGVYWAEFRGGSYSLKKVV 180

Qy  483 MMIRPNPNTFH 493
        |||||||||||
Db  181 MMIRPNPNTFH 191
```

RESULT 8
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ID   Q8N199      PRELIMINARY;   PRT;   470 AA.
AC   Q8N199;
DT   01-OCT-2002 (TrEMBLrel. 22, Created)
DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   ARP3.
GN   ARP3.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Matsumoto S., Saito Y., Masuho Y., Oike Y., Suda T.;
RL   Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Oike Y., Suda T.;
RT   "Molecular cloning of ARP3.";
RL   Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AB054064; BAB91248.1; -.
DR   InterPro; IPR002181; Fibrinogen_C.
DR   Pfam; PF00147; fibrinogen_C; 1.
DR   SMART; SM00186; FBG; 1.
DR   PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1.
SQ   SEQUENCE   470 AA;  51694 MW;  FAD20B1B0096S239 CRC64;
```

Query Match 40.7%; Score 1094.5; DB 4; Length 470;
Best Local Similarity 46.3%; Pred. No. 2.1e-68;
Matches 213; Conservative 73; Mismatches 147; Indels 27; Gaps 7;

```
Qy   44 YKRAGESQDKCTYTFIVPQQRVTGAICVNSKEPEVLLENRVHKQELELLNNELLKQKRQI 103
        :|||| :  || |||:| ||:| ||:| : |  :  :   ::|: :||:|  :: ||: :|
Db   19 WARAG--APRCTYTFVLPPQKFTGAVCWSGPASTRATPEAANASELAALRMRVGRHEHL 76

Qy  104 ETLQOLVKVDGGIVSEVKLLRKESRNMNSRVTQLYMQLLHE------IIRKRDNALEL 155
        | |  |   |||:|  |:  |||||: :||:||||:||||||      ||||||||||
Db   77 RELQRLAAADGAVAGEVRALRKESRGLSARLGQLRAQLQHEAGPGAGPGADLGAEPAAL 136

Qy  156 SQLENRILNQTADMLQLASKYKDLEHKYQHLATLAHNQSEIIAQLEEHCQRVPSARPVPQ 215
        : |  |:||:::|  :  : ::: :  ::::  ::|:|| :::|||| : :|  :  ||
Db  137 ALLGERVLNASAEAQRAAARFHQLDVKFRELAQLVTQQSSLIARLERLCPGGAGGQQVL 196

Qy  216 PPPAAPPRVYQPPTYNRIINQISTN------EIQSDQNLKVLPPLPTMPTLTSLPSS 267
        ||| . |    | .   ::  :||     : ||| |||: ::
Db  197 PPPLVPVV---PV--RLVGSTSDTSRMLDPAEPEPRDQTQRQQEPMASPMP--AGHPAV 249

Qy  268 TDKPSGPWRDCLQALEDGHDTSSIYLVKPENTNRLMQVWCDQRHDPGGWTVIQRRLDGSV 327
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  268 TDKPSGPWRDCLQALEDGHDTSSIYLVKPENTNRLMQVWCDQRHDPGGWTVIQRRLDGSV 327
```

Db 250 PTKPVGPWQDCAEARQAGHEQGSGVYELRV--GRHVSVSWCEQQLEGGGWTVIQRRQDGSV 307

```
Qy  328 NFFRNWETYKQGFGNIDGEYWLGLENIYWLTNQGNYKLLVTMEDWSGRKVFAEYASFRLE 387
        |||:.|: |: || : ||||||||| :| : :.|::::|: |||.|| ..|||||:|||
Db  308 NFFTTWQHYKAGFPGRDDGEYWLGLEPVYQLITSRGDHELLVLLEDWGGRGARAHYDGFSLE 367

Qy  388 PESEYYKLRLGRYHGNAGDSFTWHNGKQFTTLDRDHDVYTGNCAHYQKGGWWYNACAHSN 447
        |||::|:||||:|||:|||| :||:.| |:|:||| |.|:|||| ||:|||||:.||||||
Db  368 PESDHYRLRLGCYHGDAGDSLSWHNDKPFSTVDRDRDSYSGNCALYQRGGWWYHACAHSN 427

Qy  448 LNGVWYRGGHYRSRYQDGVYWAEFRGGSYSLKKVVMMIRP 487
        ||||| :|||||||||||||||||||| :||:|  ||:||
Db  428 LNGVWHHGGHYRSRYQDGVYWAEFRGGAYSLRKAAMLIRP 467
```

RESULT 9
```
ID   Q9BZZ0      PRELIMINARY;   PRT;   470 AA.
AC   Q9BZZ0;
DT   01-JUN-2001 (TrEMBLrel. 17, Created).
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   Angiopoietin-related protein 5.
GN   ARP5.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Samal B., Wu C., Dias P., Singh S.;
RT   "Molecular cloning of a novel angiopoietin-related protein.";
RL   Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF230330; AAK06404.1; -.
DR   HSSP; P02671; 1FZD.
DR   InterPro; IPR002181; Fibrinogen_C.
DR   Pfam; PF00147; fibrinogen_C; 1.
DR   SMART; SM00186; FBG; 1.
DR   PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1.
SQ   SEQUENCE   470 AA;  51693 MW;  FD64AA8DA6B6518F CRC64;
```

Query Match 40.6%; Score 1090.5; DB 4; Length 470;
Best Local Similarity 46.1%; Pred. No. 4.1e-68;
Matches 212; Conservative 74; Mismatches 147; Indels 27; Gaps 7;

```
Qy   44 YKRAGESQDKCTYTFIVPQQRVTGAICVNSKEPEVLLENRVHKQELELLNNELLKQKRQI 103
        :|||| :  || |||:| ||:| ||:| : |  :  :   ::|: :||:|  :: ||: :|
Db   19 WARAG--APRCTYTFVLPPQKFTGAVCWSGPASTRATPEAANASELAALRMRVGRHEHL 76

Qy  104 ETLQOLVKVDGGIVSEVKLLRKESRNMNSRVTQLYMQLLHE------IIRKRDNALEL 155
        | |  |   |||:|  |:  |||||: :||:||||:||||||      ||||||||||
Db   77 RELQRLAAADGAVAGKVRALRKESRGLSARLGQLRAQLQHEAGPGAGPGADLGAEPAAL 136

Qy  156 SQLENRILNQTADMLQLASKYKDLEHKYQHLATLAHNQSEIIAQLEEHCQRVPSARPVPQ 215
        : |  |:||:::|  :  : ::: :  ::::  ::|:|| :::|||| : :|  :  ||
Db  137 ALLGERVLNASAEAQRAAARFHQLDVKFRELAQLVTQQSSLIARLERLCPGGAGGQQVL 196

Qy  216 PPPAAPPRVYQPPTYNRIINQISTN------EIQSDQNLKVLPPLPTMPTLTSLPSS 267
        ||| . |    | .   ::  :||     : ||| |||: ::
Db  197 PPPLVPVV---PV--RLVGSTSDTSRMLDPAEPEPRDQTQRQQEPMASPMP--AGHPAV 249

Qy  268 TDKPSGPWRDCLQALEDGHDTSSIYLVKPENTNRLMQVWCDQRHDPGGWTVIQRRLDGSV 327
        ||||.||| ||  | : ||  :  |  :|       : |   : |  : |  :|  :|||
Db  250 PTKPVGPWQDCAEARQAGHEQGSGVYELRV--GRHVVSVSWCEQQLEGGGWTVIQRRQDGSV 307

Qy  328 NFFRNWETYKQGFGNIDGEYWLGLENIYWLTNQGNYKLLVTMEDWSGRKVFAEYASFRLE 387
        |||:.|: |: ||    ||||||||| :| : :.|::::|: |||.|| ..|||||:|||
Db  308 NFFTTWQHYKAGFGRPDGEYWLGLEPVYQLISRGDHELLVLLEDWGGRGARAHYDGFSLE 367

Qy  388 PESEYYKLRLGRYHGNAGDSFTWHNGKQFTTLDRDHDVYTGNCAHYQKGGWWYNACAHSN 447
        |||::|:||||:|||:|||| :||:.| |:|:||| |.|:|||| ||:|||||:.||||||
Db  368 PESDHYRLRLGQYHGDAGDSLSWHNDKPFSTVDRDRDSYSGNCALYQRGGWWYHACAHSN 427
```

```
Qy    448  LNGVWYRGGHYRSRYQDGVYWAEFRGGSYSLKKVVMMIRP 487
           ||||||||||||||||||||||||||||| |||||||  ||
Db    428  LNGVWHHGGHYRSRYQDGVYWAEFRGGAYSLRKAAMLIRP 467
```

RESULT 10

Query Match   36.7%;   Score 987; DB 11; Length 457;
Best Local Similarity 44.0%;   Pred. No. 6.9e-61;
Matches 195; Conservative 78; Mismatches 146; Indels 24; Gaps 7;

```
Qy     53  KCTYTFIVPQQRVTGAICVNSKEPEVLLENRVHKQELELINNELLKQKRQIETLQQLVKV 112
               :  :.:    ||     :|| |:|:|:|:| :| :||:|:|||:|:|::|  |: |:
Db     26  RCRVTLVLSPQKATSAVCRSSEATQ--------DSELATLRMRLGRHEELLRALQRRAAE 77

Qy    113  DGGIVSEVKLLRKESRNMNSRVTQLYMQLLHEIIRKRDNALE------LSQLENRILNQTAD 168
           :||:|  :| :|:::| : |  |:|| ||:| |:|:|:||::      |:.|.|:||.|:
Db     78  GGALADEVRALREHSLTINTRLGQLRAQLQQEEARAEEPDLGAEPAAALGLLAERALDAEAE 137

Qy    169  MLQLASKYKDLEHKYQHLATLAHNQSEIIAQLEEHCQRVPSARPVPQPPPAAP-----PRV 224
           ::||:.:|:|:|||:||  |.| |:.|||:|::| |:|: .:|| ::|  :|      |:|
Db    138  ARRTIARLQQLDAQLREHAQLMSQHSSLLGRLLQRACAGPERGCQQQVLPLPLAPLVPLSLV 197

Qy    225  YQPPTYRIINQISTNEIQSDQNLKVLPPPLPTMPT-LTSLPSSTDKPSGPWRDCLQALE 283
           :.|||: :|: |:::||:||:|:|:| |||: |: ||:| |::|:|  || |: ||:|:|
Db    198  GSASNTSRRLDQ--TPEHQREQSLRQQGPPSSLLPTGHLAVPT---RPVGPWRDCAEAHG 252

Qy    284  DGHDTSIYLVKPENTNRLMQVWCDQRHDPGGWTVIQRRLDGSVNFFRNWETYKQGFGNI 343
           ::||:|||||||:||||:||:|||||||||||||||||||||||||||||||||||||:
Db    253  AGHWQSGVYDLR--LGRRVAVAVWCEQDQEGGGWTVIQRRQDGSVNFFTNWQHYKAGFGRP 310

Qy    344  DGEYWLGLENIYWLTNQGNYKLLVTMEDWSGRKVFAEYASFRLEPESEYYKLRLGRYHGN 403
           |||||||||:|||||||||||||||||||||||||||||||||||||||||||||||:|:
Db    311  EGEYWLGLEPVHVQVTSRGDHELILILEDWGGRAARAHYDSFSLEPESDHYRLRLGQYHGD 370

Qy    404  AGDSFTWHNGKQFTTLDRDHDVYTGNCAHYQKGGWWYNACAHSNLNGVWYRGGHYRSRYQ 463
           |||| |:|||::||:||||||||||||||||::||||:|||||||||||| ||||||||||
Db    371  AGDSLSWHNDKPFSTVDRDRDSYSGNCALYHRGGWWYHACAHSNLNGVWHGGHYRSRYQ 430

Qy    464  DGVYWAEFRGGSYSLKKVVMMIR 486
```

RESULT 11

Query Match   34.6%;   Score 929; DB 11; Length 200;
Best Local Similarity 77.8%;   Pred. No. 2.6e-57;
Matches 153; Conservative 25; Mismatches 19; Indels 0; Gaps 0;

```
Qy    291  IYLVKPENTNRLMQVWCDQRHDPGGWTVIQRRLDGSVNFFRNWETYKQGFGNIIDGEYWLG 350
           ||:|||:||||:|||||||||||||||||||||||||||||||||||||||||:||:||||
Db      2  IYMIKPENSNGLMQLWCENSLDPGGWTVIQRRTDGSVNFFRNWENYKXGFGNIDGEYWLG 61

Qy    351  LENIYWLTNQGNYKLLVTMEDWSGRKVFAEYASFRLEPESEYYKLRLGRYHGNAGDSFTW 410
           |:|||:|||||||||||||||||||||||||||||||||||||:|:|||||||:|||| |
Db     62  LDNIYKLSNQDNYKLMIELEDWSEKKVYAEYSSFRLEPESDYYRLRLGITYQGNAGDSMMW 121

Qy    411  HNGKQFTTLDRDHDVYTGNCAHYQKGGWWYNACAHSNLNGVWYRGGHYRSRYQDGVYWAE 470
           |||||||||||||||||||||||::|||||:|||||||||||||||||||||||||||||
Db    122  HNGKQFTTLDRDKDVTGNCAHFHKGGWWYNACAHSNLNGVWHGGHYRSKHQDGIFWAE 181

Qy    471  FRGGSYSLKKVVMMIRP 487
           ||||||||||| ||:|
Db    182  YRGGSYSLRAVQMMIKP 198
```

RESULT 12

```
DR    EMBL; AF170323; AAK11499.1; -.
DR    HSSP; P02671; 1FZD.
DR    InterPro; IPR002181; Fibrinogen_C.
DR    Pfam; PF00147; fibrinogen_C; 1.
DR    SMART; SM00186; FBG; 1.
FT    NON_TER       1      1
FT    NON_TER     197    197
SQ    SEQUENCE   197 AA;  22954 MW;  3409C6314EB5S3896 CRC64;

Query Match             33.7%;  Score 906.5;  DB 13;  Length 197;
Best Local Similarity   84.9%;  Pred. No. 9.6e-56;
Matches  163;  Conservative  11;  Mismatches 15;  Indels  3;  Gaps  2;

Qy   198  AQLEEHCQRVP--SARPVPQPPPAAPPRVQPPTYNRIINQISTNEIQSDQNLKVLPPPL  255
                    :::|||||    ::|  | :||:::||||||||||||||||||||||||||||||||
Db     1  SQLEEHCRKVPPTQTKPLPQ-PPQQNKVYNPPNYNRIINQISTNEIQGDQNLKVLPPPL   59

Qy   256  PTMPTLTSLPSSTDKPSGPWRDCLQALEDGHDTSSIYLVKPENTNRLMQVWCDQRHDPGG  315
          |||||| ||||:|||||||||||||||||||||||||||||||||||||||||||||||
Db    60  PTMPLTFTSNSNSTDKPSGPWKDCLQAMEDGHDTSSIYLVKPENTNRLMQVWCDQRHDPGG  119

Qy   316  WTVIQRRLDGSVNFFRNWETYKQGFGNIDGEYWLGLENIYWLTNQGNYKLLVTMEDWSGR  375
          |||||||||||||||||||||||||| |||||||||||||||||||||||||||||||||
Db   120  WTVIQRRLDGSVNFFRNWETYKLGFGNIHGEYWLGLENIYWLTNQDNYKLLITMEDWSGR  179

Qy   376  KVFAEYASFRLE  387
               :|||||||||||
Db   180  KMFAEYASFRLE  191
```

```
RESULT 13
Q90219
ID    Q90219                PRELIMINARY;   PRT;   513 AA.
AC    Q90219;
DT    01-DEC-2001 (TrEMBLrel. 19, Created)
DT    01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT    01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE    Angiopoietin-1.
GN    ANGPT1 OR ANGI.
OS    Brachydanio rerio (Zebrafish) (Danio rerio).
OC    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC    Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC    Cyprinidae; Danio.
OX    NCBI_TaxID=7955;
RN    [1]
RP    SEQUENCE FROM N.A.
RX    MEDLINE=21916693; PubMed=11500985;
RA    Pham V.N., Roman B.L., Weinstein B.M.;
RT    "Isolation and expression analysis of three zebrafish angiopoietin
RT    genes.";
RL    Dev. Dyn. 221:470-474(2001).
DR    EMBL; AF379602; AAK83347.1; -.
DR    ZFIN; ZDB-GENE-010817-1; angpt1.
DR    InterPro; IPR002181; Fibrinogen_C.
DR    Pfam; PF00147; fibrinogen_C; 1.
DR    SMART; SM00186; FBG; 1.
DR    PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1.
SQ    SEQUENCE   513 AA;  58360 MW;  0627777A39847DBB CRC64;

Query Match             21.9%;  Score 588.5;  DB 13;  Length 513;
Best Local Similarity   30.5%;  Pred. No. 6.2e-33;
Matches  163;  Conservative  87;  Mismatches 200;  Indels  85;  Gaps  19;

Qy     9  WWLGL-LAAMGAVA---------GQEDGFEGTEEGSPREFIYLN-----RYKRAGESQDKCTYTFI   59
          ::||| |:|||||||          |  | |::|  : ||||||      ||||||||||||||||
Db     2  WWGCLFLAALLVVADCGGVEQKTDGLWSSTPKS----NSSSGRRYHRIQHGQ--CSYTFI   55

Qy    60  VPQQRVTGAICVNSKEPEVLLENRVHKQ----ELELLNNELLKQKRQIETLQQ-LVKRVDG  114
            ::||:| ::| |:||: ||:|::  |     :|::|||:|:|||||:||||| |::|| |
Db    56  LPES--DGNTCREFKSGTAYNANALQRDAPQPPEADLSNQKIQQLEHVWENYTQWLQKIEN  113

Qy   115  GIVSEVKL-------------------LRKESRNMNSRVTQLYMQLLHEI----IR  147
             :| :                         ::|   ::|:|::| :|:
Db   114  GIVSEVKL-----------------------LRKESRNMNSRVTQLYMQLLHEI----IR  147
```

```
Db   114  YIKDNMKTEMVQLQQSAVHNHTAAMLEMGTSLLSQTAEQTRKLTDVETQVLNQTSRLEIQ  173
```

```
RESULT 14
Q8C2K6
ID    Q8C2K6                PRELIMINARY;   PRT;   498 AA.
AC    Q8C2K6;
DT    01-MAR-2003 (TrEMBLrel. 23, Created)
DT    01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT    01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE    Angiopoietin.
OS    Mus musculus (Mouse).
OC    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC    Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX    NCBI_TaxID=10090;
RN    [1]
RP    SEQUENCE FROM N.A.
RC    STRAIN=NOD; TISSUE=Thymus;
RX    MEDLINE=22354683; PubMed=12466851;
RA    The RIKEN Genome Exploration Research Group Phase I & II Team;
RA    The FANTOM Consortium;
RT    "Analysis of the mouse transcriptome based on functional annotation of
RT    60,770 full-length cDNAs.";
RL    Nature 420:563-573(2002).
DR    EMBL; AK088439; BAC40354.1; -.
DR    InterPro; IPR002181; Fibrinogen_C.
DR    Pfam; PF00147; fibrinogen_C; 1.
DR    SMART; SM00186; FBG; 1.
DR    PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1.
SQ    SEQUENCE   498 AA;  57475 MW;  285D95748B5C5D800 CRC64;

Query Match             21.3%;  Score 571.5;  DB 11;  Length 498;
Best Local Similarity   29.7%;  Pred. No. 9.2e-32;
Matches  149;  Conservative  83;  Mismatches 175;  Indels  95;  Gaps  14;

Qy    43  RYKRAGESQDKCTYTFIVP--------QQRVTGAICVNSK--EP--------EVL   79
          ||||||||||||||||||:           :||:| ||:|:  :|        :|:
Db    32  RYNRIQHGQ--CAYTFILPEHDGNCRESATEQYNTNALQRDAPHVEPDFSSQKLQHLEHV   89

Qy    80  LENRVHKQELELLNNELLK-QKRQIETLQQ----------LVKVDGGIVSEVLLRKESRN  129
          ||||:| :||:|||:|:|: :|||:| |||          |:::: : : |:|:|:|||
Db    90  MEN--YTQWLQKIENYIVENMKSEMAQIQNAVQNHTATMLEIGTSLLSQT--AEQTRK  144

Qy   130  MNSRVTQLYMQLLHEIIRKRDNALELSQLENRILNQTADMLQLASKYKDLEHKY-----  183
          ::|:||:| :|:|:|::||:|||||||||||:||||||||| |::| :::|:|:
Db   145  LTDVETQVLNQTSRLEIQLLENSLLSTYKLEKQLLQQTNEILKIHEKNSLLEHKILEMGK  204

Qy   184  -------QHLATLAHNQSEIIAQLEEHCQRVPSARVPQPPPAAPPRVQPPTYN  231
                    ::||::  :||:
Db   205  ...
```

RESULT 15

```
ID   Q9BDY8
AC   Q9BDY8;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   Angiopoietin 1.
OS   Sus scrofa (Pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX   NCBI_TaxID=9823;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21153163; PubMed=11230987;
RA   Kim I., Moon S.O., Han C.Y., Pak Y.K., Moon S.K., Kim J.J., Koh G.Y.;
RT   "The angiopoietin-tie2 system in coronary artery endothelium prevents
RT   oxidized low-density lipoprotein-induced apoptosis.";
RL   Cardiovasc. Res. 49:872-881(2001).
DR   EMBL; AF232227; AAK14992.1; -.
DR   HSSP; P02671; 1FZD.
DR   InterPro; IPR002181; Fibrinogen_C.
DR   Pfam; PF00147; fibrinogen_C; 1.
DR   SMART; SM00186; FBG; 1.
DR   PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1.
SQ   SEQUENCE   498 AA;  57413 MW;  A8C1C8EF56061876 CRC64;
```

```
PRELIMINARY;        PRT;   498 AA.
```

```
Query Match             21.0%;
Best Local Similarity   28.9%;
Matches   151;  Conservative   92;

Score 565;  DB 6;  Length 498;
Pred. No. 2.6e-31;
Mismatches 195;  Indels   84;  Gaps   16;
```

```
Qy      14 LAAMGAVAGQQEDGFBGTEEGSPREFIYLNRYKRAGEGSQDKCTYTFIVPQ------QRVTG 67
              ||| :  :: ||| :   |||| : |    :|  ||  :
Db      10 LAAILTHIGCSNQRSPENGG------RRYNRIQHGQ--CAYTFILPEHDGNCRESTTD 60

Qy      68 AICVNSKE----PEV------LLENRVHKQELELLNNELLK-QKRQIETLQQ- 108
              |:| :           :||  ||  :: | :|  : || ||: |
Db      61 QYNTNALQRDAPHVEQDFSSQKLQHLEHVMEN--YTQWLQKIENYIVENMKSEMAQIQQN 118

Qy     109 ------LVKVDGGIVSEVKLLRKESRNMNSRVTQLYMQLLHEIIRKRDNALELSQLEN 160
                    |  ||:   :|| |  :  |  |||  :  : | | | |::
Db     119 AVONHTATMLEGTSLLSQT--AEQTRKLTDVETQVLNQTSRLEIQLLENSLSTYKLEK 175

Qy     161 RIILNQTADMLQLASKYKDLEHKYQHLATIAHNQSEIIAQLEEHCQRVPSARPVQPPPAA 220
              ||| :  |  ||: :|| | : :: :|:|  |: | : : ||| : :|
Db     176 QLLQQTNEILKIHEKNSLLEHKILEMEGKHKEELDTLKEEKENLQGLVTR-------- 225

Qy     221 PPRVYQPPTYNRIINQISTNE----IQSDQNLKVLPPPLPTMPTLTSLPSSTDKPS----- 272
              |   |  :| | | : |:           ||| |||| | | | ||  ||:
Db     226 --QTYIIQELKQQLNRAITNNSYLQKQQ-----------LBLMDTVHNLVNLCTKEGVLLKGG 275
```

```
Qy     273 -----GPWRDCLQALEDGHDTISSIILVKPENTNRLMQVWCDQQRHDPGGWTVIQRRLDGSV 327
             |:|:   |  :  |||||||   ::  :::: ::
Db     276 KKEEVKPFRDCADVYQAGFPNKSGIYTIYINNMPEPKKVFPRDCADVYQAGFN 335

Qy     328 NFFRNWETYKQGFGNIDGEYWLGLENIYWLTNQGNYKLLVTMEDWSGRKVFAEYASFRLE 387
             ::|::  | | : ||:: || |  :  || :  |  || |  ||
Db     336 DFQRGWKEYKQMGFGNPSGEYWLGNEFIFAITSQRQYTLRIELMDWEGNRAYSQYDRFHIG 395

Qy     388 PESEYYKLRLGRYHGNAG--DSFTWHNGKQFTTLDRDHDVYTGNCAHYQKGGWWYNACAH 445
             | |:::::  : ::   ::  ||| |||||| |||||||||||| || | |||||| |:
Db     396 NEKQNYRLYLKGHSGTAGKQSSLILH-GADFSTKDADNDNCMCKCALMLTGGWWFDACGP 454

Qy     446 SNLNGVWYRGHYRSRYQDGVYWAEFRGGSYSLKKVVVMMIRP 487
             |||||||||||||||||||| ||||||||||||||||||||
Db     455 SNLNGMFYTAGQNHGKL-NGIKWHYFKGPSYSLRSTTMMIRP 495
```

```
Qy     205 HKEELDTLKEEKENLQGLVSRQTFIIQELEKQLSRA------- 240
Qy     232 RIINQISTNEIQSDQNLKVLPPPLPTMPTLTS---LPSSTDKPSGPWRDCLQALEDGHD 287
Db     241 ------TNNNSILQKQQLBLMDAVHNLVSLCTKEGVLLKGGKREEEKPFRDCADVYQAGFN 295
Qy     288 TSSIYLVKPENTNRLMQVWCDQQRHDPGGWTVIQRRLDGSVNFFRNWETYKQGFGNIDGEY 347
Qy     296 KSGIYTIYINNMPEPKKVFCNMDVNGGGWTVIQHREDSLDFQRGWKEYKQMGFGNPSGEY 355
Qy     348 WLGLENIYWLTNQGNYKLLVTMEDWSGRKVFAEYASFRLEPESEYYKLRLGRYHGNAG-- 405
Db     356 WLGNEFIFAITSQRQYMLRIELMDWEGNRAYSQYDRFHIGNEKQNYRLYLKGHSGTAGKQ 415
Qy     406 DSFTWHNGKQFTTLDRDHDVYTGNCAHYQKGGWWYNACAHSNLNGVWYRGGHYRSRYQDG 465
Db     416 SSLILH-GADFSTKDADNDNCMCKCALMLTGGWWFDACGPSNLNGMFYTAGQNHGKL-NG 473
Qy     466 VYWAEFRGGSYSLKKVVVMMIRP 487
Db     474 IKWHYFKGPSYSLRSTTMMIRP 495
```

Search completed: July 30, 2004, 12:37:32
Job time : 46 secs

OM nucleic - nucleic search, using sw model

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

Run on: August 6, 2004, 12:25:23 ; Search time 860 Seconds
           (without alignments)
           10734.110 Million cell updates/sec

Title: US-10-018-386-1
Perfect score: 2173
Sequence: 1 gaaaatgaggctgctgcgga........aaaaaaaaaaaaaaaaaaaa 2173
Scoring table: IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0
Searched: 3373863 seqs, 212409041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   N_Geneseq_29Jan04:*
       1: geneseqn1980s:*
       2: geneseqn1990s:*
       3: geneseqn2000s:*
       4: geneseqn200as:*
       5: geneseqn2001bs:*
       6: geneseqn2002s:*
       7: geneseqn2003as:*
       8: geneseqn2003bs:*
       9: geneseqn2003cs:*
      10: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2173	100.0	2173	4	AAF29738	Human ang
2	2146.2	98.8	2288	3	AAZ52359	NSEQ gene
3	2146.2	98.8	2288	3	AAL42455	Human mat
4	2134.0	98.2	2154	3	AAI72856	cDNA clon
5	2132.6	98.1	2290	2	AAX36341	Human TIE
6	2132.6	98.1	2290	4	AAC86961	Nucleotid
7	2132.6	98.1	2290	4	AAS21377	Human CDN
8	2132.6	98.1	2290	6	AB565529	Human TIE
9	2132.6	98.1	2290	4	AAD31563	Human TIE
10	2132.6	98.1	2290	7	ACD23986	Novel hum
11	2132.6	98.1	2290	7	ACD42312	Novel hum
12	2132.6	98.1	2290	7	ACA67127	cDNA enco
13	2132.6	98.1	2290	7	ACA03736	cDNA enco
14	2132.6	98.1	2290	7	ACA04921	Novel hum
15	2132.6	98.1	2290	7	ABX89274	DNA encod
16	2132.6	98.1	2290	7	ACD41928	Human sec
17	2132.6	98.1	2290	7	ACA60451	Novel hum
18	2132.6	98.1	2290	7	ACA04441	Novel hum
19	2132.6	98.1	2290	7	ACA04157	Human hum
20	2132.6	98.1	2290	7	ACA64582	Human CDN
21	2132.6	98.1	2290	8	ADA45786	Novel hum
22	2132.6	98.1	2290	8	ADA76217	Human PRO
23	2132.6	98.1	2290	8	ADA18867	Human PRO
24	2132.6	98.1	2290	8	ADA61490	Ada61490 Homo sapi
25	2132.6	98.1	2290	8	ADB19275	Adb19275 Novel hum
26	2132.6	98.1	2290	8	ADB27816	Adb27816 cDNA enco
27	2132.6	98.1	2290	8	ADA86295	Ada86295 Novel hum
28	2132.6	98.1	2290	8	ADB15859	Adb15859 Human PRO
29	2132.6	98.1	2290	8	ADA47645	Ada47645 Novel hum
30	2132.6	98.1	2290	8	ADA67440	Ada67440 Human PRO
31	2132.6	98.1	2290	8	ADB30447	Adb30447 cDNA enco
32	2132.6	98.1	2290	8	ADA85743	Ada85743 Novel hum
33	2132.6	98.1	2290	8	ADA96955	Ada96955 Human PRO
34	2132.6	98.1	2290	8	ADA79259	Ada79259 Human PRO
35	2132.6	98.1	2290	8	ADA87398	Ada87398 Novel hum
36	2132.6	98.1	2290	8	ADB16600	Adb16600 Human PRO
37	2132.6	98.1	2290	8	ADA91692	Ada91692 Novel hum
38	2132.6	98.1	2290	8	ADB14755	Adb14755 Human PRO
39	2132.6	98.1	2290	8	ADA47327	Ada47327 Human sec
40	2132.6	98.1	2290	8	ADB18716	Adb18716 Novel hum
41	2132.6	98.1	2290	8	ADA93931	Ada93931 Novel hum
42	2132.6	98.1	2290	8	ADB19827	Adb19827 Novel hum
43	2132.6	98.1	2290	8	ADB13139	Adb13139 Human PRO
44	2132.6	98.1	2290	8	ACD98557	Acd98557 Novel hum
45	2132.6	98.1	2290	8	ADA74393	Ada74393 Human PRO

ALIGNMENTS

RESULT 1
AAF29738

ID   AAF29738 standard; cDNA; 2173 BP.
XX
AC   AAF29738;
XX
DT   05-APR-2001 (first entry)
XX
DE   Human angiopoietin-7 (ANG-7) coding sequence.
XX
KW   Human; angiopoietin-7; ANG-7; angiogenesis; cancer; wound healing;
KW   diabetic retinopathy; macular degeneration; cardiovascular disease;
KW   reproductive system; ss.
XX
OS   Homo sapiens.
XX
XX   WO20010243-4-A1.
XX
PN   WO20010243-4-A1.
XX
PD   11-JAN-2001.
XX
PF   30-JUN-2000; 2000WO-US018170.
XX
PR   02-JUL-1999; 99EP-00113502.
XX
PA   (FARB) BAYER AG.
XX
PI   Friedrich G, Hagen G, Wick M, Zubov D, Dubois-Stringfellow N;
XX
DR   WPI; 2001-123103/13.
DR   P-PSDB; AAB66340.
XX
PT   Inhibiting angiogenesis for treating cancer, wound healing, diabetic
PT   retinopathies, macular degeneration, cardiovascular diseases, by
PT   administering angiopoietin-7 polypeptide or its fragments.
XX
PS   Claim 13; Fig 1; 86pp; English.
XX
CC   The present invention describes a method of preventing angiogenesis by
CC   administering angiopoietin-7 (ANG-7) nucleic acid, protein, fragment or
CC   derivative. This can be used in the treatment of angiogenesis-related
CC   diseases, including cancer, wound healing, macular degeneration,
CC   cardiovascular diseases, diabetic retinopathies, infections and
CC   conditions of the reproductive system such as regulation of placental
CC   vascularisation, and also may be used as an abortifacient. Note: In the
CC   specification, ANG-7 is also referred to as being angiotensin-7

SQ Sequence 2173 BP; 538 A; 659 C; 611 G; 365 T; 0 U; 0 Other;
Query Match 100.0%; Score 2173; DB 4; Length 2173;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2173; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      1 GAAAATGAGGCTGCTGCGGACGGGCCGCCTGAGGATGAAACCCCAAGCCTGCGAGCG 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 GAAAATGAGGCTGCTGCGGACGGGCCGCCTGAGGATGAAACCCCAAGCCTGCGAGCG 60

Qy     61 TGGCACTGAGGCACGGGGCTGACCGTACGTGAGGGGAAAGAAGGTTGTCAGCAGCCCCGGCA 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 TGGCACTGAGGCACGGGGCTGACCGTACGTGAGGGGAAAGAAGGTTGTCAGCAGCCCCGGCA 120

Qy    121 GGACCCCTGGCCAGCCTTGGCCCCCAGCCCTTGCCCGGAGGGCAGAGAGCCAG 180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 GGACCCCTGGCCAGCCTTGGCCCCCAGCCCTTGCCCGGAGGGCAGAGAGCCAG 180
```

[DNA sequence alignment continues: Query vs Database, 100% identity, lines numbered in increments from 1 to 2173, paired Qy/Db rows with connecting identity bars; numbering continues on the right-hand column from 1021 through 2100.]

```
Qy   2101 AACTCTTTCTTTAAATAAAATTAAGTCCTACTACAATATAAAAAACAACTTGCAAAGTAAAAT 2160
          |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db   2101 AACTCTTTCTTTAAATAAAATTAAGTCTCTACAATATAAAAAACAACTTGCAAAGTAAAAT 2160

Qy   2161 AAAAAAAAAAAA 2173
          |||||||||||
Db   2161 AAAAAAAAAAA 2173
```

RESULT 2
AAZ52359

```
ID   AAZ52359 standard; cDNA; 2288 BP.
XX
AC   AAZ52359;
XX
DT   24-JUL-2000  (first entry)
XX
DE   NSEQ gene-11 associated with matrix remodelling.
XX
KW   NSEQ gene; matrix-remodeling gene; Incyte clone 2268890; cancer;
KW   matrix-remodeling disease; cardiomyopathy; arthritis; angiogenesis;
KW   diabetic necrosis; atherosclerosis; fibrosis; ulceration; cytostatic;
KW   cardioactive; antiarthritic; angiogenic; antiarteriosclerotic; antiulcer;
ss.
XX
OS   Homo sapiens.
XX
FH   Key            Location/Qualifiers
FH
FT   CDS            442..1923
FT                  /*tag= a
FT                  /product= "PSEQ protein"
FT   sig_peptide    442..507
FT                  /*tag= b
XX
PN   WO200021986-A2.
XX
PD   20-APR-2000.
XX
PF   06-OCT-1999; 99WO-US023315.
XX
PR   09-OCT-1998; 98US-00169289.
XX
PA   (INCY-) INCYTE PHARM INC.
XX
PI   Walker MG, Volkmuth W, Klingler TM;
XX
DR   WPI; 2000-317934/27.
DR   P-PSDB; AAY70745.
XX
PT   Protein co-expressed with matrix-remodeling proteins, useful in the
PT   diagnosis and treatment of cancer, cardiomyopathy, arthritis,
PT   angiogenesis, diabetic necrosis, atherosclerosis, fibrosis, and
PT   ulceration.
XX
PS   Claim 1; Page 44-45; 55pp; English.
XX
CC   The present sequence is NSEQ gene that is co-expressed with one or more
CC   known matrix-remodeling genes in a number of biological samples using an
CC   expression vector. This sequence was identified from the Incyte clone
CC   2268890. The gene, protein, and antibody sequences can be used in the
CC   diagnosis, and treatment or prevention of a disease associated with its
CC   altered expression. The diseases that can be treated are matrix-
CC   remodeling diseases, including cancer, cardiomyopathy, arthritis,
CC   angiogenesis, diabetic necrosis, atherosclerosis, fibrosis, and
CC   ulceration.
XX
SQ   Sequence 2288 BP; 548 A; 689 C; 647 G; 404 T; 0 U; 0 Other;
```

```
Query Match             98.8%;  Score 2146.2;  DB 3;  Length 2288;
Best Local Similarity   99.4%;  Pred. No. 0;
Matches 2154;  Conservative 0;  Mismatches 13;  Indels 0;  Gaps 0;

Qy      3 AAATGAGGCTGTCGGACGGCCTGAGGATGAACCCAAGCCCTTGGACTGCCGAGCGTG 62
```

```
Db  1153  TCTACCAAGGATCAGAGTGACCAGAAACCTGAAGGTGCTGCCACCCCTTGCCCACT 1212
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  1143  ATGCCCACTCTCACCACAGCCTTCCACCCACACAACCGTGGGGCCCCATGGAGAGAC 1202

Db  1213  ATGCCCACTCTCACCAGCCTCCATCTTCCACCCACACAACCGTGGGGAGAGAC 1272
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  1203  TGCCTGCCAGGCCCCTGGAGATGGGCCACACACAGCTCTCATCTTCCTTGGGTGAAGCCCGAG 1262

Db  1273  TGCCTGCCAGGCCCCTGGAGGATGGGCCACACACAGCTCTCATCTTCCTTGGGTGAAGCCGGAG 1332
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  1263  GTCATCCACGAGACACCCCTGGATGGGCTCGTTAACTTCTTCAGGAACTGGACGTACAAG 1322

Db  1333  AACACCAACCGCCTTCATGGAGGGTGGGTCGGACACAGCAGCACGAGAGGAGGCTGGACC 1392
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  1323  GTCATCCACGAGACACCCCTGGATGGGCTCGTTAACTTCTTCAGGAACTGGACGTACAAG 1382

Db  1393  GTCATCCACGAGACACCCCTGGATGGGCTCGTTAACTTCTTCAGGAACTGGACGTACAAG 1452
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  1383  CAAGGGTTTGGGAACATTGACGGGGGAAATACTGGGCTGGCCTGAGAACATTTACTGGCTG 1442

Db  1453  CAAGGGTTTGGGAACATTGACGGGGGAAATACTGGGCTGGCCTGAGAACATTTACTGGCTG 1512
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  1443  ACGAACCAAGGGACACTACAAACTCTCGGTGACCATGGAGGACTGGCTCGGGCCCAAAGTC 1502

Db  1513  ACGAACCAAGGGACACTACAAACTCTCGGTGACCATGGAGGACTGGCTCGGGCCCAAAGTC 1572
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  1503  TTTGCAGAAATACGGCCAGTTTCCCGCTGGAACCTGGAGGAGGCGAGTATTATAAGCTGCG 1562

Db  1573  TTTGCAGAAATACGGCCAGTTTCCCGCTGGAACCTGGAGGAGGCGAGTATTATAAGCTGCG 1632
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  1563  GGGGCGCTACCATGGCCAATCGGGGTGACTCCTTTACATGGCACAACGGCAAGCAGTTCACC 1622

Db  1633  GGGGCGCTACCATGGCCAATCGGGGTGACTCCTTTACATGGCACAACGGCAAGCAGTTCACC 1692
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  1623  ACCCTGACAGAGATCATGAGTCTACACAGGAAACTGTGCCCACTACCAGAAGGGAGGC 1682

Db  1693  ACCCTGACAGAGATCATGATGTCTACACAGGAAACTGTGCCCACTACCAGAAGGGAGGC 1752
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  1683  TGGTGGTATAACGGCTTGTCCCCACTCCAAACCTCAACGGGGTCTTGGTACCGCGGGGCCAT 1742

Db  1753  TGGTGGTATAACGGCTTGTCCCCACTCCAAACCTCAACGGGGTCTTGGTACCGCGGGGCCAT 1812
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  1743  TACCGGGACGCGCTACCAGACGGAGTCTACTGGGCTGAGTTCCGGAGAGGCTCTTACTCA 1802

Db  1813  TACCGGGACGCGCTACCAGACGGAGTCTACTGGGCTGAGTTCCGGAGGGCTCTTACTCA 1872
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  1803  CTCAAGAAAGTGGTGATGATGATCCGGACGGGACACCCAACACCTTCCACTAAGCCAGCTCC 1862

Db  1873  CTCAAGAAAGTGGTGATGATGATCCGGACGGGACACCCAACACCTTCCACTAAGCCAGCTCC 1932
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  1863  CCCTCCTGACCTCTCGTGGCCATTGCGAGGAGGCCACCTGGTTCACGCCTGGCGCCAGCAC 1922

Db  1933  CCCTCCTGACCTCTCGTGGCCATTGCCAGGAGGCCACCTGGTTCACGCCTGGCCCACGCAC 1992
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  1923  AAAGAACAACTCCTCACCAGTTCATCCTGAGGCTGGGAGGAGTGCTGGATTCGTGT 1982

Db  1993  AAAGAACAACTCCTCACCAGTTCATCCTGAGGCTGGGAGGAGTGCTGGATTCTGT 2052
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  1983  TTTCCGAAGTCACTGCAGCGAGATGAGATGGAACTGAATCGATACGGTGTGTTTTTCTTCCTC 2042

Db  2053  TTTCCGAAGTCACTGCAGCGGATGAGATGGAACTGAATCGATACGGTGTTTTCTGTCCCTCC 2112
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  2043  TACTTTTCCTTCACCACAGACGCCCCTCATGTCTCTCCAGGACAGGAGGACTACACAGACA 2102

Db  2113  TACTTTCCTTCACCAGACACGCCCCTCATGTCTCCAGGACAGGAGGACTACACAGACA 2172
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  2103  CTCTTCTTTAAATAAATTAAGTCTTACAATAAAAACAACTGCAAGTAAAAAAA 2162

Db  2173  CTCTTCTTTAAATAAATTAAGTCTCTACAATAAAAACAACAACTGCAAGTACCTTCATA 2232
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  2173  CTCTTCTTTAAATAAATTAAGTCTCTACAATAAAAACAACAACTGCAAGTACCTTCATA 2232

Db  2233  AATATACA 2239
          ||||||||
Qy  2233  AATATACA 2239

Qy  2163  AAAAAAA 2169
```

```
Query Match            98.8%;  Score 2146.2;  DB 6;  Length 2288;
Best Local Similarity  99.4%;
Matches 2154;          Conservative   0;  Mismatches  13;  Indels   0;  Gaps   0;

Qy     3  AAAATGAGGCTGCTGCGGGACAGGCCCTGAGGAATGAACCCCAAGCCCGGGAACCCTGAGCGGTG 62
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    73  AAAATGAGGCTGCTGCGGGACAGGCCCTGAGGAATGAACCCCAAGCCCGGGAACCCTGAGCGGTG 132

Qy    63  GCACTGAGGCAGCGGGCCTGACGCTACTGTGAGGGGGAAAGAAGAGGTTGTGAGCAGCCCCGCAGG 122
```

RESULT 4
AAI72856

```
ID   AAI72856 standard; cDNA; 2154 BP.
XX
AC   AAI72855;
XX
DT   12-AUG-2002 (first entry)
XX
DE   cDNA clone AR3, ATCC 207063.
XX
KW   Gene; angiopoietin-like protein 2; AR2; angiopoietin-like protein 3; AR3;
KW   apple crisp protein; APPLE; cocoa crisp protein; COCO;
KW   signal sequence cloning; secretory leader motif; angiogenesis;
KW   wound healing; transplantation; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             358..1839
FT                   /*tag= a
FT                   /product= "Angiopoietin-like protein-3"
XX
PN   WO200059938-A1.
XX
PD   12-OCT-2000.
XX
PF   31-MAR-2000; 2000WO-US008832.
XX
PR   01-APR-1999;  99US-01263669P.
PR   29-MAR-2000; 2000US-00538361.
XX
PA   (GEMY ) GENETICS INST INC.
XX
PI   Racie-Collins LA, Lavallie ER;
XX
DR   WPI; 2000-664990/64.
DR   P-PSDB; AAB47997.
XX
PT   New angiopoietin-like proteins 2 and 3, apple crisp and cocoa crisp
PT   proteins and polynucleotides, useful in treating e.g. autoimmune
PT   diseases, cancer, or central and peripheral nervous system disorders and
PT   neuropathies.
XX
PS   Claim 24; Page 70-71; 84pp; English.
XX
CC   The sequences given in AAI72855-58 encode angiopoietin-like protein 2
CC   (AR2), angiopoietin-like 3 protein (AR3), apple crisp protein (APPLE), or
CC   cocoa crisp protein (COCO), respectively. These sequences were isolated
CC   by indirect cloning techniques, e.g. signal sequence cloning, which
CC   isolates DNA based on the presence of well known secretory leader motifs.
CC   AR2 and AR3 promote angiogenesis and may therefore be used in wound
CC   healing and transplantation.
XX
SQ   Sequence 2154 BP; 528 A; 657 C; 607 G; 362 T; 0 U; 0 Other;
```

```
Query Match             98.2%;  Score 2134.2;  DB 3;  Length 2154;
Best Local Similarity   99.9%;
Matches 2136;  Conservative     0;  Mismatches    3;  Indels     0;  Gaps     0;
```

```
Qy    30 GATGAAACCCCAAGCCCTGGACGCCGTGGCCAGCGCAGCGCGCTGACGCTACTG   89
         ||||| |||||||||||||||||||||||||||||||||||||||||||||||
Db    16 GATGGACCCCAAGCCCTGGACGCCGTGGCCAGCGCAGCGCGCTGACGCTACTG   75

Qy    90 TGAGGGAAAGAAGGTTGTTGTGAGCAGCACCCCCGGCAGACCCCGGCAGCCCT  149
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    76 TGAGGGAAAGAAGGTTGTTGTGAGCAGCACCCCCGGCAGACCCCGGCAGCCCT  135

Qy   150 CTGCGCGGAGCCCTTCTGTGTGGAGGGCAGAGCCAGTGGAGGGCAGGGCAGG  209
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   136 CTGCGCGGAGCCCTTCTGTGTGGAGGGCAGAGCCAGTGGAGGGCAGGGCAGG  195

Qy   210 AGCCACCCGGCCCCTGCAAACTTCAGGAGAACCCCTTCAGAGGCCATTG  269
         |||||||||||||||||||||||||||||||||||||||||||||||||
Db   196 AGCACCCGGCCCCTGCAAACTTCAGGAGAACCCCTTCAGAGGCCATTG  255

Qy   270 GGCCACAGGGTGAAGCCATGTGAGGAGCCGGCCCCGGAGGCAAGCAGGAGGAGGCTTTCA  329
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   256 GGCCACAGGGTGAAGCCATGTGAGGAGCCGGCCCCGGAGGCAAGCAGGAGGAGGCTTCA  315

Qy   330 TAGAGTTCTAATTCACAAAGATAACCCATTTGCAAAGAAGACCATGTGCTG  389
         |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   316 TAGATTCTAATTCACAAAGAAGAATAACCCATTTGCAAAGAAGACCATGTGCTG  375

Qy   390 ACATGCTGGTGGGTCCGACTGCCTGGGCTGGCTGGTGCAGGGCCAGGAGGACGGT  449
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   376 ACATGCTGGTGGGTCCGGACTCGGCCATGGGGAGCTGTTGCAGGGCCAGGAGGACGGT  435

Qy   450 TTTGAGGGCCACTGAGGAGGGCTCGGCCCAAGAGAGTTCATTTTACCTAAAACACGG  509
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   436 TTTGAGGGCCACTGAGGAGGGCTCGGCCCAAGAGAGTTCATTTTACCTAAAACACGG  495

Qy   510 GCGGGGCCGAGTCCCAGACAAGTGCACCTACACCCTTCATTTGCCCCAGCGGGT  569
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   496 GCGGGGCCGAGTCCCAGACAAGTGCACCTACACCCTTCATTGTCCCAGCGGGTCACG  555

Qy   630 CAGGAGCTAGAGCTGCTCAACAAATGAGCTGCTCAAGCAGAAGGCCGAGACGCTG  689
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   616 CAGGAGCTAGAGCTGCTCAACAATGAGCTGCTCAAGCAGAAGGCCGAGACGCTG  675

Qy   690 CAGCAGCTGGTGAAGGTGGACGGGCCGCCATTGTGAGCGAGGTGAAGCTG  749
         ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   676 CAGCAGCTGGTGAAGGTGGACGGGCCGCCATTGTGAGCGAGGTGAAGCTG  735

Qy   750 AGCCGCGAACAATGAACTCGGCGGGTCACGCAGCTCTACAATGACGAGATCATC  809
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   736 AGCCGCAACATGAACTCGGCGGGTCACGCAGCTCTACAATGACGAGATCATC  795

Qy   810 CGCAAGCGGGACAACGGCTTGGAGCTCTCCCAGCTGGAGAACCAGACA  869
         |||||||||||||||||||||||||||||||||||||||||||||||
Db   796 CGCAAGCGGGACAACGGCTTGGAGCTCTCCCAGCTGGAGAACCAGACA  855

Qy   870 CGCCGACATGCTCAGCTGCCAGCAAGCAAGTACAAGGACCACCTG  929
         |||||||||||||||||||||||||||||||||||||||||||||
Db   856 GCCGACATGCTCAGCTGCCAGCAAGCAAGTACAAGGACCACCTG  915

Qy   930 GCCACAACTGGCCCCAAACAAATCAGATCATCGGCGAGTTGAGGAGCACTGCCAGAGG  989
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   916 GCCACAACTGGCCCCAAACAAATCAGATCATCGGCGAGTTGAGGAGCACTGCCAGAGG  975

Qy   990 GTGCCCCTGGGCCAGGCCGTCCCCCAGCCACCCCCCGGCCCCCGGCCAA  1049
         |||||||||||||||||||||||||||||||||||||||||||||||||
Db   976 GTGCCCCTGGGCCAGGCCGTCCCCCAGCCACCCCCCGGGGTCTACCAA  1035

Qy  1050 CCACCCACCTTACAACGCATCATCAACCAGATCCTCAACCAGATCGAGTCAGAGTGACCAG  1109
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1036 CCACCCACCTTACAACGCATCATCAACCAGATCCTCAACCAGATCGAGTCAGAGTGACCAG  1095

Qy  1110 AACCTGAAAGGTGCTACCGGCTCAGCCACCCCCTGCCACTCACCAGCCTCCATCT  1169
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1096 AACCTGAAAGGTGCTCACCGGCTCGGCCACCCCCTGCCACTCACCAGCCTCCATCT  1155

Qy  1170 TCCACCGACAAGCCGTCGGGCCCATGGAGACACTGCGTGCAGGGAGGATGGCCAC  1229
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1156 TCCACCGACAAGCCGTCGGGCCCATGGAGACACTGCGTGCAGGGAGGATGGCCAC  1215

Qy  1230 GACACCAGCTCCATCTTACCTGGTGAAGCCGGAACACAACCGCGTCATCGCAGTTGTGG  1289
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1216 GACACCAGCTCCATCTTACCTGGTGAAGCCGGAGAACCAACCGCGTCATCGCAGTGTGG  1275

Qy  1290 TGCGACCAGAGACACGACCCCGGCGTCATCCAGAGATGGCTCT  1349
         |||||||||||||||||||||||||||||||||||||||||||
Db  1276 TGCGACCAGAGACACGACCCCGGCGTCATCCAGAGGATGGCTCT  1335

Qy  1350 GTTAACTTCTTCAGGAACTGGGAGACGTACAAGCAAGGGTTGGGAACATTGACGCGGAA  1409
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1336 ...
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Db   1336  GTTAACTTCTTCAGGAACTGGGAGGACGTACAAGCAAGGGTTTGGGAACATTGACGGGCCAA  1395
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1410  TACTGGCTGGCGCCTGGAGAACATTACTGGCTGACGAACCAAGGCAACTACAAAACTCCTG  1469
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1396  TACTGGCTGGCGCCTGGAGAACATTACTGGCTGACGAACCAAGGCAACTACAAAACTCCTG  1455

Qy   1470  GTGACCATGGAGGACTGGTCTCCGGCGCGCAAAGTGCTTGCAGAATACGCCAGTTTCCGCCTG  1529
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1456  GTGACCATGGAGGACTGGTCTCCGGCGCGCAAAGTCTTTGCAGAATACGCCAGTTTCCGCCTG  1515

Qy   1530  GAACCTGAGGAGCGTAGTATTATAAGCTGGGGGCTACCATGGCCAAATCGGGGTGAC  1589
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1516  GAACCTGAGGAGCGAGTATTATAAGCTGCGGCTACCCATGGCAATGGGGGTGAC  1575

Qy   1590  TCCTTTACATGGCACAACGGGCAAGCAGTTCACCACCCCTGGACACAGAGATCATGATGTCTAC  1649
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1576  TCCTTTACATGGCACAACGGGCAAGCAGTTCACCACCCCTGGGACAGAGATCATGATGTCTAC  1635

Qy   1650  ACAGGAAACTGTGCCCACTACACGAGAAGGAGGGCTGGTGTATAACGGCTGTGCCCACTCC  1709
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1636  ACAGGAAACTGTGCCCACTACACGAGAAGGAGGGCTGGTGTATAACGGCTGTGCCCACTCC  1695

Qy   1710  AACCTCAACGGGGGTCTGGTACCCGGGGGCCATTACCTGGACGACGGAGTC  1769
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1696  AACCTCAACGGGGGTCTGGTACCCGGGGCCATTACCGGGAGCCTACCAGGACGGAGTC  1755

Qy   1770  TACTGGCTGAGTTCCGGAGGAGGCTCTTACTCACTCAAGAAGAATGGGTGATGATGATCCGA  1829
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1756  TACTGGCTGAGTTCCGGAGGAGGCTCTTACTCACTCAAGAAGATGGGTGATGATGATCCGA  1815

Qy   1830  CCGGAACCCCAACACTTCCACTAAGCAGCTCCCCTCGACCTTCGTGGTGGCCATTGCC  1889
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1816  CCGGAACCCCAACACTTCCACTAAGCAGCTCCCCTCGACCTTCGTGGTGGCCATTGCC  1875

Qy   1890  AGGAGCCCACCCTGGTCACGCTGGCCACAGCACAAGAACAACTCCTCACCAGTTCATCC  1949
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1876  AGGAGCCCACCCTGGTCACGCTGGCCACAGCACAAAGAACAACTCCTCACCAGTTCATCC  1935

Qy   1950  TGAGGCCTGGGAGGACCGGGGATGCTGGGATTCGTGTTTCTCCGAAGTCACTCCAGCGGATG  2009
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1936  TGAGGCCTGGGAGGACCGGGGATGCTGGGATTCGTGTTTCTCCGAAGTCACTCCAGGGGATGATG  1995

Qy   2010  GAACTGAATGGATTACGGTGTGTTTTCTGTCCCCTCCTACACTTCCTTCACCAACACAGCAGCCCCT  2069
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1996  GAACTGAATGGATTACGGTGTTTTCGTCCCCTCCTACTTCCTTCACCAACACAGCAGCCCCT  2055

Qy   2070  CATGTCTCCAGGACAGCAGGAACTACAGACAACTCTTCTTTAAATAAAATTAAGTCTCT  2129
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2056  CATGTCTCCAGGACAGCAGGAACTACAGACAACTCTTCTTTAAATAAAATTAAGTCTCT  2115

Qy   2130  ACAATAAAAACACAACTGCAAAGTAAAAAAAAAAAAAAAAA  2168
           |||||||||||||||||||||||||||||||||||||||||
Db   2116  ACAATAAAAACACAACTGCAAAGTAAAAAAAAAAAAAAAAA  2154
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```
RESULT 5
AAX36341

ID   AAX36341 standard; DNA; 2290 BP.
XX
AC   AAX36341;
XX
DT   01-JUL-1999   (first entry)
XX
DE   Human TIE ligand NL1 coding sequence.
XX
KW   Human TIE ligand; NL1; NL4; NL5; NL8; Ig homology domain; angiogenesis;
KW   EGF homology domain; receptor tyrosine kinase; vascular endothelial cell;
KW   early haemopoietic cell; haemopoiesis; neovascularisation; wound healing;
KW   endothelial cell; growth inhibitor; apoptosis inducer; tumour cell;
KW   vasculogenesis; detection; diagnosis; therapy; ss.
OS   Homo sapiens.
XX
PN   WO9915653-A2.
XX
PD   01-APR-1999.
XX
PF   14-SEP-1998;  98WO-US019093.
XX
PR   19-SEP-1997;  97US-00933821.
PR   29-OCT-1997;  97US-00960507.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Godowski PJ, Gurney AL, Hillan K, Botstein D, Goddard A, Roy M;
PI   Ferrara N, Tumas D, Schwall R;
XX
DR   WPI; 1999-263480/22.
DR   P-PSDB; AAY05396.
XX
PT   New isolated TIE ligand homologs for, e.g. developing products for
PT   treatment of tumors.
XX
PS   Claim 3; Fig 2; 132pp; English.
XX
CC   This sequence encodes the human tyrosine kinase containing Ig and EGF
CC   homology domains (TIE) ligand of the invention, designated NL1. The TIE
CC   receptors are receptor tyrosine kinases which are expressed in vascular
CC   endothelial cells and early haemopoietic cells. The TIE receptors are
CC   believed to be actively involved in angiogenesis, and may play a role in
CC   haemopoiesis as well. The TIE ligand homologs can promote the survival
CC   and/or growth and/or differentiation of TIE receptor expressing cells.
CC   They can be used for promoting neovascularisation in wound healing and
CC   for promoting angiogenic processes, such as for inducing collateral
CC   vascularisation in an ischaemic heart or limb, or for promoting bone
CC   development and/or maturation and/or growth in a patient or muscle growth
CC   and development. The TIE ligand homologs and antibodies can inhibit the
CC   growth of endothelial cells and induce apoptosis of cells, particularly
CC   tumour cells. They can inhibit vasculogenesis, particularly the
CC   vascularisation of tumour cells. The antibodies can also inhibit
CC   vascularisation of a cell in which a gene encoding an NL1, NL5, NL8 or
CC   NL4 polypeptide is amplified. The products can also be used for
CC   detection, diagnosis, drug screening and production of transgenic animals
XX
SQ   Sequence 2290 BP; 537 A; 692 C; 668 G; 393 T; 0 U; 0 Other;

Query Match            98.1%;  Score 2132.6;  DB 2;  Length 2290;
Best Local Similarity  99.8%;  Pred. No. 0;
Matches 2135;  Conservative   0;  Mismatches   4;  Indels   0;  Gaps 0;
```

```
Qy     3  AAATGAGGCTGCTGTGCGGACGGCCTGAGGATGAACCCCAAGCCCTGACCTGCCGAGGGTG  62
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   151  AAATGAGGCTGCTGTGCGGACGGCCTGAGGATGAACCCCAAGCCCTGACCTGCCGAGGGTG  210

Qy    63  GCACTGAGGCGACGGGTTGACCCTACGTGAGGGAAGAAGGTTGTGAGCACCCCCCAGG  122
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   211  GCACTGAGGCAGGGTGACCTACTGTGAGGGAAAGAAGGTTGTGAGCAGCCCCCGAGG  270

Qy   123  ACCCCTGGCCAGCCCTTGCCCCAGCCCTTCTGCCGGACGCCCTTCTGTGGAGGCCCAGTG  182
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   271  ACCCCTGGCCAGCCCCACCCCTGGCCCAGCCCTTCTGCCGGACGCCCTTGTGTGGAGGCAGAGCCCAGTG  330

Qy   183  GAGCCCAGTGAGGCAGGGCTGAGGCCAGCCACCGGCCGAGCCCTCGAGGAACCCCTTCAG  242
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   331  GAGCCCAGTGAGGCAGGGCTCGTTGGCAGCCACCGAGCCCTGCAACTCAGGAACCCCTCAG  390

Qy   243  AGGCCATGGACAGGGCCTGCCCGCGGGTGAAGCCATGTGAGGAGCCGCCCGG  302
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   391  AGGCCATGGACAGGGCTGCCCGCCGGCTGACGGCGGCCAGGGGTTGAAGCCATGTGAGGAGCCGCCCGG  450

Qy   303  AGCCAACCAGGAGGGGAAGGGCTTTCATAGATTCTATTCACAAAGAGAATAACCACACCATTTT  362
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   451  AGCCAAGCAGGAGGAGAAGAGGCTTTCATAGATTCTATTCACAAAGAGAATAACCACACCATTTT  510

Qy   363  GCAAAGACCATGAGGCCACTCGTGCGTGACATGCTGTGGCTCGGACTGCTGGCTGCCATG  422
```

RESULT 6
ID   AAC86961
AC   AAC86961;
XX
ID   AAC86961 standard; cDNA; 2290 BP.
XX
AC   AAC86961;
XX
DT   20-APR-2001 (first entry)
XX
DE   Nucleotide sequence of human polypeptide PRO196.
XX
KW   Human; secreted protein; transmembrane protein; PRO196; PRO183;
KW   PRO185; PRO210; PRO215; PRO217; PRO242; PRO288; PRO444; PRO183;
KW   PRO183; PRO1272; PRO1419; PRO4999; PRO170; PRO248; PRO365; PRO1361; PRO1308;
KW   PRO1600; PRO99940; PRO5333; PRO301; PRO187; PRO3337; PRO1411; PRO4356;
KW   PRO246; PRO265; PRO941; PRO10096; PRO6003; PRO6004; PRO2630;
KW   PRO6309; cell death; genetic disorder; transgenic animal; gene therapy;
KW   ss.
XX
OS   Homo sapiens.
XX
FH   Key   Location/Qualifiers
FT   CDS   520..2001
FT   /*tag= a
FT   sig_peptide   520..585
FT   /*tag= b
XX

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PN   WO200077037-A2.
XX
PD   21-DEC-2000.
XX
PF   22-MAY-2000; 2000WO-US014042.
XX
PR   15-JUN-1999; 99US-0139695P.
PR   20-JUL-1999; 99US-0145070P.
PR   26-JUL-1999; 99US-0145698P.
PR   17-AUG-1999; 99US-0149396P.
PR   01-SEP-1999; 99WO-US020111.
PR   08-SEP-1999; 99WO-US020594.
PR   15-SEP-1999; 99WO-US021090.
PR   15-SEP-1999; 99WO-US021147.
PR   30-NOV-1999; 99WO-US028313.
PR   01-DEC-1999; 99WO-US028301.
PR   02-DEC-1999; 99WO-US028565.
PR   07-DEC-1999; 99US-0169495P.
PR   05-JAN-2000; 2000WO-US000219.
PR   18-FEB-2000; 2000WO-US004341.
PR   18-FEB-2000; 2000WO-US004342.
PR   22-FEB-2000; 2000WO-US004414.
PR   01-MAR-2000; 2000WO-US005501.
PR   02-MAR-2000; 2000WO-US005841.
PR   20-MAR-2000; 2000WO-US007377.
PR   20-MAR-2000; 2000WO-US008439.
PR   15-MAY-2000; 2000WO-US013358.
PR   17-MAY-2000; 2000WO-US013705.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Ashkenazi AJ, Baker KP, Botstein DA, Desnoyers L, Eaton DL;
PI   Ferrara N, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;
PI   Godowski PJ, Gurney AL, Kljavin IJ, Mather JP, Napier MA, Pan J;
PI   Paoni NF, Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM;
PI   Wood WI, Zhang Z;
XX
DR   WPI; 2001-050091/06.
DR   P-PSDB; AAB31179.
XX
PT   Isolated nucleic acid molecule encoding a PRO polypeptide which is a
PT   transmembrane polypeptide is useful for gene therapy and identification
PT   of related polypeptides.
XX
PS   Claim 2; Fig 1; 244pp; English.
XX
CC   The present sequence encodes a human secreted and transmembrane
CC   polypeptide. The specification describes human polypeptides, designated
CC   PRO196, PRO444, PRO183, PRO185, PRO210, PRO215, PRO217, PRO242, PRO288,
CC   PRO365, PRO361, PRO1308, PRO183, PRO1272, PRO1419, PRO4999, PRO7170,
CC   PRO248, PRO353, PRO1318, PRO1600, PRO533, PRO301, PRO187,
CC   PRO337, PRO1411, PRO4356, PRO9940, PRO941, PRO10096, PRO6003,
CC   PRO6004, PRO350, PRO2630 and PRO6309. The biological activity of cells
CC   can be modulated with agents that bind to these polypeptides, resulting
CC   in the death of the cells. The polynucleotides encoding these
CC   polypeptides are useful in the recombinant production of the
CC   polypeptides, as a hybridisation probe to screen libraries to isolate
CC   homologous sequences, or to map the gene. They may also be used for
CC   analysing genetic disorders, and to produce transgenic animals which are
CC   useful for the development and screening of therapeutically useful
CC   reagents. The polynucleotides can also be used in gene therapy e.g. to
CC   replace a defective gene.
XX
SQ   Sequence 2290 BP; 537 A; 692 C; 668 G; 393 T; 0 U; 0 Other;

Query Match             98.1%;  Score 2132.6;  DB 4;  Length 2290;
Best Local Similarity   99.8%;
Matches 2135;  Conservative  0;  Mismatches  0;  Indels  4;  Gaps  0;

Qy          3 AAATCAGGCTGCTCGGGACGGCCGGCTGAGGCGCTGAGGGTGGGAAGAAGAGGGCAGG 62
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        151 AAATGAGGCTGCTCGGGACGGCCGGCTGAGGCGCTGAGGGTGGGAAGAAGAGGGCAGG 210
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Qy         63 GCACTGAGGCAGCAGCGCGCTGACGCTACTGTGAGGGAAAGAGGTTGTTGAGCAGG 122
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        211 GCACTGAGGCAGCAGCGCGCTGACGCTACTGTGAGGGAAAGAGGTTGTTGAGCAGG 270

Qy        123 ACCCCTGGGCCCAGCCCTGGCCCTGGCCCTGGCCCTACTCTGTGAGGGAGAGCCCAGTG 182
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        271 ACCCCTGGGCCCAGCCCTGGCCCTGGCCCTGGCCCTACTCTGTGAGGGAGAGCCCAGTG 330

Qy        183 GAGCCCAGTGAGGCAGGGCAGGGCTGCTTGGCAGCCACCGGGCTCCGGCCCTTCAG 242
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        331 GAGCCCAGTGAGGCAGGGCAGGGCTGCTTGGCAGCCACCGGGCTCCGGCCCTTCAG 390

Qy        243 AGGCCATGGACAGGGCTGCCCGGCTGACGCGCCAGGGTGAAGCTGTGAGGACGCCGG 302
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        391 AGGCCATGGACAGGGCTGCCCGGCTGACGCGCCAGGGTGAAGCTGTGAGGACGCCGG 450

Qy        303 AGCCAAGCAGAGAGGGAAGAGAGGGTTTCATCAGATTTCATTCACAAAAGAATACCACATTTT 362
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        451 AGCCAAGCAGAGAGGGAAGAGAGGGTTTCATCAGATTTCATTCACAAAAGAATACCACATTTT 510

Qy        363 GCAAAGACCATGAGCGCCACTGTGCCTGACATGCTTGGTCTTGGACTTGCTGCCATG 422
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        511 GCAAGGACCATGAGCGCCACTGTGCGTGACATGCTTGGTCTTGGACTTGCTGCCATG 570

Qy        423 GGAGCTGTTGCAGGGCCAGGAGGGACGGTTTGAGGGCACTGAGGAGGGCTGCTCGG 482
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Db        571 GGAGCTGTTGCAGGGCCAGGAGGGACGGTTTGAGGGCACTGAGGAGGGCTGCTCGG 630

Qy        483 TTCATTTACCTTAAACAGGTACAAGCCGCGGCGGGGGGGAGTCCCAGGACAAGTGCACCTACACC 542
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Db        631 TTCATTTACCTTAAACAGGTACAAGCCGCGGCGGGGGGAGTCCCAGGACAAGTGCACCTACACC 690

Qy        543 TTCATTGTTGCCCCAGACGGTCACGGGGTTGCCGTCAACTTCCAAGGAGCCTGAG 602
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        691 TTCATTGTTGCCCCAGACGGTCACGGGGTTGCCGTCAACTTCCAAGGAGCCTGAG 750

Qy        603 GTGGCTTCTGGGAGAACCCAGTGCATAAGCAGGCTAGAGCGTGCTCAACAAATGAGCTGCTC 662
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Db        751 GTGGCTTCTGGGAGAACCCAGTGCATAAGCAGGCTAGAGCGTGCTCAACAAATGAGCTGCTC 810

Qy        663 AAGCAGAAGCGGCGAGATCGAGAGACGCTCCAGCAGAGCTCGGTGAAGGTGGACGGACGGCATTGTG 722
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Db        811 AAGCAGAAGCGGCGAGATCGAGAGACGCTCCAGCAGAGCTCGGTGAAGGTGGACGGACGGCATTGTG 870

Qy        723 ACGGAGGTGAAGCTGCTGTGCGCAAGGAGGAGGAGGCCGCAAACATGAACTCGCGGGGGGTCACGCAGCTC 782
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        871 AGGGAGGTGAAGCTGCTGTGCGCAAGGAGGAGGAGGCCGCAAACATGAACTCGCGGGGGGTCACGCAGCTC 930

Qy        783 TACATGGAGCTCCTGCACGAGATCATCCGCAAGCGGGACAACGCGTTGGAGCTCTCCAG 842
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        931 TACATGGAGCTCCTGCACGAGATCATCCGCAAGCGGGACAACGCGTTGGAGCTCTCCAG 990

Qy        843 CTGGAGAACAGAGGATCCTGAACCAGACAGCCGACACATGCTTGGCGTTGGCCAGAAGTACAAG 902
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        991 CTGGAGAACAGAGGATCCTGAACCAGACAGCCGACACATGCTTGGCGTTGGCCAGAAGTACAAG 1050

Qy        903 GACCTGGAGCACAAGTACCAGCAGCACCTGGCCCACTGCCGCAAACCAATCAGAGATCATC 962
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Db       1051 GACCTGGAGCACAAGTACCAGCAGCACCTGGCCCACTGCCGCAAACCAATCAGAGATCATC 1110

Qy        963 GGCGGAGCTTGAGGAGCACTGCCAGGAGGTGCCCTGCCGCCGTCCCGCACACC 1022
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Db       1111 GGCGGAGCTTGAGGAGCACTGCCAGGAGGTGCCCTGCCGCCGTCCCGCACACC 1170

Qy       1023 CCCGGCTGCCCGCCCGCGGGTCCTCACCAACCACCACCCAACCGCAACCAGATC 1082
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Db       1171 CCCGGCTGCCCGCCCGCGGGTCCTCACCAACCACCACCCAACCGCAACCAGATC 1230

Qy       1083 TCTACCAACGAGAGTCACGAGTGACTGCTGCCACCCCCTCACACT 1142
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Db       1231 TCTACCAACGAGAGTCACGAGTGACTGCTGCCACCCCCTCACACT 1290

Qy       1143 ATGCCCCACTCTCACCAGCCTCCCATCTTCACCGACAAGCCGTCGGCGGCCCATGGAGAGAC 1202
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Db                                                                     1202
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Db            1291
Qy   1291  ATGCCCACTCTCACCAGAGCTCCATCTTCACGACCAAGCCGTCGGGCGCCCATGGGAGAGAC  1350
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Qy   1203  TGCCGCTGCAGGCCCTGGAGGATGGCCACGACGACCAGCTCATCTACCTGGTGAAGCCGGAG  1262
Db   1351  TGCCTGCAGGCCCTGGAGGATGGCCACGACGACCAGCTCATCTACCTGGTGAAGCCGGAG    1410
Qy   1263  AACACCAACCGCCTTCATGCAGGGTGTGGTCGCGACCAGAGACACACCCGGGGGGCTGACC   1322
Db   1411  AACACCAACCGCCTTCATGCAGGGTGTGGTCGCGACCAGAGACACACCCGGGGGGCTGACC   1470
Qy   1323  GTCATCATCCAGGAGACGGGCGGATGGGCTTCTGTTAACTTCTTTCAGGAACTGGGAGGAGAGGTACAAG 1382
Db   1471  GTCATCCAGGAGACGGGCGGATGGGCTCGTTAACTTCTTTCAGGAACTGGGAGACGTACAAG  1530
Qy   1383  CAAGGGTTTGGGAACATTGACGGGCGAATACTGGGCTGGGGCCTGGAGAACATTTACTGGCTG  1442
Db   1531  CAAGGGTTTGGGAACATTGACGGGCGAATACTGGGCTGGGGCCTGGAGAACATTTACTGGCTG 1590
Qy   1443  ACGAACCAAGGCAACTACAAACTCCTGGTGACCATGAGAGGACTTGGTCGGCCGCAAAGTC   1502
Db   1591  ACGAACCAAGGCAACTACAAACTCCTGGTGACCATGAGAGGAACTGGTCCGGCCGCAAAGTC  1650
Qy   1503  TTTGCAGAATACGGCCAGTTTTCCCGCTGGAACCTGGAACCTGAGAGACCGAGTATTATTAAAGCTGCGCGCTG 1562
Db   1651  TTTGCAGAATACGGCCAGTTTTCCCGCTGAACCTGAGAGACCGAGTATTATTAAAGCTGCGGCTG 1710
Qy   1563  GGGCGGCTACCCATGGCCAATGGCGGGTGACTCCTTTACATGGCCACAACGGCAAGCAGTTCACC  1622
Db   1711  GGGCGGCTACCCATGGCCAATGGCGGGTGACTCCTTTACATGGCCACAACGGCAAGCAGTTCACC  1770
Qy   1623  ACCCTGGACGAGAGATCATGATGTCTACACAGGAAACTGTGCCCACTACCAGAGAGGGAGGC 1682
Db   1771  ACCCTGGACAGAGAGATCATGATGTCTACACAGGAAACTGTGCCCACTACCAGAGAGGGAGGC  1830
Qy   1683  TGGTGGTATAACGGCTGTGCCCACTCCAACCTCAACGGGGGTCGTTGGTACCGCGGGGGCCAT   1742
Db   1831  TGGTGGTATAACGGCTGTGCCCACTCCAACCTCAACGGGGGTCGTTGGTACCGCGGGGGCCAT  1890
Qy   1743  TACCGGACCGCGCTACCAGGACGCGAGTCTACTGGGCTGAGTTCGGAGGGGTCTTCTTACTCA  1802
Db   1891  TACCGGACCGCGCTACCAGGACGCGAGTCTACTGGGCTGAGTTCGGAGGGGTCTTCTTACTCA  1950
Qy   1803  CTCAAGAAAGTGTGATGATGAATCAGGACGGAGTCTACTGGGCTGAGTTCGGAGTCCAGCTCC   1862
Db   1951  CTCAAGAAAGTGTGATGATGAATCAGGACGGAGTCTACTGGGCTGAGTTCGGAGTCCAGCTCC  2010
Qy   1863  CCCTCCTGACCTCTCGTGGCCATTGCCAGGAGCCCACCCTGGTCACCGCTGGCCACAGCAC   1922
Db   2011  CCCTCCTGACCTCTCGTGGCCATTGCCAGGAGCCCACCCTGGTCACCGCTGGCCACAGCAC   2070
Qy   1923  AAAGAACAAACTCCTCACCAGTTCATCCTGAGGCTGGGAGGACCGGGAATGCTGGGATTCTGT   1982
Db   2071  AAAGAACAAACTCCTCACCAGTTCATCCTGAGGCTGGGAGGACCGGGAATGCTGGGATTCTGT  2130
Qy   1983  TTTCCGAAGTCACTGCAGCGGATGATGAATCGAATACGGTGTTGTTTTCTGGTCCCTCC   2042
Db   2131  TTTCCGAAGTCACTGCAGCGGATGATGAATCGAATACGGTGTTGTTTTCTGGTCCCTCC   2190
Qy   2043  TACTTTCCTTCACACAGACAGCAGCCCCTCATGTCTTCCAGGACAGGAGGACTACAGACAA   2102
Db   2191  TACTTTCCTTCACACAGACAGCAGCCCCTCATGTCTTCCAGGACAGGAGGACTACACACAA   2250
Qy   2103  CTCTTTCTTTAAATAAAATTAAGTCTCTACAATAAAAAACA                        2141
Db   2251  CTCTTTCTTTAAATAAAATTAAGTCTCTACAATAAAAAAA                          2289
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RESULT 7
AAS21377
ID   AAS21377 standard; cDNA; 2290 BP.
XX
AC   AAS21377;
XX
DT   24-OCT-2001 (first entry)
XX
DE   Human cDNA sequence encoding for PRO196 polypeptide.
XX
KW   Human secretory and transmembrane; PRO; mammalian; cancer; lung; breast;
KW   prostate; cervical; tumour necrosis factor-alpha; TNF-alpha; cartilage;
KW   ear; proliferation; glucose; free fatty acid; skeletal muscle; adipocyte;
KW   A-peptide; factor VIIa; gene therapy; ss.
XX
OS   Homo sapiens.
XX
PN   WO200140466-A2.
XX
PD   07-JUN-2001.
XX
PF   01-DEC-2000; 2000WO-US032678.
XX
PR   01-DEC-1999; 99WO-US028301.
PR   01-DEC-1999; 99WO-US026634.
PR   02-DEC-1999; 99WO-US028551.
PR   02-DEC-1999; 99WO-US028564.
PR   02-DEC-1999; 99WO-US028565.
PR   09-DEC-1999; 99US-0170262P.
PR   16-DEC-1999; 99WO-US030095.
PR   20-DEC-1999; 99WO-US030911.
PR   20-DEC-1999; 99WO-US030999.
PR   30-DEC-1999; 99WO-US031243.
PR   30-DEC-1999; 99WO-US031274.
PR   05-JAN-2000; 99WO-US000219.
PR   06-JAN-2000; 2000WO-US000277.
PR   06-JAN-2000; 2000WO-US000376.
PR   11-FEB-2000; 2000WO-US003565.
PR   18-FEB-2000; 2000WO-US004341.
PR   18-FEB-2000; 2000WO-US004342.
PR   22-FEB-2000; 2000WO-US004414.
PR   24-FEB-2000; 2000WO-US004914.
PR   01-MAR-2000; 2000WO-US005004.
PR   02-MAR-2000; 2000WO-US005601.
PR   02-MAR-2000; 2000US-0187202P.
PR   03-MAR-2000; 2000WO-US006319.
PR   10-MAR-2000; 2000WO-US006884.
PR   15-MAR-2000; 2000US-0209832P.
PR   20-MAR-2000; 2000WO-US007377.
PR   21-MAR-2000; 2000WO-US007532.
PR   30-MAR-2000; 2000WO-US008439.
PR   17-MAY-2000; 2000WO-US013705.
PR   22-MAY-2000; 2000WO-US014042.
PR   30-MAY-2000; 2000WO-US014941.
PR   02-JUN-2000; 2000WO-US015264.
PR   05-JUN-2000; 2000US-0209832P.
PR   28-JUL-2000; 2000WO-US020710.
PR   11-AUG-2000; 2000WO-US022031.
PR   23-AUG-2000; 2000WO-US023522.
PR   24-AUG-2000; 2000WO-US023328.
PR   08-NOV-2000; 2000WO-US030952.
PR   10-NOV-2000; 2000WO-US030873.
XX
PA   (GETH) GENENTECH INC.
XX
PI   Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
PI   Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
PI   Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
XX
DR   WPI; 2001-408281/43.
DR   P-PSDB; AAU12305.
XX
PT   Isolated, secretory and transmembrane PRO polypeptide used to detect
PT   other PRO polypeptides, link bioactive molecules to cells expressing PRO
PT   polypeptides, and detect the presence of mammalian tumors e.g. lung,
PT   breast, prostate, cervical.
XX
PS   Claim 3; Fig 267; 813pp; English.

```
XX
CC   AAS21244-AAS21518 encode for novel human secretory and transmembrane PRO
CC   polypeptides. The PRO polypeptides are useful to detect other PRO
CC   polypeptides, to link bioactive molecules to cells expressing PRO
CC   polypeptides, to modulate biological activities of cells expressing PRO
CC   polypeptides, and to detect the presence of mammalian lung, colon,
CC   breast, prostate, rectal, cervical or liver tumours by comparing PRO
CC   polypeptide expression in a cell sample to that in a control sample. Some
CC   of the 275 sequences are also useful to stimulate the release of tumour
CC   necrosis factor-alpha (TNP-alpha) from human blood, the proliferation or
CC   differentiation of chondrocytes, the proliferation or gene expression in
CC   pericyte cells, the release of proteoglycans from cartilage, the
CC   proliferation of inner ear utricular supporting cells or of T-
CC   lymphocytes, the release of a cytokine from peripheral blood monocytes
CC   (PBMCs), or the proliferation of endothelial cells. Some of the PRO
CC   polypeptides may modulate glucose or free fatty acid uptake by skeletal
CC   muscle cells or by adipocytes; or inhibit binding of A-peptide to factor
CC   VIIA. The PRO polypeptides can be used in assays to identify molecules
CC   involved in binding interactions. The polynucleotides encoding PRO
CC   polypeptides can be used to generate probes, antisense RNA/DNA,
CC   transgenic or knock out animals and can be used in gene therapy
XX
SQ   Sequence 2290 BP; 537 A; 692 C; 668 G; 393 T; 0 U; 0 Other;

Query Match             98.1%;  Score 2132.6;  DB 4;  Length 2290;
Best Local Similarity   99.8%;  Pred. No. 0;  Mismatches 4;  Indels 0;  Gaps 0;
Matches  2135;  Conservative  0;  Mismatches  4;  Indels  0;  Gaps  0;
```

```
Qy      3 AAATGAGGCTGCTTGCGGACGCGCCTGAGGATGAACCCAAGCCCTTGCGAGGGTG 62
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Db    811 AAAGCAGAAGCGGCAGATCGAGACGCTGCACAGTCGTTGGTGGACGGGCATTGTG 870

Qy     63 GCACTGAGGCAGCGGCTTCACGCTACTGTGTGAGGGAAAAGAAGGTTGTGAGCAGCCCCGCAGG 122
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    871 AGCGGAGGTGAAGCGCTGCCGCCAAGGAGAGGCGCAACATGAACTCGGCGGTCTCACGGGCTC 930

Qy    123 ACCCCTGGCCACCCCTGGCCCCCAGCCTCTGCGCGAGCCCTTGTGAGGGCAGAGCCAGTG 182
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    931 TACATGCAGCTCCTTGCCACGAGGATCATCCGCAAGCGGGACAAGCGGTTGGAGCTCTCCCAG 990

Qy    183 GAGCCCAGTGAGGCAGTGAGCTGCTTGGCAGAGCCCACCCCTCCAG 242
          ||||||||||||||||||||||||||||||||||||||||||||||
Db   1023 CTGGAGAACAGATCCTGACCACAGACAGCCCACTGCCACGAGCTGCAGCTGGCCAGCAGTACAAG 1082
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[Remainder of page consists of aligned Qy/Db nucleotide sequence rows continuing through position 1802/1890, with position numbering increasing in the right column.]

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Db  1891  TACCGGAGCCGCTACCAGGACGACGGAGTCCTACTGGCGCTGAGTTCCGAGGAGGCTTACTCA  1950
Qy  1803  CTCAAGAAAGTGGTGATGAGTGAGATCGGACCGACCGACCCAACCACCTTCCACTAAGCCAGCTCC  1862
Db  1951  CTCAAGAAAGTGGTGATGAGTGAGATCGGACCGACCGACCCAACCACCTTCCACTAAGCCAGCTCC  2010
Qy  1863  CCCTCCTGACCTCCGTCGGTCCATTGCCAGGAGCGCCCACCCTGGTCTCACGGTGGCCACCAGCAC  1922
Db  2011  CCCTCCTGACCTCCGTCGGTCCATTGCCAGGAGCGCCCACCCTGGTCTCACGGTGGCCACCAGCAC  2070
Qy  1923  AAAGAACAACTCCTCACCAGTTCATCCTGAGGGTGGAGGACCGGGATGCCTGGATTCTTGT  1982
Db  2071  AAAGAACAACTCCTCACCAGTTCATCCTGAGGGTGGAGGACCGGGATGCCTGGATTCTTGT  2130
Qy  1983  TTTCCGGAGTCACTGCACGGGGATGAATGAACTGAATCATTACGGGTGTGTTTTTTCTGTTCCTCC  2042
Db  2131  TTTCCGGAGTCACTGCACGGGGATGAATGAACTGAATCATTACGGGTGTGTTTTTTCTGTTCCTCC  2190
Qy  2043  TACTTTCCTTCACACAGACAGCGCCCCCCTCATGTTCTCCAGGACGAGGACGAGGACTTACAGACAA  2102
Db  2191  TACTTTCCTTCACACAGACAGCGCCCCCTCATGTTCTCCAGGACGAGGACGAGGACTTACAGACAA  2250
Qy  2103  CTCTTTCTTTAAATAAATTAAGTCTCTACAATAAAAACA  2141
Db  2251  CTCTTTCTTTAAATAAATTAAGTCTCTACAATAAAAAAA  2289
```

```
Query Match      98.1%;  Score 2132.6;  DB 6;  Length 2290;
Best Local Similarity   99.8%;    Pred. No. 0;
Matches 2135;  Conservative  0;  Mismatches  4;  Indels  0;  Gaps  0;
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Qy   3  AAATGAGGACTTCGTGCCGGACGGCCTGAGGATGAACCCCAGACCCAAGCCCTGCCGAGCGTG  62
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Db  151  AAATGAGGACTTCGTGCCGGACGGCCTGAGGATGAACCCCAGACCCAAGCCCTGCCGAGCGTG  210
Qy   63  CGACTGAGGCCAGGCAGCCGCTGGTGACGCGGCCGTGAGGATGGACACCCAAGCCCCGCAGG  122
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Db  211  CGACTGAGGCCAGGCAGCCGCTGGTGACGCGGCCGTGAGGATGGACACCCAAGCCCCGCAGG  270
Qy  123  ACCCCTGGCCCGCCCTGGGCCCCCAGCCCTCGCCCCGGCCAGCCCCTCGCCCGAGCCCCATG  182
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Db  271  ACCCCTGGCCCGCCCTGGGCCCCCAGCCCTCGCCCCGGCCAGCCCCTCGCCCGAGCCCCATG  330
Qy  183  GAGCCCAGTGAGGCAGGGCTGCTTGGCAGGCCACCCGGCCTCGAACTCAGGAACCCCTCCAG  242
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  331  GAGCCCAGTGAGGCAGGGCTGCTTGGCAGGCCACCCGGCCTCGAACTCAGGAACCCCTCCAG  390
Qy  243  AGGCCCATGGACAGGGCTGCCCCGCGGCCAGGGTGGAAGGCATGTGAGGAGCCGCCCGCGG  302
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  391  AGGCCCATGGACAGGGCTGCCCCGCGGCCAGGGTGGAAGGCATGTGAGGAGCCGCCCGCGG  450
Qy  303  AGCCAAGCAGGAGGAAGAGCGCTTTCATAGATTCTATTCACAAAGAATAACCACATTTT  362
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  451  AGCCAAGCAGGAGGAAGAGCGCTTTCATAGATTCTATTCACAAAGAATAACCACATTTT  510
Qy  363  GCAAAGACCAATGAGGCCACTGTCGCCTGACATGCTGGTTCGGACTGCTGGCCTGCCATG  422
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Db  511  GCAAAGACCAATGAGGCCACTGTCGCCTGACATGCTGGTTCGGACTGCTGGCCTGCCATG  570
Qy  423  GGAGCTGCGTTGCAGGCCAGGAGGACGGGTTTGAGGCCACTGAGGAGGCCTCGCCAAGGAG  482
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Db  571  GGAGCTGCGTTGCAGGCCAGGAGGACGGTTTGAGGCCACTGAGGAGGCCTCGCCAAGGAG  630
Qy  483  TTCATTTACTTAAAACAGGTACAAGCCGGGCGGGGGCCGGGCAAGTGCACCTTACACC  542
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  631  TTCATTTACTTAAAACAGGTACAAGCCGGGCGGGGGCCGGGCAAGTGCACCTTACACC  690
Qy  543  TTCATTGTGCCCCAGCGACGGGTCCACGGGGTCCCATCTGCGTCAACTCCAAGGGAGCCTGAG  602
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Db  691  TTCATTGTGCCCCAGCGACGGGTCCACGGGGTCCCATCTGCGTCAACTCCAAGGGAGCCTGAG  750
Qy  603  GTGGCTTCTCGGAGAACCGAGTGCATAAGCAGGAGTGCTTCAAACAATGAAGCCTGCTC  662
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Db  751  GTGGCTTCTCGGAGAACCGAGTGCATAAGCAGGAGTGCTTCAAACAATGAAGCCTGCTC  810
Qy  663  AAGCCAGAAGCGGCGCAGATCGAGACGCTGCACAGCGGTGGAAGGGTGGACCGCGGCCATTGTG  722
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Db  811  AAGCCAGAAGCGGCGCAGATCGAGACGCTGCACAGCGGTGGAAGGGTGGACCGCGGCCATTGTG  870
Qy  723  AGCGGAGGTGAAGCTGCTGCGCGCAGGAGGAGCGGCAACATGAACTCGCGCGGGTCACGGAGCTC  782
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  871  AGCGGAGGTGAAGCTGCTGCGCGCAGGAGGAGCGGCAACATGAACTCGCGCGGGTCACGGAGCTC  930
Qy  783  TACATGCAGCTCCTGCCACGGATCATCCCAAGCGGGGACAACGCGTTGAGCTCTCCCAG  842
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Db  931  TACATGCAGCTCCTGCCACGGATCATCCCAAGCGGGGACAACGCGTTGAGCTCTCCCAG  990
Qy  843  CTGGGAGAACAGGAATCCTGAACCAGAGCCGACAATGCTGGCCAGCAAGCTACAAG  902
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  991  CTGGGAGAACAGGAATCCTGAACCAGAGCCGACAATGCTGGCCAGCAAGCTACAAG  1050
Qy  903  GACCTTGGAGCACAGTACCAGCCCACTGGCCCACACTGGCCACAACAATCAGAGATCATC  962
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1051 GACCTTGGAGCACAGTACCAGCCCACTGGCCCACACTGGCCACAACAATCAGAGATCATC  1110
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Qy    963  GCGCAGCTTGAGGAGCACTGCCAGAGAGGTGCCTCGGCCAGCCCGTCCCCAGCCACCC  1022
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1111  GCGCAGCTTGAGGAGCACTGCCAGAGAGGTGCCTCGGCCAGCCCGTCCCCAGCCACCC  1170

Qy   1023  CCCGGCTGCCCCGCCCCCGGGGTTACCAACCACCACCACCACCAACCAGATCAGCAGATC  1082
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1171  CCCGGCTGCCCCGGCGTCTACCAACCACCACCAACCCAGCCATCATCAACCAGATC  1230

Qy   1083  TCTACCAACGAGGATCAGAGTGACCAGAACCTGAAGGTGCTGCCAAGAGGGGTGCCTCC  1142
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1231  TCTACCAACGAGGATCAGAGTGACCAGAACCTGAAGGTGCTGCCAAGAGGGGCCCACT  1290

Qy   1143  ATGCCCACTCTCACCAGCCTCCCATCTTCCACGACCACAAGCCCGTCCGGCGGGCAGAGAC  1202
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1291  ATGCCCACTCTCACCAGCCTCCCATCTTCCACGACCACAAGCCCGTCCGGCCATGGGAGAC  1350

Qy   1203  TGCCTGCAGGGCCCTGGAGGATGGCCAGCAGTCCATCTCATTACTGTGGTGAAGCGGGAG  1262
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Db   1351  TGCCTGCAGGGCCCTGGAGGATGGCCACCAGAGTCCATCTCATTACTGTGGTGAAGCGGGAG  1410

Qy   1263  AACACCAAACCGCCTCATCCAGTGGTGGTGCGACCAGCAGCACGAGAGCCTGGACC  1322
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1411  AACACCAAACCGCCTCATGCAGTGTGTGCGACCAGCAGCACCCCGGGGGGCTGGACC  1470

Qy   1323  GTCATCCAGAGACGGCCTGGATGGCTCTGTTAACTTCTTCAGGAACTGGAGACGTACAAG  1382
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1471  GTCATCCAGAGACGGCCTGGATGGCTCTGTTAACTTCTTCAGGAACTGGAGACGTACAAG  1530

Qy   1383  CAAGGGTTTGGGAACATTGACGGCGGAATACTCGGCTCGCGCCTGGAGAACATTTACTGGCTG  1442
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1531  CAAGGGTTTGGGAACATTGACGGCGGAATACTGGCTCGGGCCTGGAGAACATTTACTGGCTG  1590

Qy   1443  ACGAACCAAAGGCAACTACAAAACTCCTGGTGACCCATGGAGCGGTCGGCCGGCAAAGTC  1502
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1591  ACGAACCAAAGGCAACTACAAAACTCCTGGTGACCATGGAGGAGGACGTACAAG  1650

Qy   1503  TTTGCAGAATACGGCCAGTTTCCGCCTCTGGAACCTGAGGAGCGGAGTTATTATAAGGCTG  1562
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1651  TTTGCAGAATACGGCCAGTTTCCGCCTCTGGAACCTGAGGACGCGAGTTATTATAAGGCTG  1710

Qy   1563  GGGCGGCTACCATGGCAATGCGGGGTGACTCCTTTACATGGCACAAGGCAAGCCAGTTCACC  1622
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1711  GGGCGGCTACCATGGCAATGCGGGGTGACTCCTTTACATGGCACAAGGCAAGCCAGTTCACC  1770

Qy   1623  ACCCTGGACAGAGATCATGAGTGTTCTACACAGGAAACTGTGCCCACTACCACAGAAGGGAGGC  1682
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1771  ACCCTGGACAGAGATCATGAGTGTTCCCACTACCACAGGAAACTGTGGCCAGTCC  1830

Qy   1683  TGGTGTTGTATAAGGCCCTGTCCCACTCAAACCTCAAACGGGGTGTTCTGGTTGGTACCGGGGGCCAT  1742
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1831  TGGTGGTATAACGGCTGTCCCACTCAAACCTCAAACGGGGTCTTGGTTACGGCGGGGGCCAT  1890

Qy   1743  TACCGGAGCCGCTACCAAGGACGGAGTCACTGGGCTGAGTTCCGAGGAGGCTCTTACTCA  1802
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1891  TACCGGAGCCGCTACCAAGGACGGAGTCACTGGGCTGAGTTCCGAGGAGGCTCTTACTCA  1950

Qy   1803  CTCAGAGAAAGTGGTGATGAATCGGACGAGCCCAAACCCAACACTTCCACTACAAGCCAGTCC  1862
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1951  CTCAAGAAAAGTGGTGATGAATCGGACGAGCCCAACCCCAACACACTTCCACTAAGCCAGTCC  2010

Qy   1863  CCCTCCTGACCCTCTTGTTCGGCCATTGCAGGAGCCCCACCCTGGCCACCAGCAC  1922
           |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1951  CCCTCCTGACCCTCTTGTTCGGCCATTGCAGGAGCCCCACCCTGGCCACCAGCAC  2070

Qy   1923  AAAGAACAACTCTTCACCAGTTCATCCTGAGGGTCGGGAAGGACCTGGGACTTGGAATTCGT  1982
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2071  AAAGAACAACTCTTCACCAGTTCATCCTGAGGGGAATGCTGGGAGGACCTGGGATTTCTGT  2130

Qy   1983  TTTCCGGAAGTCACTGCACGGGAGATGGAAACTGAATCGATATACGGTGTTTTTTTCTTGTCCCTCC  2042
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2131  TTTCCGGAAGTCACTGCACGGGAGATCATCATGGAACTGAATCGATACGGTGTTTTCTGTCCCTCC  2190

Qy   2043  TACTTTCCTTCACACAGACAGCGCCCTTCATGTCTCCAGGACAGCAGGAGGACTACAGACAA  2102
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2191  TACTTTCCTTCACACCAGACAGCGCCCTTCATGTCTCCAGGACAGCAGGAGGACTACAGACAA  2250

Qy   2103  CTCTTTCTTTAAATAAATTAAGTCTCTACAATAAAAACA  2141
           |||||||||||||||||||||||||||||||||||||||
Db   2251  CTCTTTCTTTAAATAAATTAAGTCTCTACAATAAAAAA  2289
```

RESULT 9

AAD31563

ID   AAD31563 standard; DNA; 2290 BP.
XX
AC   AAD31563;
XX
DT   18-JUN-2002 (first entry)
XX
DE   Human TIE ligand NL1 DNA.
XX
KW   Human; TIE ligand; NL1; cytostatic; osteopathic; vascularisation; toxin;
KW   muscular; immunoassay; therapeutic; anti-tumour agent; muscle growth;
KW   bone development; maturation; angiogenesis; ds.
XX
OS   Homo sapiens.
XX
FH
FT   Key   Location/Qualifiers
FT   CDS   520..2001
FT   /*tag= a
FT   /product= "Human NL1 protein"
XX
PN   US6350450-B1.
XX
PD   26-FEB-2002.
XX
PF   19-AUG-1998; 98US-00136828.
XX
PR   19-SEP-1997; 97US-0059588P.
XX
PA   (GETH) GENENTECH INC.
XX
PI   Godowski PJ, Gurney AL, Goddard A, Hillan K;
XX
DR   WPI; 2002-215264/27.
DR   P-PSDB; AAB19825.
XX
PT   Novel isolated antibody which specifically binds to a mammalian NL1 TIE
PT   ligand useful for immunoassays, delivery of cytotoxic molecules and as
PT   diagnostic agents to detect disease states.
XX
PS   Claim 12; Fig 2; 59pp; English.
XX
CC   The invention relates to an isolated antibody which specifically binds to
CC   a mammalian NL1 TIE (Tyrosine kinase containing Ig and EGF homology
CC   domains) ligand polypeptide which is capable of inducing vascularisation.
CC   The isolated antibody may be used in immunoassays to measure the amount
CC   of a TIE ligand in a biological sample. Additionally, the antibody may be
CC   used for the delivery of cytotoxic molecules, e.g. radioisotopes or
CC   toxins, or therapeutic agents to cells expressing a corresponding TIE
CC   receptor. The therapeutic agents may, for example, be other TIE ligands,
CC   including the TIE-2 ligand, members of the vascular endothelial growth
CC   factor (VEGF) family, or known anti-tumour agents, and agents known to be
CC   associated with muscle growth or development. Anti-TIE ligand antibodies
CC   are also suitable as
CC   maturation, or growth. Anti-TIE ligand antibodies are also suitable as
CC   diagnostic agents, to detect disease states associated with the
CC   expression of a TIE (e.g. TIE-2) receptor. These detectably labelled
CC   antibody agonists of a TIE receptor can be used for imaging the presence
CC   of angiogenesis. The present sequence is human TIE ligand NL1 DNA
XX
SQ   Sequence 2290 BP; 537 A; 692 C; 668 G; 393 T; 0 U; 0 Other;

Query Match   98.1%;   Score 2132.6;   DB 6;   Length 2290;
Best Local Similarity   99.8%;
Matches 2135;   Conservative 0;   Mismatches 4;   Indels 0;   Gaps 0;

RESULT 10
ACD23986
ID   ACD23986 standard; cDNA; 2290 BP.
XX
AC   ACD23986;
XX
DT   26-AUG-2003 (first entry)
XX
DE   Novel human secreted and transmembrane protein PRO196 cDNA.
XX
KW   Human; secreted and transmembrane protein; PRO; antiinflammatory;
KW   antiarteriosclerotic; cardiant; anti-infertility; anti-HIV; cytostatic;
KW   antidiabetic; gene therapy; tumour necrosis factor (TNF)-alpha release;
KW   TNF-alpha release; cell proliferation; cell differentiation;
KW   gene expression modulator; proteoglycan release; cytokine release;
KW   tumour; inflammatory disease; organ failure; atherosclerosis;
KW   cardiac injury; infertility; birth defect; premature aging; AIDS;
KW   acquired immunodeficiency syndrome; cancer; diabetic complication;
KW   chromosome mapping; gene mapping; pharmaceutical; diagnostic; biosensor;
KW   bioreactor; tissue typing; gene; ss.
XX
OS   Homo sapiens.
XX
PN   US20032156-A1.
XX
PD   13-FEB-2003.
XX
PF   06-MAY-2002; 2002US-0014047.
XX
PR   31-MAR-1997; 97WO-US005230.
PR   12-JUN-1998; 98WO-US012456.
PR   14-JUL-1998; 98WO-US014552.
PR   28-AUG-1998; 98WO-US017888.
PR   10-SEP-1998; 98WO-US018824.
PR   14-SEP-1998; 98WO-US019093.
PR   14-SEP-1998; 98WO-US019094.
PR   14-SEP-1998; 98WO-US019177.
PR   16-SEP-1998; 98WO-US019330.
PR   17-SEP-1998; 98WO-US019437.
PR   07-OCT-1998; 98WO-US021141.
PR   29-OCT-1998; 98WO-US022991.
PR   29-OCT-1998; 98WO-US022992.
PR   20-NOV-1998; 98WO-US024855.
PR   01-DEC-1998; 98WO-US025108.
PR   05-JAN-1999; 99WO-US000106.
PR   08-MAR-1999; 99WO-US005028.
PR   10-MAR-1999; 99WO-US005190.
PR   20-APR-1999; 99WO-US008615.
PR   14-MAY-1999; 99WO-US010733.
PR   02-JUN-1999; 99WO-US012252.
PR   01-SEP-1999; 99WO-US020111.
PR   08-SEP-1999; 99WO-US020594.
PR   13-SEP-1999; 99WO-US020944.
PR   15-SEP-1999; 99WO-US021090.
PR   15-SEP-1999; 99WO-US021547.
PR   25-OCT-1999; 99WO-US023089.
PR   29-NOV-1999; 99WO-US028214.
PR   30-NOV-1999; 99WO-US028313.
PR   30-NOV-1999; 99WO-US028409.
PR   01-DEC-1999; 99WO-US028301.
PR   01-DEC-1999; 99WO-US028634.
PR   02-DEC-1999; 99WO-US028551.
PR   02-DEC-1999; 99WO-US028564.
PR   02-DEC-1999; 99WO-US028565.
PR   16-DEC-1999; 99WO-US030095.
PR   20-DEC-1999; 99WO-US030911.
PR   20-DEC-1999; 99WO-US030999.
PR   22-DEC-1999; 99WO-US030720.
PR   30-DEC-1999; 99WO-US031243.
PR   30-DEC-1999; 99WO-US031274.
PR   05-JAN-2000; 2000WO-US000219.
PR   06-JAN-2000; 2000WO-US000277.
PR   06-JAN-2000; 2000WO-US000376.

PR   11-FEB-2000; 2000WO-US003565.
PR   18-FEB-2000; 2000WO-US004341.
PR   18-FEB-2000; 2000WO-US004342.
PR   22-FEB-2000; 2000WO-US004414.
PR   24-FEB-2000; 2000WO-US004914.
PR   24-FEB-2000; 2000WO-US005004.
PR   01-MAR-2000; 2000WO-US005601.
PR   02-MAR-2000; 2000WO-US005746.
PR   02-MAR-2000; 2000WO-US005841.
PR   10-MAR-2000; 2000WO-US006319.
PR   15-MAR-2000; 2000WO-US006884.
PR   20-MAR-2000; 2000WO-US007377.
PR   21-MAR-2000; 2000WO-US007532.
PR   30-MAR-2000; 2000WO-US008439.
PR   17-MAY-2000; 2000WO-US013705.
PR   22-MAY-2000; 2000WO-US014042.
PR   30-MAY-2000; 2000WO-US014941.
PR   02-JUN-2000; 2000WO-US015264.
PR   28-JUL-2000; 2000WO-US020710.
PR   11-AUG-2000; 2000WO-US022031.
PR   23-AUG-2000; 2000WO-US023522.
PR   24-AUG-2000; 2000WO-US023328.
PR   08-NOV-2000; 2000WO-US030952.
PR   10-NOV-2000; 2000WO-US030873.
PR   01-DEC-2000; 2000WO-US032678.
PR   20-DEC-2000; 2000US-00747259.
PR   28-FEB-2001; 2001WO-US096498.
PR   28-FEB-2001; 2001WO-US066520.
PR   01-MAR-2001; 2001WO-US002706.
PR   09-MAR-2001; 2001US-00802706.
PR   14-MAR-2001; 2001US-00806889.
PR   22-MAR-2001; 2001US-00816744.
PR   05-APR-2001; 2001US-00828366.
PR   10-MAY-2001; 2001US-00854208.
PR   10-MAY-2001; 2001US-00854280.
PR   18-MAY-2001; 2001US-00860216.
PR   25-MAY-2001; 2001US-00860028.
PR   25-MAY-2001; 2001US-00866034.
PR   01-JUN-2001; 2001WO-US017092.
PR   01-JUN-2001; 2001US-00872035.
PR   01-JUN-2001; 2001WO-US017800.
PR   05-JUN-2001; 2001US-00874503.
PR   14-JUN-2001; 2001US-00882636.
PR   19-JUN-2001; 2001US-00886342.
PR   20-JUN-2001; 2001US-00887879.
PR   21-JUN-2001; 2001US-00887879.
PR   22-JUN-2001; 2001WO-US020116.
PR   29-JUN-2001; 2001WO-US021066.
PR   09-JUL-2001; 2001WO-US021735.
PR   18-JUL-2001; 2001WO-US090827.
PR   06-AUG-2001; 2001US-00924419.
PR   09-AUG-2001; 2001US-00927796.
PR   16-AUG-2001; 2001US-00931836.
PR   19-DEC-2001; 2001US-00028072.
XX
PA   (GETH) GENENTECH INC.
XX
PI   Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
PI   Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
PI   Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
XX
DR   WPI; 2003-341980/32.
DR   P-PSDB; AB017749.
XX
PT   New secreted and transmembrane PRO nucleic acids, for treating
PT   inflammation, organ failure, atherosclerosis, cardiac injury,
PT   infertility, birth defects, premature aging, acquired immunodeficiency
PT   syndrome (AIDS), or cancer.
XX
PS   Claim 2; Fig 267; 660pp; English.
XX
CC   The invention describes an isolated nucleic acid (I) comprising, or which

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CC   has 80 % sequence identity to, or the full-length coding sequence of, one
CC   of 275 nucleotide sequences, and which encodes a corresponding
CC   polypeptide selected from 275 amino acid sequences, where all sequences
CC   are given in the specification. The polypeptide encoded by (I) is used to
CC   detect PRO polypeptides, link a bioactive molecule to a cell, stimulate a
CC   PRO polypeptide, modulate a biological activity of a cell expressing a
CC   release of PRO polypeptide, modulate a biological activity of a cell, stimulate the
CC   the uptake of glucose or free fatty acid by cells, stimulate or inhibit
CC   the proliferation or differentiation of cells or gene expression,
CC   stimulate the release of proteoglycans, stimulate the release of cytokine
CC   from peripheral blood mononuclear cells, inhibit the binding of A-peptide
CC   to factor VIIa, or detect the presence of tumour in a mammal. The nucleic
CC   acid and polypeptide encoded by it, are useful for treating inflammatory
CC   diseases, organ failure, atherosclerosis, cardiac injury, infertility,
CC   birth defects, premature aging, acquired immunodeficiency syndrome
CC   (AIDS), cancer, or diabetic complications. The nucleic acid is useful as
CC   hybridisation probes, in chromosome and gene mapping, and in generating
CC   antisense RNA or DNA. The polypeptides are useful as pharmaceuticals,
CC   diagnostics, biosensors or bioreactors. Both are useful in tissue typing.
CC   This sequence encodes a novel human secreted and transmembrane PRO
CC   polypeptide.
XX
SQ   Sequence 2290 BP; 537 A; 692 C; 668 G; 393 T; 0 U; 0 Other;
```

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Query Match             98.1%;  Score 2132.6;  DB 7;  Length 2290;
Best Local Similarity   99.8%;  Pred. No.0;
Matches  2135;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;
```

```
Qy      3 AAATGAGGGCTGCTGCCGACGGCGGCGTCGAGGATGAAACCCCAAGACCCTGGACCTGCCGAGCGTG 62
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    151 AAATGAGGGCTGCTGCCGACGGCGGCGTCGAGGATGAAACCCCAAGACCCTGGACCTGCCGAGCGTG 210

Qy     63 GCACTGAGGCAGCCGGCCGCTGACCGCTACTGTGTGAGGAAAAGAAAGGTTGTGAGCCAGCCCCGAGG 122
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    211 GCACTGAGGCAGCCGGCCGCTGACCGCTACTGTGTGAGGAAAAGAAAGGTTGTGAGCCAGCCCCGAGG 270

Qy    123 ACCCCTGGGCGCAGCCCTGGGCCCCAGCCTCTGTGGAGGGCAGAGCCAGTG 182
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db    271 ACCCCTGGGCGCAGCCCTGGGCCCCAGCCTCTGTGGAGGGCAGAGCCAGTG 330

Qy    183 GAGCCCAGTGATCGAGGCCAGGGCTGCTTGTTGCCGCACCACCGGGCCCGCTGAACTCAGGGAACCCCTTCCAG 242
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    331 GAGCCCAGTGATCGAGGCCAGGGCTGCTTGTTGCCGCACCACCGGGCCCGCTGAACTCAGGGAACCCCTTCCAG 390

Qy    243 AGGCCATGGACAGGCTGCCCCGCTGACGGCGCGAAGCTGAGTGACGAGGAGGCGGAGCGGGAG 302
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    391 AGGCCATGGACAGGCTGCCCCGCTGACGGCGCGAAGCTGAGTGACGAGGAGGCGGAGCGGGAG 450

Qy    303 AGCCAAGCAGAGAGGGAAGAGGCCTTCATGAGATTCTATTCACAAGAGAATAACCACCACCATTTT 362
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    451 AGCCAAGCAGAGAGGGAAGAGGCCTTCATGAGATTCTATTCACAAGAGAATAACCACCACCATTTT 510

Qy    363 GCAAAGACCATGAGGCCACTGTGCGTGACATGCTGGCCTCGGACTGCTCGGCCATG 422
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    511 GCAAAGACCATGAGGCCACTGTGCGTGACATGCTGGCCTCGGACTGCTCGGCCATG 570

Qy    423 GGAGCTGTTGCAGGCCAGGAGGACGGGTTTTGAGGGACTGCTCGCCCAGAGAG 482
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    571 GGAGCTGTTGCAGGCCAGGAGGACGGGTTTTGAGGGACTGCTCGCCCAGAGAG 630

Qy    483 TTCATTTACCTTAAACAGGTACAAGCGGGCGGGGGGCGGGGCGCACCTACACC 542
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    631 TTCATTTACCTTAAACAGGTACAAGCGGGCGGGGGGCGGGGCGCACCTACACC 690

Qy    543 TTCATTGTGCCCCAGCAGCGCGGGGTCCCATCTGGCTGCAACTCCAAGGACCCTGAG 602
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    691 TTCATTGTGCCCCAGCAGCGCGGGGTCCCATCTGGCTGCAACTCCAAGGACCCTGAG 750

Qy    603 GTGCCTTCTGGAGGAACCGGAGTGCATAAGCAGGACTAGAGCGTCTCAACAATGAGGCTGCTC 662
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    751 GTGCCTTCTGGAGGAACCGGAGTGCATAAGCAGGACTAGAGCGTCTCAACAATGAGGCTGCTC 810

Qy    663 AAGCAGAAGCGGCAGATCGAGACGCTGGTGAAGGTGGAGCGCGGGCGGCCATTGTG 722
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    811 AAGCAGAAGCGGCAGATCGAGACGCTGGTGAAGGTGGAGCGCGGGCGGCCATTGTG 870

Qy    723 ACGGAGGTGAACCTGCTGTGCGGCAAGGAGAGAGCCGCCAACATGAACGTCCAGCTC 782
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    871 ACGGAGGTGAACCTGCTGTGCGGCAAGGAGAGAGCCGCCAACATGAACGTCCAGCTC 930

Qy    783 TACATGCAGCTCCTGCACGAGATCATCCGGACAACGGCGGTTGGAGTCTCCCAG 842
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    931 TACATGCAGCTCCTGCACGAGATCATCCGGACAACGGCGGTTGGAGTCTCCCAG 990

Qy    843 CTGGAGAACAGGATCCTGAACCAGACCAGCAGCCGGCTGCGCCCAGCCAGTCAAG 902
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    991 CTGGAGAACAGGATCCTGAACCAGACCAGCAGCCGGCTGCGCCCAGCCAGTCAAG 1050

Qy    903 GACCTGGAGCACAAGTACCAGCACCTGGCCCACACTGGCCCACAACCAAATCAGAGATCATC 962
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1051 GACCTGGAGCACAAGTACCAGCACCTGGCCCACACTGGCCCACAACCAAATCAGAGATCATC 1110

Qy    963 GCGCAGCTTGAGGAGCACTGCCAGAGGCGTGCCCTCGGCCAGCCCGTCCCCAGCCACCC 1022
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1111 GCGCAGCTTGAGGAGCACTGCCAGAGGCGTGCCCTCGGCCAGCCCGTCCCCAGCCACCC 1170

Qy   1023 CCCGCTGCCCCGCCCCCGGGGGTCTTACACAACACCACTCATCACAACAGAATC 1082
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1171 CCCGCTGCCCCGCCCCCGGGGGTCTTACACAACACCACTCATCACAACAGAATC 1230

Qy   1083 TCTACCAACGGAATCCAGAGTGACCAGAACCTGAAGGTGCTGCACCCCTCTGCCCACT 1142
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1231 TCTACCAACGGAATCCAGAGTGACCAGAACCTGAAGGTGCTGCACCCCTCTGCCCACT 1290

Qy   1143 ATGCCCACTCTTCACCAGCCTCCCATCTTCACCGACAAGCCGTCGGGCCCATGGAGAC 1202
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1291 ATGCCCACTCTTCACCAGCCTCCCATCTTCACCGACAAGCCGTCGGGCCCATGGAGAC 1350

Qy   1203 TGCCTGCAGGGCCCTGGAGGATGGCCAGACGACACAGCTCAATCACTGGTGGAAGCCGGAG 1262
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1351 TGCCTGCAGGGCCCTGGAGGATGGCCAGACGACACAGCTCAATCACTGGTGGAAGCCGGAG 1410

Qy   1263 AACACCAACCCCTCATGCAGGTGTGGTGCACGAACAGAGACACAGCCCCGGGGGCTGGACC 1322
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1411 AACACCAACCCCTCATGCAGGTGTGGTGCACGAACAGAGACACAGCCCCGGGGGCTGGACC 1470

Qy   1323 GTCATCCAGACAGACCGCCTGGATGGCCTCTTGTTTAACTTCTTCAGGAACTGGGGACCTTACAAG 1382
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1471 GTCATCCAGACAGACCGCCTGGATGGCCTCTTGTTTAACTTCTTCAGGAACTGGGGACCTTACAAG 1530

Qy   1383 CAAGGGTTTGGGGAACATTGACGGCGGAAATACTGGGCTGGGCTGGAGAACATTTACTGGCTG 1442
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Db   1531 CAAGGGTTTGGGGAACATTGACGGCGGAAATACTGGGCTGGGCTGGAGAACATTTACTGGCTG 1590

Qy   1443 ACGAACCAAGGCAACTACAAACTCCTGGTGACCATGGAGGACTGGTTCCGGCCAAAGTC 1502
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1591 ACGAACCAAGGCAACTACAAACTCCTGGTGACCATGGAGGACTGGTTCCGGCCAAAGTC 1650

Qy   1503 TTTGCAGAATACGCCAGTTTCCGCCTGGAACCTGAGAGGGGACTGGTCGCGGGGTG 1562
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1651 TTTGCAGAATACGCCAGTTTCCGCCTGGAACCTGAGAGGGGACTGGTCGCGGGGTG 1710

Qy   1563 GGGCGCTACCATGGCAATGCGGGTGACTCCTTTCTTTACATTGCCAACGGCCAGTTCACC 1622
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1711 GGGCGCTACCATGGCAATGCGGGTGACTCCTTTCTTTACATTGCCAACGGCCAGTTCACC 1770

Qy   1623 ACCCTGGACAGAGATCATGAGTCTACACAGGAGAAACTGCCCACTACCACTACCAGAGGAGGC 1682
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1771 ACCCTGGACAGAGATCATGAGTCTACACAGGAGAAACTGCCCACTACCACTACCAGAGGAGGC 1830

Qy   1683 TGGTGGTATAACGCCGTGCCCACTCCAACCTCAACCTGAGGGGGTTCGGTATACGGGCCAT 1742
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1831 TGGTGGTATAACGCCGTGCCCACTCCAACCTCAACCTGAGGGGGTTCGGTATACGGGCCAT 1890

Qy   1743 TACCCGAGCCGCACCAGGACGGAGAGTCTACTGGGCTGAGTTCCGAGCTCTTACTCA 1802
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Db  1891  TACCGGAGCCGGCTACCAGGACCGGAGTCTACTCGGGCTGAGTTCCGAGGAGGCTCTTACTCA  1950
Qy  1803  CTCAAGAAAAGTGGTGATGATGATCCAGCAACCCAAACACCTTCACTAAGCCAGCTCC  1862
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1951  CTCAAGAAAAGTGGTGATGATGATCCAGCAACCCAAACACCTTCACTAAGCCAGCTCC  2010
Qy  1863  CCCTCCTGACCTCTCGTTGGCCATTGCCAGGAGACCCAACCCTGGTCACCGCTGCCACAGCAC  1922
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2011  CCCTCCTGACCTCTCGTTGGCCATTGCCAGGAGACCCAACCCTGGTCACCGCTGCCACAGCAC  2070
Qy  1923  AAAGAACAAACTCCTCACCAGTTCATCCTGAGGCTGGGAGGAGACCGGGAGATGCTGGATTCTGT  1982
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2071  AAAGAACAAACTCCTCACCAGTTCATCCTGAGGCTGGGAGGAGACCGGGAGATGCTGGATTCTGT  2130
Qy  1983  TTTCCGAAGTCACTGCGAGGGATGATGGAAACTGAATCGATACGGGTGTTTTCGTCCCTCC  2042
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Db  2131  TTTCCGAAGTCACTGCGAGGGATGATGGAAACTGAATCGATACGGGTGTTTTCGTCCCTCC  2190
Qy  2043  TACTTTCCTTCACACAGACAGCCCCCTCCATGTCTCAGGACAGGACAGGACTACAGACAA  2102
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Db  2191  TACTTTCCTTCACACAGACAGCCCCCTCCATGTCTCAGGACAGGACAGGACTACAGACAA  2250
Qy  2103  CTCTTTCTTTAAATAAAATTAAGTCTCTTACAATTAAAAAACA  2141
          ||||||||||||||||||||||||||||||||||||||
Db  2251  CTCTTTCTTTAAATAAAATTAAGTCTCTTACAATTAAAAAA  2289
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RESULT 11

ACD42312

ID   ACD42312 standard; cDNA; 2290 BP.
XX
AC   ACD42312;
XX
DT   05-SEP-2003 (first entry)
XX
DE   Novel human secreted and transmembrane protein PRO196 cDNA.
XX
KW   Human; secreted and transmembrane protein; PRO; antidiabetic;
KW   ophthalmological; cytostatic; immunostimulant; gene therapy;
KW   vascular endothelial growth factor inhibitor; hypertrophy of adult heart;
KW   protein secretion disorder; pancreas disorder; diabetes;
KW   vascular permeability; retinal neuron cell survival; retinal disorder;
KW   immune response; inflammation; mononuclear cell infiltration;
KW   eosinophil infiltration; apoptosis; neoplastic growth; gene; ss.
XX
OS   Homo sapiens.
XX
PN   US2003040014-A1.
XX
PD   27-FEB-2003.
XX
PF   01-FEB-2002; 2002US-00066269.
XX

PR 09-SEP-1998; 98US-0099601P.
PR 18-AUG-1998; 98US-0097000P.
PR 10-AUG-1998; 98US-0095998P.
PR 14-JUL-1998; 98WO-US014552.
PR 08-APR-1998; 98US-0081049P.
PR 25-MAR-1998; 98US-0079294P.
PR 09-FEB-1998; 98US-0074092P.
PR 09-FEB-1998; 98US-0074086P.
PR 16-DEC-1997; 97US-0069694P.
PR 25-NOV-1997; 97US-0066800P.
PR 21-NOV-1997; 97US-0066364P.
PR 29-OCT-1997; 97US-0063733P.
PR 27-OCT-1997; 97US-0063329P.
PR 24-OCT-1997; 97US-0063082P.
PR 24-OCT-1997; 97US-0062816P.
PR 17-OCT-1997; 97US-0062295P.
PR 19-SEP-1997; 97US-0059588P.
PR 18-SEP-1997; 97US-0059263P.
PR 17-SEP-1997; 97US-0059115P.
PR 26-AUG-1997; 97US-0056974P.
XX
PR 15-NOV-2001; 2001US-00002796.
PR 09-JUL-2001; 2001WO-US021735.
PR 29-JUN-2001; 2001US-0021066.
PR 20-JUN-2001; 2001WO-US019692.
PR 01-JUN-2001; 2001WO-US017800.
PR 30-MAY-2001; 2001WO-US017443.
PR 28-FEB-2001; 2001WO-US005520.
PR 01-DEC-2000; 2000WO-US032678.
PR 24-AUG-2000; 2000WO-US023522.
PR 23-AUG-2000; 2000WO-US023328.
PR 11-AUG-2000; 2000WO-US022031.
PR 02-JUN-2000; 2000WO-US015264.
PR 30-MAY-2000; 2000WO-US014941.
PR 22-MAY-2000; 2000WO-US014042.
PR 17-MAY-2000; 2000WO-US013705.
PR 15-MAY-2000; 2000WO-US013358.
PR 30-MAR-2000; 2000WO-US008439.
PR 20-MAR-2000; 2000WO-US007377.
PR 09-MAR-2000; 2000WO-US005841.
PR 02-MAR-2000; 2000WO-US005601.
PR 01-MAR-2000; 2000WO-US004414.
PR 22-FEB-2000; 2000WO-US004442.
PR 18-FEB-2000; 2000WO-US004341.
PR 05-JAN-2000; 2000WO-US000219.
PR 20-DEC-1999; 99WO-US030999.
PR 07-DEC-1999; 99US-0169495P.
PR 02-DEC-1999; 99US-0285565.
PR 01-DEC-1999; 99US-0285001.
PR 30-NOV-1999; 99US-0028313.
PR 15-SEP-1999; 99US-0028347.
PR 15-SEP-1999; 99US-0021090.
PR 08-SEP-1999; 99US-0025094.
PR 01-SEP-1999; 99US-0020011.
PR 17-AUG-1999; 99US-0149396P.
PR 26-JUL-1999; 99US-0145698P.
PR 20-JUL-1999; 99US-0145070P.
PR 15-JUN-1999; 99WO-0139695P.
PR 02-JUN-1999; 99US-0125252.
PR 23-MAR-1999; 99US-0125778P.
PR 08-MAR-1999; 98US-0025028.
PR 01-DEC-1998; 98US-0025190.
PR 25-NOV-1998; 98US-0024855.
PR 20-NOV-1998; 98US-0103040P.
PR 28-OCT-1998; 98US-0106020P.
PR 24-SEP-1998; 98US-0101922P.
PR 17-SEP-1998; 98US-0100858P.
PR 17-SEP-1998; 98WO-US019437.
PR 16-SEP-1998; 98WO-US019330.
PR 14-SEP-1998; 98WO-US019093.
PR 10-SEP-1998; 98US-0018824.
PR 10-SEP-1998; 98US-0099812P.
PR 10-SEP-1998; 98US-0099811P.
PR 10-SEP-1998; 98US-0099803P.
XX
PA (GETH) GENENTECH INC.
XX
PI Ashkenazi AJ, Baker KP, Botstein DA, Desnoyers L, Eaton DL;
PI Ferrara N, Fong S, Gao W, Gerber H, Goddard A;
PI Godowski PJ, Gurney AL, Kljavin IU, Mather JP, Napier MA, Pan J;
PI Paoni NF, Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM;
PI Wood WI, Zhang Z;
XX
DR WPI; 2003-503396/47.
DR P-PSDB; AB025150.
XX

PT   New secreted and transmembrane PRO polypeptides, useful for treating
PT   diabetes, retinal disorders and stimulating an immune response.
XX
PS   Claim 2; Fig 1; 254pp; English.
XX
CC   The invention describes an isolated polypeptide (I) having at least 80 %

CC amino acid sequence identity to 30 secreted and transmembrane
CC polypeptides. PRO polypeptides are also useful for stimulating
CC hypertrophy of adult heart, for inhibiting vascular endothelial growth
CC factor stimulated proliferation of endothelial cells, stimulating
CC proliferation of stimulated T-lymphocytes and for inducing
CC proliferation of stimulated T-lymphocytes and for inducing proliferation
CC of PDB12 pancreatic ductal cells and are thus useful in the treatment of
CC disorders which involve protein secretion by the pancreas, including
CC diabetes. PRO polypeptides are useful for inducing vascular permeability
CC and in enhancing survival of retinal neurons cells and are thus useful
CC for the treatment of retinal disorders. PRO polypeptides are also useful
CC for stimulating an immune response and inducing inflammation by inducing
CC mononuclear cell and eosinophil infiltration at the site of infection of
CC an animal. The PRO polypeptides are further useful for inducing apoptosis
CC in endothelial cells for inhibiting neoplastic growth. This sequence
CC encodes a novel human secreted and transmembrane PRO polypeptide
XX
SQ Sequence 2290 BP; 537 A; 692 C; 668 G; 393 T; 0 U; 0 Other;

Query Match   98.1%; Score 2132.6; DB 7; Length 2290;
Best Local Similarity   99.8%; Pred. No. 0; Mismatches 4;
Matches 2135; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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Qy       3 AAATGAGGCTGCTGCGGACGGGCCTGAGGATGAACCCAAGCCCTGCGACGGTG      62
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     151 AAATGAGGCTGCTGCGGACGGGCCTGAGGATGAACCCAAGCCCTGCGACGGTG     210

Qy      63 GCACTGAGGCAGCGGCGGCTACTGTGAGGGAAAGAAGGTTGTGAGCACCCCCAGG     122
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     211 GCACTGAGGCAGCGGCGGCTACTGTGAGGGAAAGAAGGTTGTGAGCACCCCCAGG     270

Qy     123 ACCCCTGGCCAGCCCTGGCCCTGGGAGGCAGAGCCAGTG     182
           |||||||||||||||||||||||||||||||||||||||
Db     271 ACCCCTGGCCAGCCCTGGCCCTGGGAGGCAGAGCCAGTG     330

Qy     183 GAGCCCAGTGAGGCCAGGGCTGCTTGGCAGCCAGAACCCTCAG     242
           |||||||||||||||||||||||||||||||||||||||||||
Db     331 GAGCCCAGTGAGGCCAGGGCTGCTTGGCAGCCAGAACCCTCAG     390

Qy     243 AGGCCCATGGACAGGCCTGCCCCGTGACGGTGAAGTGAGGGAGCGCGCCCCCG     302
           |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     391 AGGCCCATGGACAGGCCTGCCCCGTGACGGTGAAGTGAGGGAGCGCGCCCCCG     450

Qy     303 AGCCAAGCAGGAGGACAGAGGCTTTCAATAGATTCTATTCACAAAGAATAAACCACAATTTT     362
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     451 AGCCAAGCAGGAGGAGAAGAGGCTTTCAATAGATTCTATTCACAAAGAATAAACCACAATTTT     510

Qy     363 GCAAAGACCCATGAGGCCACTGTGTGCGTGGACACATGGTCGGTCGGTCTGCCATG     422
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     511 GCAAAGACCCATGAGGCCACTGTGTGCGTGGACACATGGTCGGTCGGTCTGCCATG     570

Qy     423 GGAGCTGTTGCAGGCCAGGAGGACAGGGTTTTGAGGGGCCACTGAGGAGGCCTCAAGAGAG     482
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     571 GGAGCTGTTGCAGGCCAGGAGGACAGGGTTTTGAGGGGCCACTGAGGAGGCCTCAAGAGAG     630

Qy     483 TTCAATTTACCTAAACAGGTACAAGCGGGCGCGGCAGTCGCACCTACACC     542
           ||||||||||||||||||||||||||||||||||||||||||||||||||
Db     631 TTCAATTTACCTAAACAGGTACAAGCGGGCGCGGCAGTCGCACCTACACC     690

Qy     543 TTCATTGTGCCCCAGCAGCGGCGGTCAACGGGGTGCCATCTGCCGTCAAGCTCCAGGAGCCTGAG     602
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     691 TTCATTGTGCCCCAGCAGCGGCGGTCAACGGGGTGCCATCTGCCGTCAAGCTCCAGGAGCCTGAG     750

Qy     603 GTGCTTCTGGGAGAACCAGTGCATAAGCAGAGCTAGAGCTGCTCAACAATGAGCGCTC     662
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     751 GTGCTTCTGGGAGAACCAGTGCATAAGCAGAGCTAGAGCTGCTCAACAATGAGCGCTC     810

Qy     663 AAGCAGAAGCGGCAGGATCGAGCGCTCGCAGCAGTCGGTAGAAGGTGGCACGGGCCATTGTG     722
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     811 AAGCAGAAGCGGCAGGATCGAGCGCTCGCAGCAGTCGGTAGAAGGTGGCACGGGCCATTGTG     870

Qy     723 ACGGAGGTGAAGCTGCTGCGAGGAGAACGCTCGCGGGGTCACGCAGCTC     782
           |||||||||||||||||||||||||||||||||||||||||||||||||
Db     871 ACGGAGGTGAAGCTGCTGCGGAAGGAGAGAGCCGCACACATGAACTCGCGGGGTCACGCAGCTC     930
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Qy   1863 CCCTCCTTGACCTTCTGCTGGCCATTGCCAGGAGCCCACCTGGTCACGCTGGCCACAGCAC 1922
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2011 CCCTCCTTGACCTTCTGCTGGCCATTGCCAGGAGCCCACCTGGTCACGCTGGCCACAGCAC 2070

Qy   1923 AAAGAACAACTCCTTCACCCAGTTCATCCTGAGGCCTGGGAGGACCCGGAGGATGCTGGATTCTGT 1982
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2071 AAAGAACAACTCCTTCACCCAGTTCATCCTGAGGCCTGGGAGGACCCGGAGGATGCTGGATTCTGT 2130

Qy   1983 TTTCCGAAGTCACTGCACGGATGAGAACTGAAATCGATACGGTGTTTTTCTGTCCTCC 2042
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2131 TTTCCGAAGTCACTGCACGGATGAGAACTGAAATCGATACGGTGTTTTTCTGTCCTCC 2190

Qy   2043 TACTTTCCTTCACACCAGACACCAGCGCCCTCATGTCTCCAGGACAGGACAGGACTACAGGACA 2102
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2191 TACTTTCCTTCACACCAGACACCAGCGCCCTCATGTCTCCAGGACAGGACAGGACTACAGGACA 2250

Qy   2103 CTCTTTCTTTAAAATAAATTAAGTCTCTACAATAAAAACA 2141
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Db   2251 CTCTTTCTTTAAAATAAATTAAGTCTCTACAATAAAAAAA 2289
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RESULT 12
ACA67127

ID   ACA67127 standard; cDNA; 2290 BP.
XX
AC   ACA67127;
XX
DT   23-JUN-2003 (first entry)
XX
DE   cDNA encoding human PRO polypeptide #134.
XX
KW   Human; PRO polypeptide; secreted and transmembrane protein;
KW   anti-PRO antibody; diagnostic assay; gene expression; diabetes;
KW   bone disorder; cartilage disorder; rheumatoid arthritis; obesity;
KW   sports injury; osteoarthritis; hyper-insulinaemia; hypo-insulinaemia;
KW   hearing loss; coagulation disorder; stroke; heart attack; cardiant;
KW   antidiabetic; anorectic; vulnerary; antiarthritic; osteopathic;
KW   antirheumatic; auditory; cerebroprotective; angiogenic; gene; ss.
XX
OS   Homo sapiens.
XX
PN   US2003004311-A1.
XX
PD   02-JAN-2003.
XX
PF   19-DEC-2001; 2001US-00028072.
XX
PR   18-JUN-1997; 97US-0049911P.
PR   26-AUG-1997; 97US-0056974P.
PR   17-SEP-1997; 97US-0059113P.
PR   17-SEP-1997; 97US-0059115P.
PR   17-SEP-1997; 97US-0059117P.
PR   17-SEP-1997; 97US-0059122P.
PR   17-SEP-1997; 97US-0059184P.
PR   17-SEP-1997; 97US-0059263P.
PR   18-SEP-1997; 97US-0059352P.
PR   19-SEP-1997; 97US-0059588P.
PR   24-SEP-1997; 97US-0059836P.
PR   17-OCT-1997; 97US-0062250P.
PR   17-OCT-1997; 97US-0062285P.
PR   17-OCT-1997; 97US-0062287P.
PR   17-OCT-1997; 97US-0062755P.
PR   17-OCT-1997; 97US-0062814P.
PR   24-OCT-1997; 97US-0062816P.
PR   24-OCT-1997; 97US-0063045P.
PR   24-OCT-1997; 97US-0063082P.
PR   24-OCT-1997; 97US-0063127P.
PR   27-OCT-1997; 97US-0063327P.
PR   28-OCT-1997; 97US-0063329P.
PR   28-OCT-1997; 97US-0063550P.
PR   29-OCT-1997; 97US-0063561P.
PR   29-OCT-1997; 97US-0063704P.
PR   29-OCT-1997; 97US-0063739P.
PR   29-OCT-1997; 97US-0063735P.
PR   29-OCT-1997; 97US-0063738P.
PR   03-NOV-1997; 97US-0064248P.
PR   07-NOV-1997; 97US-0064809P.
PR   12-NOV-1997; 97US-0065186P.
PR   17-NOV-1997; 97US-0065846P.
PR   21-NOV-1997; 97US-0065364P.
PR   24-NOV-1997; 97US-0066453P.
PR   24-NOV-1997; 97US-0066511P.
PR   24-NOV-1997; 97US-0066770P.
PR   11-DEC-1997; 97US-0069212P.
PR   11-DEC-1997; 97US-0069278P.
PR   16-DEC-1997; 97US-0069334P.
PR   16-DEC-1997; 97US-0069694P.
PR   23-JAN-1998; 97US-0072320P.
PR   04-FEB-1998; 97US-0073612P.
PR   09-FEB-1998; 98US-0074086P.
PR   09-FEB-1998; 98US-0074092P.
PR   12-MAR-1998; 98US-0077791P.
PR   20-MAR-1998; 98US-0078910P.
PR   25-MAR-1998; 98US-0079294P.
PR   26-MAR-1998; 98US-0079663P.
PR   27-MAR-1998; 98US-0079728P.
PR   31-MAR-1998; 98US-0080165P.
PR   12-JUN-1998; 98US-0012456.
PR   14-JUL-1998; 98US-0014552.
PR   28-AUG-1998; 98WO-US017888.
PR   10-SEP-1998; 98WO-US018824.
PR   14-SEP-1998; 98WO-US019093.
PR   14-SEP-1998; 98WO-US019094.
PR   14-SEP-1998; 98WO-US019177.
PR   16-SEP-1998; 98WO-US019330.
PR   17-SEP-1998; 98WO-US019437.
PR   07-OCT-1998; 98WO-US022991.
PR   29-OCT-1998; 98WO-US022991.
PR   29-OCT-1998; 98WO-US022992.
PR   20-NOV-1998; 98WO-US024855.
PR   01-DEC-1998; 98US-0025108.
PR   05-JAN-1999; 99US-0000106.
PR   08-MAR-1999; 99US-0005028.
PR   10-MAR-1999; 99US-0005190.
PR   20-APR-1999; 99US-0008615.
PR   14-MAY-1999; 99WO-US010733.
PR   01-JUN-1999; 99WO-US012252.
PR   02-JUN-1999; 99WO-US012111.
PR   08-SEP-1999; 99WO-US020594.
PR   13-SEP-1999; 99WO-US020944.
PR   15-SEP-1999; 99WO-US021090.
PR   15-SEP-1999; 99WO-US021547.
PR   05-OCT-1999; 99WO-US023089.
PR   29-NOV-1999; 99WO-US028214.
PR   30-NOV-1999; 99WO-US028313.
PR   30-NOV-1999; 99WO-US028409.
PR   01-DEC-1999; 99WO-US028301.
PR   01-DEC-1999; 99WO-US028634.
PR   02-DEC-1999; 99WO-US028551.
PR   02-DEC-1999; 99WO-US028564.
PR   16-DEC-1999; 99WO-US028865.
PR   20-DEC-1999; 99WO-US030095.
PR   20-DEC-1999; 99WO-US030911.
PR   30-DEC-1999; 99WO-US030999.
PR   30-DEC-1999; 99US-0031243.
PR   05-JAN-2000; 2000WO-US031274.
PR   06-JAN-2000; 2000WO-US002019.
PR   06-JAN-2000; 2000WO-US000277.
PR   11-FEB-2000; 2000WO-US003576.
PR   18-FEB-2000; 2000WO-US003665.
PR   18-FEB-2000; 2000WO-US004341.
PR   22-FEB-2000; 2000WO-US043442.
PR   24-FEB-2000; 2000WO-US004414.
PR   24-FEB-2000; 2000WO-US004914.
PR   01-MAR-2000; 2000US-US005004.
PR   01-MAR-2000; 2000WO-US005601.

```
PR   02-MAR-2000; 2000WO-US005746.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
PI   Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
PI   Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
XX
DR   WPI; 2003-352836/33.
DR   P-PSDB; ABU81003.
XX
PS   Claim 2; Fig 267; 643pp; English.
XX
CC   The present invention relates to the isolation of novel human PRO
CC   polypeptides, and the polynucleotide sequences encoding them. The PRO
CC   polypeptides are secreted and transmembrane proteins. The PRO
CC   polypeptides and polynucleotides are useful for preparing a medicament
CC   useful in the treatment of diabetes, bone and/or cartilage disorders
CC   (e.g. rheumatoid arthritis, sports injuries, osteoarthritis), obesity,
CC   hyper- or hypo-insulinaemia, hearing loss, and coagulation disorders
CC   (e.g. stroke, heart attack). Anti-PRO antibodies are useful in diagnostic
CC   assays for PRO, by detecting its expression in specific cells, tissues or
CC   serum, and for affinity purification of PRO from recombinant cell culture
CC   or natural sources. ACA66994-ACA67268 represent cDNA sequences encoding
CC   the human PRO polypeptides of the invention. Note: The sequence data for
CC   this patent was obtained in electronic format directly from the USPTO web
CC   site at seqdata.uspto.gov/psipsDIDEntry.html
XX
SQ   Sequence 2290 BP; 537 A; 692 C; 668 G; 393 T; 0 U; 0 Other;
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Query Match   98.1%;   Score 2132.6;   DB 7;   Length 2290;
Best Local Similarity   99.8%;   Pred. No. 0;   Matches 2135;   Conservative 0;   Mismatches 4;   Indels 0;   Gaps 0;

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Qy   1623  ACCCTCGGACAGAGATCATGATGTCTACACAGCAGGAACCTGTGCCACTACCAGAAGGGAGGC  1682
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Db   1771  ACCCTCGGACAGAGATCATGATGTCTACACAGCAGGAAACTGTGCCACTACCAGAAGGGAGGC  1830

Qy   1683  TGGTGGTTATAACGGCTTGTGCCCATCCCAACCTCAACGGAGGTTCTTGTCTACCCGGGGGCCAT  1742
           |||||||||||||||||||||||||  |||||||||||||  |  |||||  |||||||||||||
Db   1831  TGGTGGTTATAACGGCTTGTGCCCACTCCAACCTCAACGGGGTCTGGTTCTTGGTACCCGGGGGCCAT  1890

Qy   1743  TACCGGAGCCGCTACCAGGACGGAGTCTACTGGGGCTTACTGA        TTACTCA  1802
           |||||||||||||||||||||||||||||||||||||||  |              ||||||
Db   1891  TACCGGAGCCGCTACCAGGACGGAGTCTACTGGGGCTTCCGAGGAGGGCTCTTACTCA  1950

Qy   1803  CTCAAGAAAGTGGTGATGATCCGACCGAAC    CCCTTCCACTAAGCCAGCTCC  1862
           ||||||||||||||||||||||||||||||        |||||||||||||||||
Db   1951  CTCAAGAAAGTGGTGATGATCCGACCGAACACCACCTTCCACTAAGCCAGCTCC  2010

Qy   1863  CCCTCCTGACCTCTCGTGGCCATTGCCAGGAGCCCACCCGTCAGGCTGCCACAGCAC  1922
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2011  CCCTCCTGACCTCTCGTGGCCATTGCCAGGAGCCCACCCGTCAGGCTGCCACAGCAC  2070

Qy   1923  AAAGAACAACTCCTCACCACCAGTTCATCCTGAGGCTGGGGAGGATGCTGGATTTCTGT  1982
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2071  AAAGAACAACTCCTCACCACCAGTTCATCCTGAGGCTGGGGAGGATGCTGGATTTCTGT  2130

Qy   1983  TTTCCGGAAGTCACTGCAGCGGATGAGGAACTGAATCCGATACGGTGTTTCTGTCCCTCC  2042
           |||||||||||||||||||||||||||||||||||||  ||||||||||  |||||||||
Db   2131  TTTCCGGAAGTCACTGCAGCGGATGAGGAACTGAATCGATACGGTGTTTTCGTGTCCCTCC  2190

Qy   2043  TACTTTCCTTCACACAGAGACACGCCCCCCTCATGTCTCTCAGGACAGGAGGACTACAGACAA  2102
           |||||||||||||||||  ||| ||||| ||||||||| ||||||||| |||||||||||||
Db   2191  TACTTTCCTTCACACAGGACAGCCCCTTCATGTCTCCAGGACAGCAGGACTACAGACAA  2250

Qy   2103  CTCTTTCTTAAATAAATTAAGTCTCTACAATAAAAACA  2141
           |||||||||  |||||||||||||||||||||||||
Db   2251  CTCTTTCTTTAAATAAATTAAGTCTCTACAATAAAAAAA  2289
```

RESULT 13
ACA03736

ID   ACA03736 standard; cDNA; 2290 BP.
XX
AC   ACA03736;
XX
DT   23-MAY-2003 (first entry)
XX
DE   cDNA encoding human PRO polypeptide #134.
XX
KW   Human; PRO polypeptide; secreted and transmembrane protein;
KW   tumour necrosis factor-alpha; TNF-alpha; blood; proliferation;
KW   differentiation; chondrocyte; tumour; genetic disorder; cytostatic; gene;
KW   ss.
XX
OS   Homo sapiens.
XX
PN   US20030036180-A1.
XX
PD   20-FEB-2003.
XX
PF   09-MAY-2002; 2002US-00143114.
XX
PR   31-MAR-1997; 9WO-US005230.
PR   12-JUN-1998; 98WO-US012456.
PR   14-JUL-1998; 98WO-US014552.
PR   28-AUG-1998; 98WO-US017888.
PR   10-SEP-1998; 98WO-US018824.
PR   14-SEP-1998; 98WO-US019093.
PR   14-SEP-1998; 98WO-US019094.
PR   14-SEP-1998; 98WO-US019177.
PR   16-SEP-1998; 98WO-US019330.
PR   17-SEP-1998; 98WO-US019437.
PR   07-OCT-1998; 98WO-US021141.
PR   29-OCT-1998; 98WO-US022991.
PR   29-OCT-1998; 98WO-US022992.
PR   20-NOV-1998; 98WO-US024855.
PR   01-DEC-1998; 98WO-US025108.
PR   05-JAN-1999; 99WO-US000106.
PR   08-MAR-1999; 99WO-US005028.
PR   10-MAR-1999; 99WO-US005190.
PR   20-APR-1999; 99WO-US008615.
PR   14-MAY-1999; 99WO-US010733.
PR   02-JUN-1999; 99WO-US012252.
PR   01-SEP-1999; 99WO-US020111.
PR   08-SEP-1999; 99WO-US020594.
PR   13-SEP-1999; 99WO-US020944.
PR   15-SEP-1999; 99WO-US021090.
PR   15-SEP-1999; 99WO-US021547.
PR   30-SEP-1999; 99WO-US023089.
PR   05-OCT-1999; 99WO-US028214.
PR   29-NOV-1999; 99WO-US028313.
PR   30-NOV-1999; 99WO-US028409.
PR   30-NOV-1999; 99WO-US028301.
PR   01-DEC-1999; 99WO-US028634.
PR   01-DEC-1999; 99WO-US028551.
PR   02-DEC-1999; 99WO-US028564.
PR   02-DEC-1999; 99WO-US028551.
PR   16-DEC-1999; 99WO-US030095.
PR   20-DEC-1999; 99WO-US030911.
PR   20-DEC-1999; 99WO-US030720.
PR   22-DEC-1999; 99WO-US031243.
PR   30-DEC-1999; 99WO-US031274.
PR   30-DEC-1999; 2000WO-US000219.
PR   05-JAN-2000; 2000WO-US000277.
PR   06-JAN-2000; 2000WO-US000376.
PR   06-JAN-2000; 2000WO-US003565.
PR   11-FEB-2000; 2000WO-US004441.
PR   18-FEB-2000; 2000WO-US004342.
PR   18-FEB-2000; 2000WO-US004414.
PR   22-FEB-2000; 2000WO-US004914.
PR   24-FEB-2000; 2000WO-US005004.
PR   24-FEB-2000; 2000WO-US005601.
PR   01-MAR-2000; 2000WO-US005746.
PR   02-MAR-2000; 2000WO-US005841.
PR   02-JUN-2000; 2000WO-US006319.
PR   10-MAR-2000; 2000WO-US006884.
PR   15-MAR-2000; 2000WO-US007377.
PR   20-MAR-2000; 2000WO-US007532.
PR   21-MAR-2000; 2000WO-US007705.
PR   30-MAR-2000; 2000WO-US008439.
PR   17-MAY-2000; 2000WO-US013705.
PR   22-MAY-2000; 2000WO-US014042.
PR   30-MAY-2000; 2000WO-US014941.
PR   28-JUL-2000; 2000WO-US015264.
PR   11-AUG-2000; 2000WO-US020710.
PR   23-AUG-2000; 2000WO-US022031.
PR   24-AUG-2000; 2000WO-US023522.
PR   08-NOV-2000; 2000WO-US023328.
PR   10-NOV-2000; 2000WO-US030952.
PR   01-DEC-2000; 2000WO-US032678.
PR   20-DEC-2000; 2000WO-US033073.
PR   20-DEC-2000; 2000US-00742259.
PR   28-FEB-2001; 2000US-00744956.
PR   28-FEB-2001; 2001WO-US0796498.
PR   01-MAR-2001; 2001WO-US006520.
PR   09-MAR-2001; 2001WO-US006666.
PR   14-MAR-2001; 2001US-00802706.
PR   22-MAR-2001; 2001US-00808689.
PR   05-APR-2001; 2001US-00816744.
PR   10-MAY-2001; 2001US-00828366.
PR   18-MAY-2001; 2001US-00854208.
PR   25-MAY-2001; 2001US-00854280.
PR   25-MAY-2001; 2001US-00860216.
PR   01-JUN-2001; 2001US-00866028.
PR   01-JUN-2001; 2001US-00866034.
PR   01-JUN-2001; 2001WO-US017092.
PR   25-MAY-2001; 2001WO-US017800.

PR   05-JUN-2001; 2001US-00874503.
PR   14-JUN-2001; 2001US-00882636.
PR   19-JUN-2001; 2001US-00886342.
PR   20-JUN-2001; 2001WO-US019692.
PR   21-JUN-2001; 2001US-00887879.
PR   22-JUN-2001; 2001WO-US020116.
PR   29-JUN-2001; 2001WO-US021066.
PR   09-JUL-2001; 2001WO-US021735.
PR   18-JUL-2001; 2001US-00908827.
PR   06-AUG-2001; 2001US-00924419.
PR   09-AUG-2001; 2001US-00927796.
PR   16-AUG-2001; 2001US-00931836.
PR   19-DEC-2001; 2001US-00028072.
XX
PA   (GETH) GENENTECH INC.
XX
PI   Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
PI   Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
PI   Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
XX
DR   WPI; 2003-332040/31.
DR   P-PSDB; ABU66703.
XX
PT   New secreted and transmembrane PRO nucleic acids, useful for gene
PT   therapy, in chromosome and gene mapping, as chromosome markers, in tissue
PT   typing, and in chromosome identification.
XX
PS   Claim 2; Fig 267; 660pp; English.
XX
CC   The present invention relates to the isolation of novel human PRO
CC   polypeptides, and the polynucleotide sequences encoding them. The PRO
CC   polypeptides are secreted and transmembrane proteins. The PRO
CC   polypeptides are useful for detecting other PRO polypeptides, for linking
CC   bioactive molecules to cells expressing PRO polypeptides, for modulating
CC   biological activities of cells expressing PRO polypeptides, and for for
CC   identifying agonists or antagonists. The PRO polypeptides are useful for
CC   for stimulating the release of tumour necrosis factor (TNF)-alpha from
CC   human blood, for stimulating the proliferation or differentiation of
CC   chondrocytes, and detecting the presence of tumours. The polynucleotide
CC   sequences encoding PRO polypeptides are useful as hybridisation probes,
CC   in chromosome and gene mapping, in the generation of antisense RNA and
CC   DNA, in the preparation of PRO polypeptides, for generating transgenic
CC   animals or knockout animals, for the genetic analysis of individuals with
CC   genetic disorders, and in gene therapy. ACA03603-ACA03877 represent cDNAs
CC   encoding the human PRO polypeptides of the invention. Note: The sequence
CC   data for this patent was obtained in electronic format directly from the
CC   USPTO web site at seqdata.uspto.gov/psipsIDEntry.html
XX
SQ   Sequence 2290 BP; 537 A; 692 C; 668 G; 393 T; 0 U; 0 Other;

Query Match   98.1%; Score 2132.6; DB 7; Length 2290;
Best Local Similarity   99.8%; Pred. No. 0; Mismatches 0;
Matches 2135;   Conservative   0; Mismatches   4; Indels   0; Gaps   0;

Qy   3 AAATGAGGCTGCTGTCGCGACGGCCCTGAGGATGAACCCCAAGCGCCTGGCCAGCCTGGACGGTG   62
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Db   151 AAATGAGGCTGCTGTCGCGACGGCCCTGAGGATGAACCCCAAGCGCCTGGCCAGCCTGGACGGTG 210

Qy   63 GCACTGAGGCAGCGGCGGCTGACCGTACTGTGAGGGAAAGAAGGTTGTGAGCAGCCCCGCAGG 122
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   211 GCACTGAGGCACGGGCGGCTGACCGTACTGTGAGGGAAAGAAGGTTGTGAGCAGCCCCGCAGG 270

Qy   123 ACCCCTGGCCAGCCTTGCCGGAGCCCTCTGTGGAGGCGAGAGCCCAGTG 182
              |||||||||||||||||||||||||||||||||||||||||||||||||
Db   271 ACCCCTGGCCAGCCTTGCCGGAGCCCTCTGTGGAGGCGAGAGCCCAGTG 330

Qy   183 GAGCCCAGTGAGGCAGGAGGCCTGCTTGGCCAGCCCACCGGCCCGGCCTTCCCAG 242
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   331 GAGCCCAGTGAGGCAGGAGGCCTGCTTGGCCAGCCCACCGGCCCGGCCTTCCCAG 390

Qy   243 AGGGCCATGGACAGGGCCCCGGTGAACGGCCAGGGTGAAGGAGGAGGAGGAGCCGGCCCCCG 302
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   391 AGGGCCATGGACAGGGCCCCGGTGAACGGCCAGGGTGAAGGAGGAGGAGGAGCCGGCCCCCG 450

Qy   303 AGGCCAACGCAGGAGGAGGGGGAGGGGGAGGGTTTCATTAGAGTTCTATTCACAAAAGAATAACACCATTTT 362
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   451 AGGCCAACGCAGGAGGAGGGGGAGGGGGAGGGTTTCATTAGAGTTCTATTCACAAAAGAATAACACCATTTT 510

Qy   363 GCAAAGACCCATGAGGCCACTGTGCGGTGACATGCTGGTTGGTTCGGGACTGCTGGCCATG 422
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   511 GCAAAGACCCATGAGGCCACTGTGCGGTGACATGCTGGTTGGTTCGGGACTGCTGGCCATG 570

Qy   423 GGGAGCTGGTTGCAGGCCCAGGAGGACGGCGGTTTTGAGGGGACTGAGGAGGAGGTCGGCCAAGGAG 482
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   571 GGAGCTGGTTGCAGGCCCAGGAGGACGGCGGTTTTGAGGGGCACTGAGGAGGAGGTCGGCCAAGGAG 630

Qy   483 TTCATTTACCTTAAACAGGTACAAAGCAGGTACAAAGCGGGCGGGCGGGGCGGGGCGGGGCGCATGTG 542
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   631 TTCATTTACCTTAAACAGGTACAAAGCAGGTACAAAGCGGGCGGGCGGGGCGGGGCGGGGCGCACCTCACC 690

Qy   543 TTCATTGTTGCCCCAGCAGGCGGTCACGGGTGCCATCTGCCGTCAAACTCCAAGGAGCCTGAG 602
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Db   691 TTCATTGTTGCCCCAGCAGCGGGTCAGGGGTGCCATCTGCCGTCAAACTCCAAGGAGCCTGAG 750

Qy   603 CTGGCTTCTTGGAGAACCGGAGTGCATAAAGCAGGAGGAGCTAGAGCTGCTCAAACAATGAGCTGCTC 662
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Db   751 GTGCTTCTTGGAGAACCGGAGTGCATAAAGCAGGAGGAGCTAGAGCTGCTCAACAATGAGCTGCTC 810

Qy   663 AAGCAGAAGCGGGCAGAATCGAGACGCTGCAGCAGGCTGGTGAAGGTGGAGCGGCCATTGTG 722
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Db   811 AAGCAGAAAGCGGGCAGAATCGAGACGCTGCAGCAGGCTGGTGAAGGTGGAGCGGCCATTGTG 870

Qy   723 AGGGAGGTGAAGCTGCTGCCAAGGAGGAGCGGCAACATGAAACTCGGGGGTGGCAGCAGCTC 782
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Db   871 AGGGAGGTGAAGCTGCTGCCAAGGAGGAGCGGCAACATGAAACTCGGGGGTGGCAGCAGCTC 930

Qy   783 TACATCGAGTCTCCTGCAGAGATCATCCGGACGACAACGCGGACAGCGTCTTCGGGTCTCCCAG 842
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Db   931 TACATCGAGCTTCCTGCAGAGATCATCCGGACGACAACGCGGACAGCGTCTTCCCCCAG 990

Qy   843 CTGGAGAACCAGGATCCTGAACCAGCAGCCACAATGCTGCAGCTGCTGCTGCAAGTACAAG 902
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   991 CTGGAGAACCAGGATCCTGAACCAGCAGCCACAATGCTGCAGCTGCTGCTGCAAGTACAAG 1050

Qy   903 GACCTGGAGCAGAAGTACACCAGCACCTGGCCCCACACTGGCCCACCAAATCAGAGGATCATC 962
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1051 GACCTGGAGCAGAAGTACACCAGCACCTGGCCCCACACTGGCCCACCAAATCAGAGGATCATC 1110

Qy   963 GCGCAGCTTGAGGAGGCACTGCCCGAGGGGTGCCCTGGCCAGGGCCCGTCCCCAGCCACC 1022
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Db   1111 GCGCAGCTTGAGGAGGCACTGCCCGAGGGGTGCCCTGGCCAGGGCCCGTCCCCAGCCACC 1170

Qy   1023 CCCGGCTGCCCCGCCCCCGGGTCTTACCAACCACCCACCACCGATCATCAACCAGATC 1082
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Db   1171 CCCGGCTGCCCCGCCCCCGGGTTCTTACCAACCACCCACCACCGATCATCAACCAGATC 1230

Qy   1083 TCTACCAACAGATCGACAGTGACCAGAACCTGAAGTGCTGCCACCCCACTCCTGCCCACT 1142
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Db   1231 TCTACCAACAGATCGACAGTGACCAGAACCTGAAGGTGCTGCCACCCCACTCCTGCCCACT 1290

Qy   1143 ATGCCCACTCTCACCCAGCTCTCCATTCTTCCACCACCAAGCCGTCGGGGTCCCATGGAGAGAGAC 1202
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1291 ATGCCCACTCTCACCCAGCTCTCCATTCTTCCACCACCAAGCCGTCGGGGTCCCATGGAGAGAGAC 1350

Qy   1203 TGCCTGCAGGCCCCTGGAGGATGGCCAGCGACCACCAGCTCCATCTACCTGGTGAAGCCGGGAG 1262
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Db   1351 TGCCTGCAGGCCCCTGGAGGATGGCCAGCGACAGCACCAGCTCCATCTACCTGGTGAAGCCGGGAG 1410

Qy   1263 AACACCAACCGCCCTCATGCGAGGTTGTGGTCGGACAGACAGAGACAGACACCGGGGGTGGACC 1322
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1411 AACACCAACCGCCCTCATGCGAGGTTGTGGTCGGACGAGAACAGAGACAGACACCGGGGGTGGACC 1470

Qy   1323 GAGCCCAGTGAGGCGAGGGCCTGGATGCTCTCGTTTAACTTCTTCAGGAACTGGGGACGTACAAG 1382
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1471 GTCATCCAGAGACGGCCTGGATGGCCTCGTTTAACTTCTTCAGGAACTGGGGACGTACAAG 1530

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Qy  1383 CAAGGGTTTGGGAACATTGACGGCGAATACTGGCTGGGCCTGGGAACATTTACTGGCTG 1442
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Db  1531 CAAGGGTTTGGGAACATTGACGGCGAATACTGGCTGGGCCTGGGAACATTTACTGGCTG 1590

Qy  1443 ACGAACCAAGCGAACTACAACTCCTCGTGACCATGGACGACTGGTTCGGCCCGCAAAGTC 1502
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1591 ACGAACCAAGCGAACTACAAACTCCTGGTGACCATGGAGGACTTGGTTCGGCCCGCAAAGTC 1650

Qy  1503 TTTGCAGAATACGGCAGTTTCCGGCTGGGAACGTGGAGCGGAGTATTATAAGGCTGGGGCTG 1562
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Db  1651 TTTGCAGAATACGGCAGTTTCCGCCCTGGAACCTGAGAGCGAGTATTATAAGCTGCGGCTG 1710

Qy  1563 GGGCGCGTACCATGGCAATGCGGGGTGACTCCTTCCTTTACATGGCACAACGGCACAGCCAAGCCAGTTCACC 1622
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Db  1711 GGGCGCGTACCCATGGCAATGCGGGGTGACTCCTTCCTTTACATGGCACAACGGCAAGCCAGTTCACC 1770

Qy  1623 ACCCTGGACAGAGATCATGATGTCTACACAGCAGGAAAACGTGCCCACTACCAGAAGGGGGGC 1682
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Db  1771 ACCCTGGACAGAGATCATGATGTCTACACAGCAGGAAAACGTGCCCACTACCAGAAGGGGGGC 1830

Qy  1683 TGGTGGTTATAACGGCCCGTGCCCACTCCAACCTCAACGGGGGTCTGGTTACGGGGGGGGCCCAT 1742
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1831 TGGTGGTTATAACCCTGTGCCCACTCCAACCTCAACGGGGGTCTGGTTACCGGGGGGGGCCCAT 1890

Qy  1743 TACCCGGAGCCGGCTACCAGGAGTCTTACTGGGCTGAGTTCCGGAGTTCTTTACTCA 1802
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1891 TACCCGGAGCCGGCTACCAGGAGTCGTACTGGGCTGAGTTCCGGAGGGCTCTTACTCA 1950

Qy  1803 CTCAAGAAAGTGGTGATGATCGATCCGACCGGAACCCAAACACCTTCCACTAAAGCCAGCTCC 1862
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1951 CTCAAGAAAGTGGTGATGATCGATCCGACCGGAACCCAACACCTTCCACTAAAGCCAGCTCC 2010

Qy  1863 CCCTCCTGACCTCTCGTGGCCATTGCCAGGACCCACCTGGCCGCCACAGCAC 1922
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1951 CTCAAGAAAGTGGTGATGATCGATCCGACCGGAACCCAACACCTTCCACTAAAGCCAGCTCC 2010

Qy  1923 AAAGAACAACTCCTCACCAGTTCATCCTGAGGCTGGAGGACGCGGATGCTGGATTCTGT 1982
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2011 CCCTCCTGACCTCTCGTGGCCATTGCCAGGACCCACCTGGCCGCCACAGCAC 2070

Qy  1983 TTTCCGAAGTCACTGCAGCGGATGAAATCGAATACGGGTGTTTTTCTGTCCCTCC 2042
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2071 AAAGAACAACTCCTCACCAGTTCATCCTGAGGCTGGGAGGACCGGGATGCTGGATTCTGT 2130

Qy  2043 TACTTTCCTTCACCACCAGAGCCCCTTCATGTCTCCAGGAGGACAGGAGGACTACAGACAA 2102
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Db  2131 TTTCCGAAGTCACTGCAGCGGATGGAAATCGAATACGGGTGTTTTCTGTCCCTCC 2190

Qy  2103 CTCTTTCTTAAATAAATTAAGTCTCTACAATAAAAACA 2141
         |||||||||||||||||||||||||||||||||||||||
Db  2191 TACTTTCCTTCACCACCAGAGCCCCTTCATGTCTCCAGGAGGACAGGAGGACTACAGACAA 2250

Qy  2103 CTCTTTCTTAAATAAATTAAGTCTCTACAATAAAAACA 2141
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Db  2251 CTCTTTCTTAAATAAATTAAGTCTCTACAATAAAAAA 2289
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RESULT 14

ACA04921

ID   ACA04921 standard; cDNA; 2290 BP.
XX
AC   ACA04921;
XX
DT   28-MAY-2003 (first entry)
XX
DE   Novel human secreted and transmembrane protein PRO196 cDNA.
XX
OS   Homo sapiens.
XX
XX
PN   US2003032063-A1.
XX
PD   13-FEB-2003.
XX
XX
PF   01-FEB-2002; 2002US-00064994.
XX
PR   26-AUG-1997; 97US-0059974P.
PR   17-SEP-1997; 97US-0059115P.
PR   18-SEP-1997; 97US-0059263P.
PR   19-SEP-1997; 97US-0059588P.
PR   17-OCT-1997; 97US-0062285P.
PR   24-OCT-1997; 97US-0062816P.
PR   24-OCT-1997; 97US-0063082P.
PR   27-OCT-1997; 97US-0063209P.
PR   29-OCT-1997; 97US-0063733P.
PR   21-NOV-1997; 97US-0063264P.
PR   25-NOV-1997; 97US-0068040P.
PR   16-DEC-1997; 97US-0069694P.
PR   09-FEB-1998; 98US-0074086P.
PR   09-FEB-1998; 98US-0074092P.
PR   25-MAR-1998; 98US-0080049P.
PR   08-APR-1998; 98US-0081049P.
PR   10-AUG-1998; 98US-0095998P.
PR   18-AUG-1998; 98US-0097000P.
PR   09-SEP-1998; 98US-0099601P.
PR   10-SEP-1998; 98US-0099803P.
PR   10-SEP-1998; 98US-0099811P.
PR   10-SEP-1998; 98US-0099812P.
PR   14-SEP-1998; 98WO-US019093.
PR   16-SEP-1998; 98US-0100058P.
PR   17-SEP-1998; 98WO-US019330.
PR   17-SEP-1998; 98US-0100588P.
PR   24-SEP-1998; 98US-0101922P.
PR   28-OCT-1998; 98US-0106032P.
PR   20-NOV-1998; 98US-0109304P.
PR   20-NOV-1998; 98WO-US024855.
PR   25-NOV-1998; 98WO-US025190.
PR   01-DEC-1998; 98WO-US025108.
PR   08-MAR-1999; 99WO-US005028.
PR   23-MAR-1999; 99US-0125778P.
PR   02-JUN-1999; 99US-0131252.
PR   15-JUN-1999; 99US-0139695P.
PR   20-JUL-1999; 99US-0145070P.
PR   26-JUL-1999; 99US-0145698P.
PR   17-AUG-1999; 99US-0149396P.
PR   01-SEP-1999; 99WO-US020111.
PR   08-SEP-1999; 99WO-US020594.
PR   15-SEP-1999; 99WO-US021090.
PR   15-SEP-1999; 99WO-US021547.
PR   30-NOV-1999; 99WO-US028313.
PR   01-DEC-1999; 99US-0028301.
PR   02-DEC-1999; 99US-0028565.
PR   07-DEC-1999; 99US-0169495P.
PR   20-DEC-1999; 99WO-US030999.
PR   05-JAN-2000; 2000WO-US000219.
PR   18-FEB-2000; 2000WO-US004341.
PR   18-FEB-2000; 2000WO-US004342.
PR   22-FEB-2000; 2000WO-US004414.
PR   01-MAR-2000; 2000WO-US005601.
PR   02-MAR-2000; 2000WO-US005841.
PR   09-MAR-2000; 2000WO-US006471.
PR   20-MAR-2000; 2000WO-US007377.
PR   30-MAR-2000; 2000WO-US008439.
PR   15-MAY-2000; 2000WO-US013358.
PR   17-MAY-2000; 2000WO-US013705.
PR   22-MAY-2000; 2000WO-US014042.
PR   30-MAY-2000; 2000WO-US014941.
PR   02-JUN-2000; 2000WO-US012264.
PR   11-AUG-2000; 2000WO-US022031.
PR   23-AUG-2000; 2000WO-US023522.
PR   24-AUG-2000; 2000WO-US023328.

XX
KW   Secreted and transmembrane polypeptide; PRO polypeptide; PRO533; PRO301;
KW   PRO187; PRO337; PRO1411; PRO10096; PRO246; PRO6307; PRO6003; PRO6004;
KW   PRO4356; PRO2630; PRO265; PRO941; FGFR; bioactive molecule;
KW   fibroblast growth factor receptor; cell death; chromosome mapping;
KW   gene mapping; transgenic animal; knockout animal; gene therapy; tumour;
KW   obesity; diabetes; insulinaemia; vascular permeability;
KW   cardiac insufficiency disorder; immune response; hearing loss;
KW   auditory hair cell regeneration; bone disorder; cartilage disorder;
KW   sports injury; arthritis; gene; ss.

PR 01-DEC-2000; 2000WO-US032678.
PR 28-FEB-2001; 2001WO-US065520.
PR 30-MAY-2001; 2001WO-US017443.
PR 01-JUN-2001; 2001WO-US017800.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 15-NOV-2001; 2001US-00002796.
XX
PA (GTTH) GENENTECH INC.
XX
PI Ashkenazi AJ, Baker KP, Botstein DA, Desnoyers L, Eaton DL;
PI Ferrara N, Fong S, Gao W Gerber H, Gerritsen ME, Goddard A;
PI Godowski PJ, Gurney AL, Kljavin IJ, Mather JP, Napier MA, Pan J;
PI Paoni NF, Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM;
PI Wood WI, Zhang Z;
XX
DR WPI; 2003-341964/32.
DR P-PSDB; ABU67268.
XX
PT The invention describes an isolated, secreted and transmembrane
PT polypeptide (I), termed PRO polypeptide. (I) is useful for detecting
PT polypeptides, useful for modulating biological activity of cell
PT expressing the polypeptide, and in chromosome and gene mapping.
XX
PS Claim 2; Fig 1; 255pp; English.
XX
CC The invention describes an isolated, secreted and transmembrane
CC polypeptide (I), termed PRO polypeptide. (I) is useful for detecting
CC PRO533, PRO301, PRO187, PRO337, PRO1411, PRO10096, PRO246, PRO6307,
CC PRO6003, PRO6004, PRO4356, PRO630, PRO265, PRO941, fibroblast growth
CC factor receptor (FGFR)-4, FGFR-3, FGFR-2 or FGFR-1 polypeptide, and for
CC linking a bioactive molecule e.g. toxin, radiolabel or antibody, to a
CC cell expressing the polypeptide. The bioactive molecule causes cell
CC death. (II) is useful as hybridisation probes, in chromosome and gene
CC mapping, in generation of antisense RNA and DNA, in the preparation of
CC PRO polypeptide, for generating transgenic animals or knockout animals
CC which in turn are useful in the development and screening of
CC therapeutically useful reagents, and for the genetic analysis of
CC individuals with genetic disorders, in gene therapy, and for chromosome
CC identification. (I) Or Ab is useful for the preparation of medicament for
CC treating conditions which are responsive to the PRO polypeptide or anti-
CC PRO antibody e.g. a tumour. (I) is useful for treating obesity, diabetes
CC or hypo- or hyper-insulinaemia, and cardiac insufficiency disorders, for
CC inhibiting tumour growth, enhances vascular permeability and immune
CC response, for inducing regeneration of auditory hair cells and for
CC treating hearing loss in mammals, and for treating bone and/or cartilage
CC disorders such as sports injuries and arthritis. This sequence encodes a
CC novel human secreted and transmembrane polypeptide associated
CC oligonucleotide
XX
SQ Sequence 2290 BP; 537 A; 692 C; 668 G; 393 T; 0 U; 0 Other;

Best Local Similarity   98.1%;   Score 2132.6;   DB 7;   Length 2290;
Query Match   99.8%;   Pred. No. 0;
Matches 2135; Conservative   0; Mismatches   4; Indels   0; Gaps   0;

Qy   3 AAATGAGGCTGCTGCGGACGGCGGCCTGAGGATGAACCCCAAGCCCTGGCACCTGCGACGGGTG 62
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   151 AAATGAGGCTGCTGCGGACGGCGGCCTGAGGATGAACCCCAAGCCCTGGCACCTGCGACGGGTG 210

Qy   63 GCACTGAGGCAGCGGGCTGACGGCTACTGTGAGGAAAGAAGGTTGTGAGCAGCCCCGCAGG 122
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   211 GCACTGAGGCAGCGGGCTGACGGCTACTGTGAGGAAAGAAGGTTGTGAGCAGCCCCGCAGG 270

Qy   123 ACCCCTGGCCAGCCCTGGCCCAGCCTTCTCGTGGAGGCAGAGAGCCAGTG 182
           ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   271 ACCCCTGGCCAGCCCTGGCCCAGCCTTCTCGTGGAGGCAGAGAGCCAGTG 330

Qy   183 GAGCCCAGTGAGGCAGGGCGCTGCTTGGCAGCCACCAGGGTGAAGCATGTGAGGACGGCGCCCGG 242
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   331 GAGCCCAGTGAGGCAGGGCGCTGCTTGGCAGCCACCAGGGTGAAGCATGTGAGGACGGCGCCCGG 390

Qy   243 AGGCCATGGACACGGCTCCCCCGCCCTGACGGCGGCGGGTGAAGCATGTGAGGAGGACGCGCCCGG 302
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   391 AGGCCATGGACAGGCTGCCCCCGCCCGCCGCCGGCCAGGGTGGAAGGCATGTGAGGAGCGCCCGG 450

Db   391 AGGCCATGGACAGGCTGCCCCCGCCCGCCGCCGGCCAGGGTGGAAGGCATGTGAGGAGCGCCCGG 450
Qy   303 AGCCCAAGCCAGGAGGGGAAGAGAGGCTTCATAGAGTTCTATTCACAAAGAATAACCACATTTT 362
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   451 AGCCCAAGCCAGGAGGGGAAGAGAGGCTTTCATAGAGTTCTATTCACAAAGAATAACCACATTTT 510

Qy   363 GCAAAGACCCATGAGCCCACTGGTGCCGGTGACATGCTGGTCGGACTGTGGCTGCCATG 422
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   451 GCAAAGACCCATGAGCCCACTGGTGCCGGTGACATGCTGGTCGGACTGTGGCTGCCATG 510

Qy   423 TTCATTTGTTGCCCCAGGCCGGGGGTTGCCAGGGTGGCTGGGGGGCGGGGCCTGGCCAGGAG 482
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   511 GCAAGGACCCAATGAGGCCCACTGTGCCGGTGACATGCTGGTCGGACTGTGGCTGCCATG 570

Db   511 GCAAGGACCCAATGAGGCCCACTGTGCCGGTGACATGCTGGTCGGACTGTGGCTGCCATG 570
Qy   483 TTCATTTAACCTAAAACAGGTACAAAGCGGGCGGGCGGGCGGGGCCTGGCCAGGAG 542
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   571 TTCATTTGTTGCCCCAGGCCGGGGGTTGCCAGGGTGGCTGGGGGGCGGGGCCTGGCCAGGAG 630

Qy   543 TTCATTTAACCTAAAACAGGTACAAAGCGGGCGGGCGGGCGGGGCCTGGCCAGGAG 602
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   631 TTCATTTAACCTAAAACAGGTACAAAGCGGGCGGGCGGGCGGGGCCTGGCCAGGAG 690

Qy   603 GTGCTTCTGGAGAACCGAGTGCATAAGCAGGAGTGCTTCAAACAATGAGTGCTC 662
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   691 GTGCTTCTGGAGAACCGGAGTGCATAAGCAGGAGCTTAGAGCTGCTCAAACAATGAGTGCTC 750

Qy   663 AAGCAGAAGCGGCAGATCGAGAACGGCGCTGCAGCAGCTGGTGAAGGTGGACGGCGGCATTGTG 722
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   751 GTGCTTCTGGAGAACCGGAGTGCATAAGCAGGAGCTTAGAGCTGCTCAAACAATGAGTGCTC 810

Qy   723 AGGCGAGGTGAAGCTGCTCGCCCAAGGACAGAGCGGCGCAACAATGAACTGGGGGTCACCCAGCTC 782
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   811 AAGCAGAAGCGGCAGATCGAGAACGGCGCTGCAGCAGCTGGTGAAGGTGGACGGCGGCATTGTG 870

Qy   783 TACATCCAGCTTCCTGCCACGAGATCATCCGACGAGATCAAGCGGCACGCAAGGCGTTGGGAGCTCTCCCAG 842
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   871 AGGCGAGGTGAAGCTGCTCGCCCAAGGACAGAGCGGCGCAACAATGAACTGGGGGTCACCCAGCTC 930

Qy   843 CTGGAGAACAGGATCCTGAACCAGACAGCAGCCGACATCGCGAGCTGGCCAGCAGTACAAG 902
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   931 TACATCCAGCTTCCTGCCACGAGATCATCCGACGAGATCAAGCGGCACGCAAGGCGTTCTCCCAG 990

Qy   903 GACCTGGAGCACAAGTACACCAGCACCTGGCCACAGCACTGGCCCCAACAATCAGAGATCATC 962
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   991 CTGGAGAACAGGATCCTGAACCAGACAGCAGCCGACATCGCGAGCTGGCCAGCAGTACAAG 1050

Qy   963 GCGCACTTGAGGAGGCACTCGCCAGAGGGGTGCCCTGGGCCCAGGGCCGTTCCCCAGCACCC 1022
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1051 GACCTGGAGCACAAGTACACCAGCACCTGGCCACAGCACTGGCCCCAATCAGAGATCATC 1110

Qy   1023 CCGGCGTGCCCCGCCCCGGGGGTTCTACCAACCACCACTACTCCAACACCGGATCATCAACCAGATC 1082
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1111 GCGCACTTGAGGAGGCACTCGCCAGAGGGGTGCCCTGGGCCCAGGGCCGTTCCCCAGCACCC 1170

Qy   1083 TCTACCAACGAGATCCAGAGTGACCAGAGTGACCAGAAGCTGGGGCCCATGGGACTGGAGAGAC 1142
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1171 CCGGCGTGCCCCGCCCCGGGGTTCTACCAACCACCACTACTCCAACACCGGATCATCAACCAGATC 1230

Qy   1143 ATGCCCACTCTTCACCAGCCTCCCATCTTCCACCGACCAACAGCCCATGGACTGGAGAGAC 1202
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1231 TCTACCAACGAGATCCAGAGTGACCAGAGTGACCAGAAGCTGCCACCCCCTCCTGCCCACT 1290

Qy   1203 TGCCTGCAGCCCCTGGAGGATGGGCCACGACACCAGCTCCATCTACCTGTGTGAACGGGGAG 1262
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1291 ATGCCCACTCTTCACCAGCCTCCCATCTTCCACCGACCAACAGCCCATGGACTGGAGAGAC 1350

Qy   1263 AACACCAACAACGGCCCTCATGCAGGTGTGGTCGGACAGAGACCAGAGGACACGGACC 1322
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1351 TGCCTGCAGCCCCTGGAGGATGGGCCACGACACCAGCTCCATCTACCTGTGTGAACGGGAG 1410

Qy   1323 GTCATCCAGAGACGGCCTGGAATGGGCTCGTTAACTTCTTCAGGAACTGGGGAGACGTACAAG 1382
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1411 AACACCAACAACGGCCCTCATGCAGGTGTGGTCGGACAGAGACCAGAGGACACGGACC 1470

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Db 1471 GTCATCCAGAGACGCCTGCGATGGCTTCGTTAACTTCTTCAGGAGGAGGGGACGTACAAG 1530
Qy 1383 CAAGGGTTTGGGAACATTGACGGCGAATACTGGCTG|GTCCTGGGAGAACATTTACTGGCTG 1442
Db 1531 CAAGGGTTTGGGAACATTGACGGCGAATACTGGCTG|GTCCTGGGAGAACATTTACTGGCTG 1590
Qy 1443 ACGAACCAAGGCAACTACAAACTCCTGGTGACCATGGAGGAGGACTGGTCGGCCGCAAAGTC 1502
Db 1591 ACGAACCAAGGCAACTACAAACTCCTGGTGACCATGGAGGAGGACTGGTCGGCCGCAAAGTC 1650
Qy 1503 TTTGCAGAATAGGCCAGTTTCCGCCTGGAACCTGAGAGCGGAGTATTATAAGCTGCGGCTG 1562
Db 1651 TTTGCAGAATAGGCCAGTTTCCGCCTGGAACCTGAGAGCGGAGTATTATAAGCTGCGGCTG 1710
Qy 1563 GGGCGCTACCATGGCAATGCGGGTGACTCCTTTACATGGCAACGCGCAAGCAGTTCACC 1622
Db 1711 GGGCGCTACCATGGCAATGCGGGTGACTCCTTTACATGGCAACGCGCAAGCAGTTCACC 1770
Qy 1623 ACCCTGACAGAGATCATGATGTGTCTACACACGAAAACTTGTGCCCACTACCACGAAAGGAGGC 1682
Db 1771 ACCCTGACAGAGATCATGATGTGTCTACACACGAAAACTTGTGCCCACTACCACGAAAGGAGGC 1830
Qy 1683 TGGTGGTATAACGGCCTTGTGCCCACTCCAACTTCAACCGGGGTCTGGGTTACCGCGCCCGGGGGGCCAT 1742
Db 1831 TGGTGGTATAACGGCCTTGTGCCCACTCCAACTTCAACCGGGGTCTGGGTTACCGCGCCCGGGGGGCCAT 1890
Qy 1743 TACCGGAGCCGGCTACCAGGAGTCTACTGGGCTGAGTTCCGAGGAGGCTCTTACTCA 1802
Db 1891 TACCGGAGCCGGCTACCAGGAGTCTACTGGGCTGAGTTCCGAGGAGGCTCTTACTCA 1950
Qy 1803 CTCAAGAAAGTGGTGATGATGAATCGACCGGAGACCCCAACACCTTCACTAAGCCAGTCC 1862
Db 1951 CTCAAGAAAGTGGTGATGATGAATCGACCGGAGACCCCAACACCTTCACTAAGCCAGTCC 2010
Qy 1863 CCCTCCTGACCTCTCGTGGCCATTGCCAGGGACGTCAGGTCAGCGTCGGCCACAGCAC 1922
Db 2011 CCCTCCTGACCTCTCGTGGCCATTGCCAGGGACGTCAGGTCAGCGTCGGCCACAGCAC 2070
Qy 1923 AAAGAACAAACTCCTCACCCTCTCCAGTTCATCCTGAGGCTGGAGGAGTGCTGGATTCTGT 1982
Db 2071 AAAGAACAAACTCCTCACCCTCTCCAGTTCATCCTGAGGCTGGAGGAGTGCTGGATTCTGT 2130
Qy 1983 TTTCCGAAGTCACTGCAGCCGGATGAGTGAATCGAATACGGTGTTTTCTGTCCCTCC 2042
Db 2131 TTTCCGAAGTCACTGCAGCCGGATGAGTGAATCGAATACGGTGTTTTCTGTCCCTCC 2190
Qy 2043 TACTTCCTTCACACCAGACGCCCTCATGTCTCCAGGACAGCAGGACTACAGAGACA 2102
Db 2191 TACTTCCTTCACACCAGACGCCCTCATGTCTCCAGGACAGCAGGACTACAGAGACA 2250
Qy 2103 CTCTTTCTTTAAATAAAATTAAGTCTCTACAATAAAAAACA 2141
Db 2251 CTCTTTCTTTAAATAAAATTAAGTCTCTACAATAAAAAAA 2289
)
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PR 28-JUL-2000; 2000WO-US020710.
PR 11-AUG-2000; 2000WO-US022031.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000WO-US074259.
PR 20-DEC-2000; 2000US-0747259.
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PR 28-FEB-2001; 2001US-0796520.
PR 01-MAR-2001; 2001WO-US006666.
PR 09-MAR-2001; 2001US-0802706.
PR 14-MAR-2001; 2001US-0808689.
PR 22-MAR-2001; 2001US-0816744.
PR 05-APR-2001; 2001US-0828366.
PR 10-MAY-2001; 2001US-0854208.
PR 10-MAY-2001; 2001US-0854280.
PR 18-MAY-2001; 2001US-0860216.
PR 25-MAY-2001; 2001US-0866028.
PR 25-MAY-2001; 2001US-0866034.
PR 25-MAY-2001; 2001US-0872035.
PR 01-JUN-2001; 2001US-0017092.
PR 01-JUN-2001; 2001US-0017800.
PR 05-JUN-2001; 2001US-0874503.
PR 14-JUN-2001; 2001US-0882336.
PR 19-JUN-2001; 2001US-0886342.
PR 20-JUN-2001; 2001US-0019692.
PR 21-JUN-2001; 2001US-0887879.
PR 22-JUN-2001; 2001WO-US020116.
PR 29-JUN-2001; 2001US-0021066.
PR 09-JUL-2001; 2001US-0021735.
PR 18-JUL-2001; 2001US-0908827.
PR 06-AUG-2001; 2001US-0924419.
PR 09-AUG-2001; 2001US-0927796.
PR 16-AUG-2001; 2001US-0931836.
PR 19-DEC-2001; 2001US-00028072.
XX
SQ Sequence 2290 BP; 537 A; 692 C; 668 G; 393 T; 0 U; 0 Other;
XX
PA (GETH) GENENTECH INC.
XX
PI Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
XX
DR WPI; 2003-148238/14.
DR P-PSDB; ABU59784.
XX
PT Two hundred and seventy five nucleic acids encoding PRO polypeptides,
PT useful for treating pericyte-associated tumors, diabetes and various bone
PT and/or cartilage disorders, e.g. arthritis.
XX
PS Claim 2; Fig 267; 659pp; English.
XX
CC The invention describes an isolated human PRO polypeptide. The PRO
CC polypeptides are useful in detecting PRO polypeptides in a sample, in
CC linking a bioactive molecule to a cell expressing a PRO polypeptide, and
CC in modulating at least one biological activity of a cell expressing a PRO
CC polypeptide. PRO1312 stimulates hypertrophy of neonatal heart and is thus
CC useful for treating cardiac insufficiency disorders. PRO1154 and PRO1186
CC stimulate adrenal cortical capillary endothelial growth, and PRO1536,
CC PRO943, PRO828, PRO1068 or PRO535, PRO826, PRO819, PRO1126,
CC PRO1360 and PRO1387 induce c-fos in endothelial cells, and are thus
CC useful for treating conditions or disorders where angiogenesis would be
CC beneficial, e.g. wound healing and antagonist of this polypeptide are
CC useful for treating cancerous tumours. PRO812 inhibits vascular
CC endothelial growth factor (VEGF) stimulated proliferation of endothelial
CC cells and is thus useful for inhibiting endothelial cell growth in
CC mammals which would be beneficial in inhibiting tumour growth. PRO826,
CC PRO1068, PRO1184, PRO1346 and PRO1375 stimulate proliferation of
CC immune stimulated T-lymphocytes and are therapeutically useful for enhancing
CC immune response. PRO828, PRO826, PRO1068 or PRO1132 enhance survival of
CC retinal neurons cells (PRO1132 is also enhances survival/proliferation of
CC rod photoreceptor cells) and therefore are useful for treating retinal

CC disorders of injuries, e.g. retinitis pigmentosum, AMD. PRO819, PRO813
CC and PRO1066 induce proliferation of mammalian kidney mesangial cells,
CC and therefore are useful for treating kidney disorders associated with
CC decreased mesangial cell function such as Berger disease or other
CC nephropathies associated with dermatitis, herpetiformis or Crohn's
CC disease. PRO1310, PRO844, PRO1312, PRO1192 and PRO1387 induce the
CC proliferation and/or redifferentiation of chondrocytes in culture and are
CC thus useful for treating sports injuries, and arthritis. This sequence
CC encodes a novel human PRO protein

Query Match   98.1%; Score 2132.6; DB 7; Length 2290;
Best Local Similarity   99.8%; Pred. No. 0;
Matches 2135; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy   3 AAAATGAGGGCTTGCTTGGCGACACGGCCCTGAGGATGAAACCCCAACCCCTCTGGACTGTGCCCAGCGTG 62
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   151 AAAATGAGGGCTCCTGCCGACACGGCCCTGAGGATGGAAACCCCAAGCCCTCCCGAGCGTG 210

[Sequence alignment data continues...]

Qy   843 CTGGAGAACAGGAATCCTGAACCAGACAGCCGACATGCTGCAGCGTCGGCAAGTACAAG 902

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Qy   991 CTGGGAAACAGAGATCCTGAACACGAGACAGCCGACATCTGCAGCTGCGAAGTACAAG 1050
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Db   903 GACCTGGAGCACAAGTACAGCACCTGGCCACACTGGCCCACAACCAATCAGAAGATCATC  962

Qy   903 GACCTGGAGCACAAGTACAGCACCTGGCCACACTGGCCCACAACCAATCAGAGATCATC  962
Db  1051 GACCTGGACGACAAGTACCAGACCTGGCCACACTGGCCCAACAATCAGAAGATCATC 1110

Qy  1051 GACCTGGACGACAAGTACCAGACCTGGCCACACTGGCCCAACAATCAGAGATCATC 1110
Db   963 GCGCAGCTTGAGGAGCACTGCCAGAGGGGTGCCCTGCCCAGCCACCC 1022

Qy   963 GCGCAGCTTGAGGAGCACTGCCAGAGGGGTGCCCTGCCCAGCCACCC 1022
Db  1111 GCGCAGCTTGAGGAGCACTGCCAGAGGGGTGCCCTGCCCAGCCACCC 1170

Qy  1111 GCGCAGCTTGAGGAGCACTGCCAGAGGGGTGCCCTGCCCAGCCACCC 1170
Db  1023 CCGGCTGCCCCCGCCCCGGGTCTACCAACCACCACCCACCCAAACAGATC 1082

Qy  1023 CCGGCTGCCCCCGCCCCGGGTCTACCAACCACCACCCACCCAAACAGATC 1082
Db  1171 CCGGCTGCCCCCGCCCCGGGTCTACCAACCACCACCCACCCAAACAGATC 1230

Qy  1171 CCGGCTGCCCCCGCCCCGGGTCTACCAACCACCACCCACCCAAACAGATC 1230
Db  1083 TCTACCAAACGAGATCAGAGTGACCAGAACCTGAAGGTGCTGCCACCCCCCTGCCCACT 1142

Qy  1083 TCTACCAAACGAGATCAGAGTGACCAGAACCTGAAGGTGCTGCCACCCCCCTGCCCACT 1142
Db  1231 TCTACCAAACGAGATCAGAGTGACCAGAACCTGAAGGTGCTGCCACCCCCCTGCCCACT 1290

Qy  1231 TCTACCAAACGAGATCAGAGTGACCAGAACCTGAAGGTGCTGCCACCCCCCTGCCCACT 1290
Db  1143 ATGCCCACTCTCACCAGCCTCCCATCTTCCACCGACAAGCCGTCGGGCCCCATGGAGAGAC 1202

Qy  1143 ATGCCCACTCTCACCAGCCTCCCATCTTCCACCGACAAGCCGTCGGGCCCCATGGAGAGAC 1202
Db  1291 ATGCCCACTCTCACCAGCCTCCCATCTTCCACCGACAAGCCGTCGGGCCCCATGGAGAGAC 1350

Qy  1291 ATGCCCACTCTCACCAGCCTCCCATCTTCCACCGACAAGCCGTCGGGCCCCATGGAGAGAC 1350
Db  1203 TGCCTGCAGGGCCCTGGAGGATGGCCAGCACCACCAGCTCCATCTACCTGTGAAGCCGGAG 1262

Qy  1203 TGCCTGCAGGGCCCTGGAGGATGGCCAGCACCACCAGCTCCATCTACCTGTGAAGCCGGAG 1262
Db  1351 TGCCTGCAGGGCCCTGGAGGATGGCCACGACCAGCTCCATCTACCTGTGAAGCGGGAG 1410

Qy  1351 TGCCTGCAGGGCCCTGGAGGATGGCCACGACCAGCTCCATCTACCTGTGAAGCGGGAG 1410
Db  1263 AACACCAAACCCCTCATGCAGGTGTGGTGCCAGACACACGACCCCGAGGGGGCTGGACC 1322

Qy  1263 AACACCAAACCCCTCATGCAGGTGTGGTGCCAGACACACGACCCCGAGGGGGCTGGACC 1322
Db  1411 AACACCAAACCCCTCATGCAGGTTGTGGTGCGAGACAGAGACCCCAGAGAAGGGGCTGGACC 1470

Qy  1411 AACACCAAACCCCTCATGCAGGTTGTGGTGCGAGACAGAGACCCCAGAGAAGGGGCTGGACC 1470
Db  1323 GTCATCCAGAGACGCCTGGATGGCTCGTCGTTAACTTCTTCAGGAACTGGGAGGTACAAG 1382

Qy  1323 GTCATCCAGAGACGCCTGGATGGCTCGTCGTTAACTTCTTCAGGAACTGGGAGGTACAAG 1382
Db  1471 GTCATCCAGAGACGCCTGGATGGCTCGTTAACTTCTTCAGGAACTGGGAGGACGTACAAG 1530

Qy  1471 GTCATCCAGAGACGCCTGGATGGCTCGTTAACTTCTTCAGGAACTGGGAGGACGTACAAG 1530
Db  1383 CAAGGGTTTGGGAACATTGACGGCGGAATACTGGCTGGGCCTGGAGAACATTACTGGCTG 1442

Qy  1383 CAAGGGTTTGGGAACATTGACGGCGGAATACTGGCTGGGCCTGGAGAACATTACTGGCTG 1442
Db  1531 CAAGGGTTTGGGAACATTGACGGCGGAATACTGGCTGGGCCTGGAGAACATTACTGGCTG 1590

Qy  1531 CAAGGGTTTGGGAACATTGACGGCGGAATACTGGCTGGGCCTGGAGAACATTACTGGCTG 1590
Db  1443 ACGAACCAAGGCCAACTACAAACTCCCTGGGTGACCATGGAGGAGGACTGGTCCGGCGCAAAGTC 1502

Qy  1443 ACGAACCAAGGCCAACTACAAACTCCCTGGGTGACCATGGAGGAGGACTGGTCCGGCGCAAAGTC 1502
Db  1591 ACGAACCAAGGCCAACTACAAACTCCTGGGTGACCATGGAGGACTGGTCCGGCCGCAAAGTC 1650

Qy  1591 ACGAACCAAGGCCAACTACAAACTCCTGGGTGACCATGGAGGACTGGTCCGGCCGCAAAGTC 1650
Db  1503 TTTGCAGAATACGCCAGTTTCCGCCTGAGCGGTGAGTA 1562

Qy  1503 TTTGCAGAATACGCCAGTTTCCGCCTGAGCGGTGAGTA 1562
Db  1651 TTTGCAGAATACGCCAGTTTCCGCCTGGGAACCTGAGCGTATTATAAGCTGGCGCTG 1710

Qy  1651 TTTGCAGAATACGCCAGTTTCCGCCTGGGAACCTGAGCGTATTATAAGCTGGCGCTG 1710
Db  1563 GGGCGCCTACCATGGCAATGCGGGGTGACTCCTTTACATGGCACAAGGGCAAGCAGTTCACC 1622

Qy  1563 GGGCGCCTACCATGGCAATGCGGGGTGACTCCTTTACATGGCACAAGGGCAAGCAGTTCACC 1622
Db  1711 GGGCGCGTTACCATGCCGGGTGACTTCCTTTACATGGCACAACCAGGAAACTGTGCCCACT 1770

Qy  1711 GGGCGCGTTACCATGCCGGGTGACTTCCTTTACATGGCACAACCAGGAAACTGTGCCCACT 1770
Db  1623 ACCCTGGACAGAGATCATGAATTCTCACACAGGAAACTGTGCCCACTTACCACCAGAAGGGAGGC 1682

Qy  1623 ACCCTGGACAGAGATCATGAATTCTCACACAGGAAACTGTGCCCACTTACCACCAGAAGGGAGGC 1682
Db  1771 ACCCTGGACACAGATCATGATGAGTGTGCCCACTTACCACCTACCAGAAGGGAGGC 1830

Qy  1771 ACCCTGGACACAGATCATGATGAGTGTGCCCACTTACCACCTACCAGAAGGGAGGC 1830
Db  1683 TGGTGGTTATAACGCCTGTGCCCACTCCAACCTCAACCGGGGTCTGGTTACCGGGGGGCCCAT 1742

Qy  1683 TGGTGGTTATAACGCCTGTGCCCACTCCAACCTCAACCGGGGTCTGGTTACCGGGGGGCCCAT 1742
Db  1831 TGGTGGTATAACGCCTGTGCCCAACCTCAACCGGGGTCTGGTTACCGGGGGCCAT 1890

Qy  1831 TGGTGGTATAACGCCTGTGCCCAACCTCAACCGGGGTCTGGTTACCGGGGGCCAT 1890
Db  1743 TACCGGAGCCGCTACCAGGAGTCTACTCGGGTGAGTTCCGAGGAGGCCTCTCTTACTCA 1802

Qy  1743 TACCGGAGCCGCTACCAGGAGTCTACTCGGGTGAGTTCCGAGGAGGCCTCTCTTACTCA 1802
Db  1891 TACCGGAGCCGCTACCAGGAGTCTACTCGGGGTGAGTTCCGAGGAGGCTCTTACTCA 1950

Qy  1891 TACCGGAGCCGCTACCAGGAGTCTACTCGGGGTGAGTTCCGAGGAGGCTCTTACTCA 1950
Db  1803 CTCAAGAAAGTGGTGATGAGATGATCCGACCGAACACCTTCCACTAAGCCCAGCCTCC 1862

Qy  1803 CTCAAGAAAGTGGTGATGAGATGATCCGACCGAACACCTTCCACTAAGCCCAGCCTCC 1862
Db  1951 CTCAAGAAAGGGTGATGATGATCCGACACCCCAAACACCTTCCACTAAGCCACCTCC 2010

Qy  1951 CTCAAGAAAGGGTGATGATGATCCGACACCCCAAACACCTTCCACTAAGCCACCTCC 2010
Db  1863 CCCTCCTGACCTTCTGTGGCCATTGCCAGGAGCCCAGCCACCCTGGCCTGGCCACCCAGCAC 1922

Qy  1863 CCCTCCTGACCTTCTGTGGCCATTGCCAGGAGCCCAGCCACCCTGGCCTGGCCACCCAGCAC 1922
Db  2011 CCCTCCTGACCTTCTCGTGGCCATTGCCAGCTGCCACCCCAGCAC 2070

Qy  2011 CCCTCCTGACCTTCTCGTGGCCATTGCCAGCTGCCACCCCAGCAC 2070
Db  1923 AAAGAACAACTCCTCACCAGTTCATCCTGAGGCTGGGAGGACCGGGGAGTGCTGGATTCTGT 1982

Qy  1923 AAAGAACAACTCCTCACCAGTTCATCCTGAGGCTGGGAGGACCGGGGAGTGCTGGATTCTGT 1982
Db  2071 AAAGAACAACTCCTCACCAGTTCATCCTGAGGCTGGGAGGACCGGGGAGTGCTGGATTCTGT 2130
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OM nucleic - nucleic search, using sw model

GenCore version 5.1.6
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Run on: August 6, 2004, 12:27:03 ; Search time 8364 Seconds
(without alignments)
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    Listing first 45 summaries

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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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6	2132.6	98.1	2290	6	BD222237	Human nuc
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ALIGNMENTS

RESULT 1
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DEFINITION  Sequence 1 from Patent WO0102434.
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VERSION     AX069013.1  GI:12578833
KEYWORDS    .
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            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Friedrich,G., Hagen,G., Wick,M., Zubov,D. and
            Dubois-Stringfellow,N.
  TITLE     Methods for modulating angiogenesis by using the anti-angiogenic
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Pred. No. is the number of results predicted by chance to have a

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JOURNAL    angiotensin-7 and polynucleotides encoding therefor
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VERSION     BC012368.1  GI:15214488
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  AUTHORS   Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
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  TITLE     Generation and initial analysis of more than 15,000 full-length
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  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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   PUBMED    12477932
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  AUTHORS   Strausberg,R.
  TITLE     Direct Submission
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            Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
            USA
REMARK      NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT     Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
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            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Baylor College of Medicine Human Genome
            Sequencing Center
            Center code: BCM-HGSC
            Web site: http://www.hgsc.bcm.tmc.edu/cdna/
            Contact: amg@bcm.tmc.edu
            Contact: Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged, H.,
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Qy     63 GCACTGAGGCAGCGCGGCTGACGCTACTCTGTGAGGGAAAGAAAGGTTGTGAGCGACCAGG 122
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Db     65 GCACTGAGGCACGGCTGACGCTACTCTGTGAGGGAAAGAAAGGTTGTGAGCGACCCCGCAGG 124

Qy    123 ACCCCTGGCCCAGCCCTGGCCCCCAGCCCTGCGCGGAGCCCTGTGGAGCGAGCAGACCAGTG 182
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Db    125 ACCCCTGGCCCAGCCCTGGCCCCCCAGCCCTGCGCGGAGCCCTGTGGAGCGAGCCCAGTG 184

Qy    183 GAGCCCAGTGAGGCCAGGGCTCGTTGGCAGCCACCGGCCCGCCGCGCTCAGGAGACCCCTCAG 242
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Db    185 GAGCCCAGTGAGGCCATGGGCTCGTTGGCAGCCACCGGCCCGCCGCCGCTCAGGAGACCCCTCAG 244

Qy    243 AGGCCCATGGACACAGGCGTGCCCGGCCTGACGGCCGTGAGGCAGTGTGAGGAGCGCGCCGG 302
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Db    245 AGGCCCATGGACACAGGCGTGCCCGGCCTGACGGGTCAAGCATGTGAGGAGCGCGCCCCCGG 304

Qy    303 AGCCAAGCCAGGAGGGAAGGAAGGCTTTCATAGATTCTATTCACCAAGAATAACCACCATTTT 362
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Qy    363 GCAAAGACCATGAGGCCCACTGTTGCGTGACATGCTGGTTGGCTGGACTGCTGGCGTCCTGCCATG 422
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Qy    423 GGAGCTGTTGCAGGCCAGGAGGACGGTTTTGAGGGCACTGAGGAGGGCTCGCGCAAGAGAG 482
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Qy    483 TTCATTTACCTAAACACAGGTACAAGCGGCGGCGGGGGGAGTCCCAGGACAAGTGCACCTACACC 542
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Qy    543 TTCATTGTTGCCCCAGCAGCAGCGGGTCACGGGTGCCATCTGCGTCAAACTCCAAGAGCTGAG 602
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Db    545 TTCATTGTTGCCCCAGCAGCAGCGGGTCACGGGTGCCATCTGCGTCAAACTCCAAGAGCTGAG 604

Qy    603 GTCCTTCTCGGGAGAACCGAGTGCATAAGCAGGCTAGAGCTCGCTCAACAATGAGCTGCTC 662
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Qy    663 AAGCCAGAGACGGGCAGGATGGAGAGCCGTGCAGCACTCAGACAGAGGGGAGGGGAGCCCAT 722
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Qy    723 AGGGAGGGTGAAGTGCTGCTCGCGAGAGAGCCCGCAAACATGAAACTCCGGGTCACGCAGCTC 782
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Qy   1803 CTCAAGAAAGTGGTGGATGGGATCCGGACCGGAGAACCCAACAACCCTGTGGGTCACGCGCAGCTC 1862
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Qy   1863 CCCTCCTGACCTTCTGGTGGCCATTGCCAGGAGGGACCGGGAGATCCGGACAGGCTGGCCACAGCAC 1922
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Db   1865 CCCTCCTGACCTTCTGGTGGCCATTGCCAGGAGGCCCACCCGGGAGATCCGGACGGCTGGCCCACAGCAC 1924

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Qy   2103 CTCTTTCTTTAAATAAAATTAAGTCTCTACAATAAAAACACAACAACTGCAAAGTACCTTCAAA 2162
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Db   2105 CTCTTTCTTTAAATAAAATTAAGTCTCTACAATAAAAACACAACAACTGCAAAGTACCTTCAAA 2164

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FEATURES    Key             Location/Qualifiers
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ORIGIN

Query Match    98.8%;    Score 2146.2;    DB 6;    Length 2288;
Best Local Similarity    99.4%;    Pred. No. 0;    Mismatches    13;    Indels    0;    Gaps    0;
Matches 2154;    Conservative    0;    Mismatches    13;    Indels    0;    Gaps    0;
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Db       73 AAATGAGGCTGCTTGCGGACGGGCCTGAGGATGAACCCCAAGCCCTGGACCTGCGAGCGTG 132

Qy       63 GCACTGAGGCAGCGGCTGACGCTACTGTGAGGAAAGAGAGGTTGTGAGCAGCCCCGCGAGG 122
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      133 GCACTGAGGCAGCGGCTGACGCTACTGTGAGGAAAGAGAGGTTGTGAGCAGCCCCGCGAGG 192

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Db      193 ACCCCTGGCCCAGCCCTGGCCCCAGCGCTCTCTTGTGGTGCAGCAGAGCCAGTG 252

Qy      183 GAGCCCAGTGAGGCAGCGGCTGCTTGGCGAGCCACACCCCTTGGGAGCCAGTG 242
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Qy      243 AGGCCATGGCAGGCTCGCCCGCCTGAGGCGCCAAGGGTGAAGCAATGGACCCGCGCGGG 302
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      313 AGGCCATGGCAGGCTCGCCCGCCTGAGGCGCCAAGGGTGAAGCAATGGACCCGCGCGGG 372

Qy      303 AGCCAAGCAGGAGGGAAGAGGCTTTCATAGATTCTATTCACAAAAGAATAACCACCATTTT 362
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Qy      783 TACATGCAGCTCCTTGCACGAGATCATCCGCAAGGCGGACAACGCGTTGGAAGCTCTTG 842

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RESULT 4

LOCUS   AX014411

LOCUS   AX014413   3541 bp   DNA   linear   PAT 07-SEP-2000

DEFINITION Sequence 125 from Patent WO9954353.

ACCESSION   AX014413

VERSION   AX014413.1   GI:10040712

KEYWORDS   .

SOURCE   Homo sapiens (human)

ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE   1
  AUTHORS   Schmitt,A., Specht,T., Dahl,E., Hinzmann,B., Rosenthal,A. and
            Pilarsky,C.
  TITLE   Human nucleic acid sequences of normal uterus tissue
  JOURNAL   Patent: WO 9954353-A 125 28-OCT-1999;
            SCHMITT ARMIN (DE); SPECHT THOMAS (DE); DAHL EDGAR (DE); HINZMANN
            BERND (DE); ROSENTHAL ANDRE (DE); METAGEN GES FUER GENOMFORSCHUN
            (DE); PILARSKY CHRISTIAN (DE)

FEATURES   Location/Qualifiers
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ORIGIN

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Qy   2043 TACTTTCCTTCACCACCAGACAGCCCTCATGTGTCTCCAGGACCTACACAGACAA 2102
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Db   2113 TACTTTCCTTCACCACCAGACAGCCCCTCATGTGTCTCCAGGACGACAGGACTACACGAACA 2172

Qy   2103 CTCTTTCTTAAATAAATAAGTCTCTACAATAAAAACACAACCAACCTGCAAAGTAACCTTCATA 2162
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Qy   2163 AAAAAAA 2169
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Qy   483 TTCATTTACTTAAACAGGTACAAAGCGGGGGGGGGGGGGGAGTCCAAGACAGAGCAACACC 542
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Qy   543 TTCAGTTGTGCCCCAGCAGCGCGGGTCACGGGGTGCCATCTGCGTCAACTCAAGGAGGCTGAG 602
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RESULT 5

LOCUS       BD222237
LOCUS       BD222237      3541 bp    DNA    linear    PAT 17-JUL-2003
DEFINITION  Human nucleic acid sequence originating in normal uterine tissue.
ACCESSION   BD222237
VERSION     BD222237.1  GI:33032007
KEYWORDS    JP 2002512017-A/66.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 3541)
  AUTHORS   Specht,T., Hinzmann,B., Schmitt,A., Pilarsky,C., Dahl,E. and
            Rosenthal,A.
  TITLE     Human nucleic acid sequence originating in normal uterine tissue
  JOURNAL   Patent: JP 2002512017-A 66 23-APR-2002;
            METAGEN GESELLSCHAFT FUER GENOM FORSCHUNG MBH
  OS        Homo sapiens (human)
  PN        JP 2002512017-A/66
  PD        23-APR-2002
  PF        15-APR-1999 JP 2000546691
  PR        17-APR-1998 DE 198 17 946.4
  PI        THOMAS SPECHT, BERND HINZMANN, ARMIN SCHMITT, CHRISTIAN PILARSKY,
  PI        ANDRE ROSENTHAL
  PI        EDGAR DAHL;
  PC        C12N15/09,A61K38/00,A61K48/00,A61P35/00,C07K14/47,C07K16/18,
  PC        C12N1/19,
  PC        C12N1/21,C12N5/00,C12P21/08,C12P21/08,G01N33/68,C12N15/00, PC
  PC        A61K37/02,
  PC        C12N5/00
COMMENT     Human nucleic acid sequence originating in normal uterine    CC
            tissue

FEATURES             Location/Qualifiers
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FT                   /organism="Homo sapiens (human)".
     source          1..3541
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"

ORIGIN
Query Match             98.2%;  Score 2133.2;  DB 6;  Length 3541;
Best Local Similarity   99.3%;
Matches 2152; Conservative 0; Mismatches 14; Indels 1; Gaps 1;
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Qy      3 AAATGAGGCTGCTGCGGACGGCCTCAGGAGATGAACCCCAAGCCCTGGACTGCCGAGCGTG 62
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Db     75 AAATGAGGCTGCTGCGGACGGCCTCAGGAGATGAACCCCAAGCCCTGGACTGCCGAGCGTG 134

Qy     63 GCACTGAGGCAGCGGCGCTGACCCTACTGTGAGGGAAAGAAGGTTGTGAGCAGCCCCAGCAGG 122
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    135 GCACTGAGGCAGCGGCGCTGACCCTACTGTGAGGGAAAGAAGGTTGTGAGCAGCCCCAGCAGG 194

Qy    123 ACCCCTGGCCAGCCCCCAGCCTTCTGGCCGGAGCCCCTTGTGGGAGCCAGAGTG 182
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Db    195 ACCCCTGGCCAGCCCCCAGCCTTCTGGCCGGAGCCCCTTGTGGGAGCCAGAGTG 254

Qy    183 GAGCCCAGTGAGGCAGGGCTGCTTGGCCGCCACCGGCCTGCAACTCAGGAACCCCTCCAG 242
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy    243 AGGCCCATGGACAGGCTGCCCCGCTGACCGGCCCAGGGTGAAGCGATGTGAGGAGCCGCCGG 302
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    315 AGGCCCATGGACAGGCTGCCCCGCTGACCGGCCCAGGGTGAAGCGATGTGAGGAGCCGCCGG 374

Qy    303 AGCCAAGCAGGAGGGGAAGAGGCCTTCATCAGATTCATTCACAGAAGAAGTA 362
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Db    375 AGCCAAGCAGGAGGGGAAGAGGCCTTCATCAGATTCATTCACAGAAGAAGTA 434

Qy    363 GCAAAGACCATGAGAGGCCACTGTGCGTGACCATGCTGGCTGCTCGGACTGCTGGCCATG 422
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    435 GCAAAGACCATGAGAGGCCACTGTGCGTGACCATGCTGGCTGCTCGGACTGCTGGCCATG 494

Qy    423 GGAGCTGTTGCAGGGCCAGGAGGACGGTTTTGAGGGCCAGGAGGCTCGCAGAGAG 482
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Db    495 GGAGCTGTTGCAGGGCCAGGAGGACGGTTTTGAGGGCCAGGAGGCTCGCAGAGAG 554

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Qy    1443 ACGAACCAAGGCAAACTACACAAACTCCTGGTGACCATGGAGAGGACTGGGTCCGGCCGCAAAGTC 1502
Db    1514 ACGAACCAAGGCAAACTACAAAACTCCTGGTGACCATGGAGAGGACTGGGTCCGGCCGCAAAGTC 1573
Qy    1503 TTTGCAGAATACGCCAGTTTTCCGCCTGGAGCGGAGTATTATAAGCTTGCCGGCTG 1562
Db    1574 TTTGCAGAATACGCCAGTTTTCCGCCTGGAGCGGAGTATTATAAGCTTGCGGGCTG 1633
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Qy    1623 ACCCTGGACAGAGATCATGATTGCTACACAGGAAAACTGTGCCCACTACCAGAAGGGGAGGC 1682
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Db    1754 TGGTGGTTATAACGGCCTGTGCCCAACTCCAACACGGGGTGTCTACCGGCCGGGGGCCAT 1813
Qy    1743 TACCGGCAGCCCTACCAGGAGGGGAGTTCACTGAGTCCGAGGAGCCTCTTTACTCA 1802
Db    1814 TACCGGCAGCCGGCCTACCAGGAGTCTGAGTTCCGAGGAGGCTCTTTACTCA 1873
Qy    1803 CTCAAGAAAGTGGTGAATGATGCTACCGACCGGGGACTCCAACTAAGCCAGCTCC 1862
Db    1874 CTCAAGAAAGTGGTGATGATGATCCGACCGGAACCCCAACACACTTCCACTAAGCAGCTCC 1933
Qy    1863 CCCTCCTGACCTCTCGTGGCCATTGCCTGGAGAGCCACAGCAC 1922
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Qy    1923 AAAGAACAAACTCTCACCAGTTCATCTCGAGGCTGTGGGAGGACCCGGAGGCCACAGCAC 1982
Db    1994 AAAGAACAAACTCTCACCAGTTCATCCTGAGGCTGGGGAGGACCCGGAGGCCACAGTGT 2053
Qy    1983 TTTCCGAAGTCACTGCAGCGGATGGAATCGAATCGAAGGGTGTTTTCTGTCCCTCC 2042
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Qy    2163 AAAAAAA 2169
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Db        675 GTGCTTCTGGAGAACCGAGTGCATAAGCAGGAGCTAGAGCTGCTCAACAATGAGCTGCTC 734

Qy        663 AAGCAGAAGCGGCAGATCGAGACGCTGCAGCAGCTGGTGAAGGTGGACGGCGGCATTGTG 722
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Db        735 AAGCAGAAGCGGCAGATCGAGACGCTGCAGCAGCTGGTGGAGGTGGACGGCGGCATTGTG 794

Qy        723 AGCGAGGTGAAGCTGCTGCGCAAGGAGAGCCGCAACATGAACTCGCGGGTCACGCAGCTC 782
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Db        795 AGCGAGGTGAAGCTGCTGCGCAAGGAGAGCCGCAACATGAACTCGCGGGTCACGCAGCTC 854

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Qy        903 GACCTGGAGCACAAGTACCAGCACCTGGCCACACTGGCCCACAACCAATCAGAGATCATC 962
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RESULT 6
AR081094
LOCUS       AR081094                2290 bp    DNA     linear   PAT 31-AUG-2000
DEFINITION  Sequence 1 from patent US 5972338.
ACCESSION   AR081094
VERSION     AR081094.1  GI:10007822
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 2290)
  AUTHORS   Godowski,P.J. and Gurney,A.L.
  TITLE     Tie ligands homologues
  JOURNAL   Patent: US 5972338-A 1 26-OCT-1999;
FEATURES             Location/Qualifiers
     source          1. .2290
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match             98.1%;  Score 2132.6;  DB 6;  Length 2290;
  Best Local Similarity   99.8%;  Pred. No. 0;
  Matches 2135;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          3 AAATGAGGCTGCTGCGGACGGCCTGAGGATGAACCCCAAGCCCTGGACCTGCCGAGCGTG 62
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Qy        123 ACCCCTGGCCAGCCCTGGCCCCAGCCTCTGCCGGAGCCCTCTGTGGAGGCAGAGCCAGTG 182
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        271 ACCCCTGGCCAGCCCTGGCCCCAGCCTCTGCCGGAGCCCTCTGTGGAGGCAGAGCCAGTG 330

Qy        183 GAGCCCAGTGAGGCAGGGCTGCTTGGCAGCCACCGGCCTGCAACTCAGGAACCCCTCCAG 242
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Qy    331 GAGCCCAGTGAGGCAGGAGGCTGCTTGGCCAGCCACCGGCCTGCAAACTCAGGAACCCTTCCAG 390
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Db   1323 ...

Qy    243 AGGGCCATGGACAGGCTGGCCCGCGGCGGCCAGGGTGGAGGCTGAGCGGAGCGGCCGGCCGGG 302
Db   1383 ...

Qy    391 AGGGCCATGGGACCAGGCTCCCGCGCTGAAGCATGTGAGGAGCCGGCCCGG 450

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Qy    451 AGCCAAGCACGGCGGAGGGGAAGAGGCTTTCATAGATTCTAATCACAAAGAATAACCACCATTTT 510

Qy    363 GCAAAGACCATGAGGCCACTGGTGCGTTGGCTTCGGAGCTGCTGCCATG 422

Qy    511 GCAAGGACCATGAGGCGCACTGTTGCGTGGACTATGTCTGGCTTGGCTGCTGCCATG 570

Qy    423 GGGAGCTTGGTTGCAGGGCCAGGAGGCACTGAGGAGGGGCTTGGCCAAGGAGAG 482

Qy    571 GGAGCTGTTGCAGGGCCAGGAGGCACTGAGGAGGGCTCCCAGAGAG 630

Qy    483 TTCATTTACCTAAACAGGTACAAGCGGGGGGGGGGGGGGCGCACCTACACC 542

Qy    631 TTCATTTACCTAAACAGGTACAAGTGCACCTACACC 690

Qy    543 TTCATTGTGCCCAGCAGCGGGGTCACCGGGTGCCATCTCTGCGGTCAACTTCCAAGGAGCTGAG 602

Qy    691 TTCATTGTTGCCCCAGCAGCGGGGTCACCGGGTCAACTTCCAAGGAGCCTGAG 750

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Qy    751 GTGCTTCTGGGAGAACCGAGTGCATAACCAGGAGAGCTGCTCAACAATGAGTTGCTC 810

Qy    663 AAGCAGAAGCGGCGCAGAGATCGAGAGCGGCTTCCAGCAGCGGTGGTGAAGGTGGAGGCCATTGTG 722

Qy    811 AAGCAGAAAGCCGGCAGATCGAGAGCGCTGCAGCGACGGCGGGCCATTGTG 870

Qy    723 AGCGAGGTGAACGTGCTTCGGCCAAGGAGGGGCCCAACCAACCATGAAACTCGGAGGCAGCTC 782

Qy    871 AGCGAGGTGAACGTGCTGCGGGCCCAACATGAACTCGGGAGGCAGCTC 930

Qy    783 TACATGCAGCTCCCTGCGACGAGATCATCCGGGACACACGGGTTGGAGCTCTCCCAG 842

Qy    931 TACATGCAGCTCCTGCGACGAGATCATCCGGGACAACGGGTTTGGAGCTCTTCCCAG 990

Qy    843 CTGGAGAACAGGATCTTGAACCAGACAGCCGAGTCGCAGCTGCCCAGCGAGTACAAG 902

Qy    991 CTGGAGAACAGGATCCTGAAACCAGAGACCGCCAGCTGCCCAGCAAGTACAAG 1050

Qy    903 GACCTGGAGCACACAAGTACCAGAGACCCTGGCCCACACACAGAGATCATC 962

Qy   1051 GACCTGGAGCACAAGTTACCAGACACCTGGCCCACCCTGTCACGCTGGCACAGGATCATC 1110

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Qy   1231 TCTACCAACGAGATCCAGAGTGACCAGAGGTGCTCCACCCCTGCCCCACT 1290

Qy   1203 TGCCTGCAGGCCCCTGGAGGAATGGCCACGACCACCAGCTCCATCTACTCACTGGTGAAGCCGGGAG 1262

Qy   1351 TGCCTGCAGGCCCCTGGAGGATGGCCCAGAGACACACGACACCCCATCTACTCACTGGTGAAGCCTGGAG 1410

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Query Match    98.1%;  Score 2132.6;  DB 6;  Length 2290;
Best Local Similarity   99.8%;  Pred. No. 0;
Matches 2135;  Conservative   0;  Mismatches   4;  Indels   0;  Gaps   0;

Qy        3 AAATGAGGCTGTGCGGACGGGCTGAGGAATGAACCCAAGCCCTGGACCTGCCGAGGCGTG 62
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Db      211 GCACTGAGGCAGCGGGCTGACGTCTACTGTGAGGGAAAGAAGGTTGTGAGCACCCCGCAGG 270

Qy      123 ACCCCTGCCCACGCCCTGGCCCCAGCCCTCTGCCGCAGGCCCTCTGTTGGAGGGCAGGTG 182
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Db      271 ACCCCTGCCCACGCCCTGGCCCCAGCCCTCTGCCGCAGGCCCTCTGTTGGAGGGCAGGTG 330

Qy      183 GAGCCCAGTGAGGCAGGCTGCTGCTTGGCCAGCCCTGCACTCAGGAGAGCCCAGTG 242
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      331 GACCCCAGTGAGGCAGGCTGCTGCTTGGCCAGCCCTGCACTCAGGAGAGCCCAGTG 390

Qy      243 AGGCCATGGACAGGCTGCCCCGCTGACCCAGGGTGAAGCATGTGAGGAGCGCGCCCCGG 302
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Db      391 AGGCCATGGACAGGCTGCCCCGCTGACCCAGGGTGAAGCATGTGAGGAGCGCGCCCCGG 450

Qy      303 AGCCAAGGAGGAGGGAAGAGAGGCTTTCATTGAATTCTATTCACAAAGAATAAACCACCATTTT 362
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Qy      423 GGAGCTGTTGCAGGGCACGGTTTTGAGGGAGGGCTCGCCCAAGAGAG 482
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Qy      483 TTCATTTACCTAAAACAGGTACAAGCGGGGCGGGGGGGACCAAGTGCACCTACACC 542
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Qy      543 TTCATTGTGCCCCAGCACGCGGGTCACGGGTGCCATCTGCGTCAACTTCAAGGAGCCTGAG 602
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Qy      603 GTGCTTCTGGGAGAACCCAGTGCATAAGCAGACTAGAGCGCGTCAAAATGAGTGCTCTC 662
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Db      751 GTGCTTCTGGGAGAACCCAGTGCATAAGCAGACTAGAGCTTGCCTCAAAATGAGCTGCTC 810

Qy      663 AAGCAGAAGCGGCAGATTGGACGCGTCAGCACGCTGTGAGGTGGACGGCGGGCATTGTG 722
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Db      811 AAGCAGAAGCGGCAGATTGGACGCGTCAGCACGCTGTGAGGTGGACGGCGGGCATTGTG 870

Qy      723 ACGGAGGTGAAGCTGCTTGCGCGAGGAGGAGCGCGACACATGAAACTCGCGGGTCAGCTC 782
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Db      871 ACGGAGGTGAAGCTGCTTGCGCGAGGAGGAGCGCGACACATGAAACTCGCGGGTCAGCTC 930

Qy      783 TACATGCAGCTCCTGCACGAGGATCATCCGCAAGCGGGGACAACGGCGTTGGAGCTCTCCAG 842
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Db      931 TACATGCAGCTCCTGCACGAGATCATCCGCAAGCGGGGACAACGGCGTTGGAGCTCTCCAG 990

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Db      991 CTGGAGAACAGCAGGATCCTGAAACAGACAGCCGCCGACATGCTGCTGCACAGTCAAGTACAAG 1050

Qy      903 GACCTGGAGCACAAGTACCAGCACCCTGGCCACTGGCCACAACCAATCAGAGAGATCATC 962
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RESULT 8
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LOCUS       AR205229                2290 bp    DNA        linear   PAT 20-JUN-2002
DEFINITION  Sequence 1 from patent US 6368853.
ACCESSION   AR205229
VERSION     AR205229.1  GI:21502759
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 2290)
  AUTHORS   Godowski,P.J. and Gurney,A.L.
  TITLE     Tie ligand homologues
  JOURNAL   Patent: US 6368853-A 1 09-APR-2002;
FEATURES             Location/Qualifiers
     source          1..2290
                     /organism="unknown"
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ORIGIN

Query Match          98.1%;  Score 2132.6;  DB 6;  Length 2290;
Best Local Similarity  99.8%;  Pred. No. 0;
Matches 2135;  Conservative  0;  Mismatches  4;  Indels  0;  Gaps  0;
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Db     63 GCACTGAGGCGACGGCGGCTGACCGTACTGTGAGGGAAAAGAGAAGGTTGTGAGCGCAGG 122
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Qy    211 GCACTGAGGCGACGGCGGCTGACCCTACGTGAGGGAAAGAAGGTTGTGAGCACCGCCGCAGG 270

Qy    123 ACCCCTGGCCCAGCCCTTGGCCCCCAGCCCTTCGTGTGGAGGGCAGAGGCCAGTG 182
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Db    183 GAGCCCCAGTGAGGCAGGCCTGCTTGCCAGCCACCCGGCCACCCCTTCCAG 242
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Qy    243 AGGCCAAGCACAGGGCTCCCCCGCCCTGACGGCGTGAGCCATGGTGAGGACGCGCCGG 302
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Db    391 AGGCCAAGCACAGGAGGGAAGAGGCTTCCCCCGCCCTGACGGCGTGAGCCATGGTGAGGACGCGCCGG 450

Db    303 AGCCAAGCAGAGGGGAAGAGGCTTTCATAGAGATTCTATTCACAAAAGAAATAACCACCATTTT 362
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Qy    451 AGCCAAGCAGAGGAGGAAGAGGCTTTCATAGAGATTCTATTCACAAAAGAAATAACCACCATTTT 510

Qy    363 GCAAAGACCCATGAGGCCCCAACTGTGCCGGTGGCTGGCTGACAGCTGCTGGCTGCCATG 422
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Db    511 GCAAGAGACCATGAGGCCCCACTGTGGCCGGTGACACTGCTGGCTCGGACTGCCATG 570

Db    423 GGAGCTGTTGCAGGCCCCAGGCCACGGGTTTGAGGGGGCACTGAGGAGGGCTCGCCAAGAGAG 482
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Qy    483 TTCATTTACCTAAACAGGTACAAGCGCGGCGAGTGCCACCTACACC 542
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Db    631 TTCATTTACCTAAACAGGTACAAGCGCGGCGAGTGCCACCTACACC 690

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Qy    691 TTCATTGTGTGCCCCAGCCAGCAGCGGGTCAGGGGTGCCATCTCCACCGGAGCCTGAG 750

Qy    603 GTGCTTCTGGAGAACCGGAGTGCATAAGCACGAGAGCCTAGAGCTGCTCAAACAATGAGCTGCTC 662
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Db    663 AAGCAGAAGCGGCCAGATCGAGACGCTGCACGAGTGGTGAAGGTGATCACGCGCATTGTG 722
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Qy    811 AAGCAGAAGCGGGCCAGATCGAGACACGCTGCACGAGTGGTGAAGGTGATCACGCGGCATTGTG 870

Qy    723 AGCGAGGTGAAGCTGCTGCCCAAGCAAGCAAGCAGCCGCAAACATGAAACTCCCGGGTCAGCGGTC 782
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Db    871 AGCGAGGTGAAGCTGCTGCCCAAGCAAGAAGCCGCAACATGAAACTCCCGGGTCAGCGGTC 930

Db    783 TACATGCCAGCTCCTGCCACGGATCATCCGCAAGGGGCACAAGCGGCTCTCCCCAG 842
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Qy   1051 GACCTGGAGCACAAGTACCAGCACCTGGCCCACCTGCCCCCACAGAGATCATC 1110

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Qy   1083 TCTACCAACGAGATCCAGAGTGACCAGAACCTGAAGGTGCTGCACCACCCCTGCCACT 1142
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Db   1231 TCTACCAACGAGATCCAGAGTGACCAGAACCTGAAGGTGCTGCACCACCCCTGCCACT 1290

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Qy   1291 ATGCCCACTCTCACAGAGCCTCCAATCTTCACGGCACGAAGCGCGTCGGGCCCATGGAGACGAC 1350

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Db   1351 TGCCTGCAGGCCCTGGAGGATGGCCACGGACAGCCAGTCAGTCCATCTACCTGGTGAAGCCGGAG 1410

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Qy   1443 ACGAACCAAGCGCAACTACAAAACTCCTGGTGAGGAGAACACTGGGCGGCCGCCCAAAGTC 1502
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Db   1623 ACCCTGGACAGAGATCATGATGTCTACACAGGGAAAACTGTGCCACTACACAGAAGGGAGGC 1682
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Qy   1771 ACCCTGGACAGAGATCATGATGTCTACACAGGGAAAACTGTGCCACTACACAGAAGGGAGGC 1830

Qy   1683 TGGGTGGTATAAGCGCCTGTGCCCACTCCAACCCTCAACGGGGGTTCTGCTACCGGTGGGCCAT 1742
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Qy   2103 CTCTTTTCTTTAAAATAAATTAAGTCTCTTACAATAAAAAACA 2141
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Db   2191 TACTTTTCCTTCACACCAGACAGCACCCCTCATGTCTCCAGGACAGGAGGACTACAGACAA 2250
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RESULT 9
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LOCUS       AR266344                2290 bp    DNA        linear   PAT 10-APR-2003
DEFINITION  Sequence 1 from patent US 6492331.
ACCESSION   AR266344
VERSION     AR266344.1  GI:2695273
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 2290)
  AUTHORS   Godowski,P.J. and Gurney,A.L.
  TITLE     NL8 tie ligand homologues
  JOURNAL   Patent: US 6492331-A 1 10-DEC-2002;
FEATURES             Location/Qualifiers
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ORIGIN

Query Match     98.1%;  Score 2132.6;  DB 6;  Length 2290;
Best Local Similarity   99.8%;  Pred. No. 0;
Matches 2135;  Conservative   0;  Mismatches   4;  Indels   0;  Gaps   0;
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(The remainder of the page consists of paired Qy / Db nucleotide sequence alignment rows with their base-position numbering, running the length of the aligned sequences.)

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RESULT 10
LOCUS       AR307688                2290 bp    DNA        linear   PAT 12-JUN-2003
DEFINITION  Sequence 1 from patent US 6651822.
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VERSION     AR307688.1  GI:31698425
KEYWORDS    .
SOURCE      unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 2290)
  AUTHORS   Godowski,P.J., Gurney,A.L., Hillan,K., Botstein,D., Goddard,A.,
            Roy,M., Ferrara,N., Tumas,D. and Schwall,R.
  TITLE     NL4 tie ligand homologue
  JOURNAL   Patent: US 6651822-A 1 22-APR-2003;
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ORIGIN

Query Match   98.1%; Score 2132.6; DB 6; Length 2290;
Best Local Similarity   99.8%; Pred. No. 0;
Matches 2135; Conservative   0; Mismatches   4; Indels   0; Gaps   0;

RESULT 11

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DEFINITION  Sequence 1 from patent US 6586397.
ACCESSION   AR350376
VERSION     AR350376.1  GI:33751435
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 2290)
  AUTHORS   Godowski,P.J. and Gurney,A.L.
  TITLE     Tie ligand homologues
  JOURNAL   Patent: US 6586397-A 1 01-JUL-2003;
FEATURES             Location/Qualifiers
     source          1..2290
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

Query Match             98.1%;  Score 2132.6;  DB 6;  Length 2290;
Best Local Similarity   99.8%;  Pred. No. 0;
Matches 2135;  Conservative   0;  Mismatches   4;  Indels   0;  Gaps   0;
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Qy      3 AAAATGAAGGCTTGCTCGGAGACCCAAGGCCCTGAGGATGAACCCAAGGCCTGGACCTGGACCTGCGTG 62
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(sequence alignment continues; Query (Qy) / Database (Db) rows)

Qy   1023 CCCGCGCTGCCCGCGGCCCCGCGGGGTTACCAAACCACCAACCGCATCATCAACCAGATC 1082
Db   1171 CCCGCTGCCCGCGGCCCCGCGGGGTCTACCAAACCACCAACCGCATCATCAACCAGATC 1230

Qy   1083 TCTACCAAACGAGGAGGATCCAGAGTGACCAGAGAACCTTGAGCGGTGCTGCCACCCCTTCTGCCCACT 1142
Db   1231 TCTACCAAACGAGAAGGATCCAGAGTGACCAGAGAACCTTGAAGGTGCTGCCACCCCTTCTGCCCACT 1290

Qy   1143 ATGCCCACTCTCACCAGCCTTCCCATCTTCCACCGACACGCAAGCCGTCGGGCCCATGGAGAGAC 1202
Db   1291 ATGCCCACTCTCACCAGCCTCCCATCTTCCACCGACACGCAAGCCGTCGGGCCCATGGAGAGAC 1350

Qy   1203 TGCCTGCAGGCCCTGGAGGATGGCCACGAGCACCAGCTTCCATCTCATTCACTTGGGAAGCCGGGAG 1262
Db   1351 TGCCTGCAGGCCCTGGAGGATGGCCACGAGCACCAGCTTCCATCTCATTCACTTGGGAAGCCGGGAG 1410

Qy   1263 AACACCAACCGCCTCATGCAGGTGTGGTTGGTGGTCACAGACAGACCACCCCGGGGGGGGGGGGACC 1322
Db   1411 AACACCAACCGCCTCATGCAGGTGTGGTTGGTGGTCACAGACAGACCACCCCGGGGGGGGGGGGACC 1470

Qy   1323 GTCATCCAGAGACGACCCTGGATGGCTCTCGTTAACTTCTTCTTCAGGAACTGGGAGACGTACAAG 1382
Db   1471 GTCATCCAGAGACGACCCTGGATGGCTCTCGTTAACTTCTTCTTCAGGAACTGGGAGACGTACAAG 1530

Qy   1383 CAAGGGGTTTGGGAACCATTGACCGGCGGATACTGGCTGGCCTGGAGAACATTTACTGGCTG 1442
Db   1531 CAAGGGGTTTGGGAAACCATTGACCGGCGGAATACTGGCTGGGCCTGGAGAACATTTACTGGCTG 1590

Qy   1443 ACGAACCAAGGCAACTACAAAACTCCTGGTGACCATGGAGGACTGGTCGGCGGCGCCAAAGTC 1502
Db   1591 ACGAACCAAGGCAACTACAAAACTCCTGGTGACCATGGAGGACTGGTCGGCGGCGCCAAAGTC 1650

Qy   1503 TTTGCAGAATAGCGCCAGTTTCCGCCCTGGAAACTGAGAGCGAGTATTATAAGCTGCGGCTG 1562
Db   1651 TTTGCAGAATAGCGCCAGTTTCCGCCCTGGAAACTGAGAGCGAGTATTATAAGCTGCGGCTG 1710

Qy   1563 GGGCGCTACCATGGCAATGCGGGTGACTCCTTTACTCACATGGCACAACGGCAAGCAGTTCACC 1622
Db   1711 GGGCGCTACCATGGCAATGCGGGTGACTCCTTTACTCACATGGCACAACGGCAAGCAGTTCACC 1770

Qy   1623 ACCCTGACAGAGATGTCTACACAGAGAAACTGTGCCCACTACCACAGAAGGGAGGC 1682
Db   1771 ACCCTGACAGAGATGTCTACACAGAGAAACTGTGCCCACTACCACAGAAGGGAGGC 1830

Qy   1683 TGGTGGTATAACCCTGTGCCCACTCCAACCTCAACCTCAACGGGGGTCTGGTTACCGGCGGGGCGCCAT 1742
Db   1831 TGGTGGTATAACCCTGTGCCCACTCCAACCTCAACCTCAACGGGGGTCTGGTTACCGGCGGGGCGCCAT 1890

Qy   1743 TACCGGAGCGCTACCAGGACGGAGTCTACTGGGCTGGAGTTCCGAGGAGGCTCTTACTCA 1802
Db   1891 TACCGGAGCGCCGTTACCAGGACGGAGTCTACTGGGCTGGAGTTCCGAGGAGGCTCTTACTCA 1950

Qy   1803 CTCAAGAAAAGTGGTGATGATGATGATCGGACGGAACCCCAACACACTTCCACTAAGCCAGCTCC 1862
Db   1951 CTCAAGAAAAGTGGTGATGATGATGATCGGACGGAACCCCAACACACTTCCACTAAGCCAGCTCC 2010

Qy   1863 CCCTCCTGACCTCTCGTTGTCAGGAGCCCACCCTGCCCTGGCCACAGCAC 1922
Db   2011 CCCTCCTGACCTCTCGTTGTCAGGAGCCCACCCTGCCCTGGCCACAGCAC 2070

Qy   1923 AAAGACAAACTCCTCACCAGTTCATCCTCGAGCGTACAAGGGGGGGGGGGGGAATGCTCGGATTCTGT 1982
Db   2071 AAAGAACAAACTCCTCACCAGTTCATCCTCGAGCGTACAAGTGCCACTTACACC 2130

Qy   1983 TTTCCGGAAGTCACTGCAGCGGATGATGGAACTGAATCGATAGGGTGTGTTTTTCTGGTCCCTCC 2042
Db   2131 TTTCCGGAAGTCACTGCAGCGGATGATGGAACTGAATCGATAGGGTGTGTTTTTCTGGTCCCTCC 2190

Qy   2043 TACTTTCCTTCACACAGACAGCCCTCATTGTTCCAGGACAGGACAGGACTACAGACAA 2102
Db   2191 TACTTTCCTTCACACAGACAGCCCTCATTGTTCCAGGACAGGACAGGACTACAGACAA 2250

Qy   2103 CTCTTTCTTTCTTTAAATAAATTAAGTCTCTACAAATAAAAACA 2141
Db   2251 CTCTTTCTTTCTTTAAATAAATTAAGTCTCCTACAAATAAAAAA 2289

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Qy    663 AAGCAGAAGCCGGCAGATCGAGACGCTGCAGCAGCTGCAGGTGGAGGTGGACGGGCATTGTG  722
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    811 AAGCAGAAGCCGGCAGATCGAGACGCTGCAGCAGCTGCAGGTGGAGGTGGACGGGCATTGTG  870

Qy    723 AGCGAGGTGAAGCTGCGCGCGCAAGGAGAGCCCGGTCAGCAGCTCGGCGGGGGCATTGTG   782
          |||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db    871 AGCGAGGTGAAGCTGCGTGCGCAAGGAGAGCCCGGTCAGCAGCTCGGCGGGGGCATTGTG   930

Qy    783 TACATGGCAGCTCCTCTGCGACGAGCATCCTGCGACGAGCCGGGACAAGCGCGTTTGGGCTTCTCCCAG  842
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    931 TACATGGCAGCTCCTCTGCGACGAGCATCCTGCGACGAGCCGGGACAAGCGCGTTTGGGCTTCTCCCAG  990

Qy    843 CTGGAGAACAGGATCCTGAACCAGACAGCAGCCGACATGCTGCAGCTGGCCAGCAGCTTAGACAGCAAG  902
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    991 CTGGAGAACAGGATCCTGAACCAGACAGCAGCCGACATGCTGCAGCTGGCCAGCAGCTTAGACAGCAAG 1050

Qy    903 GACCTGGAGCACAAGTACCAGCACCTGGCCCACCTGGCCCACCTGGCCCACTCAGACTGAGAGATCATC  962
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Db   1051 GACCTGGAGCACAAGTACCAGCACCTGGCCCACCTGGCCCACCTGGCCCACTCAGACTGAGAGATCATC 1110

Qy    963 GCGCAGCTTGAGGAGCACTGCGCAGAGGGTGCCCTCGGCCAGCGCCCGTCCCCAGCCACCC         1022
          ||||||||||||||||||||||||||||||||||||||||||||||||
Db   1111 GCGCAGCTTGAGGAGCACTGCGCAGAGGGTGCCCTCGGCCAGCGCCCGTCCCCAGCCACCC         1170

Qy   1023 CCCGCTGCCCCCCGGGTCTACCAACCCGCCACCACCAATCAACCAGATC                 1082
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Db   1171 CCCGCTGCCCCCCGGGTCTACCAACCCGCCACCACCAATCAACCAGATC                 1230

Qy   1083 TCTACCAAACGAGATCCAGAGTGACCAGAACCTGAAGGTGCTGCCACCCCCTCTGCCCACT     1142
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Db   1231 TCTACCAAACGAGATCCAGAGTGACCAGAACCTGAAGGTGCTGCCACCCCCTCTGCCCACT     1290

Qy   1143 ATGCCCACTCTCACCACCAGCCTCCCATCTTCCACGACAAGCCCGTTCGCGGCCCATGGAGGAGAC     1202
          ||||||||||||||||||||||||||||||||||||||||||||
Db   1291 ATGCCCACTCTCACCACCAGCCTCCCATCTTCCACGACAAGCCCGTTCGCGGCCCATGGAGGAGAC     1350

Qy   1203 TGCCTGCAGGCCCTGGAGGATGGCCCACGACCACCAGCTCCCATTACCTGGTGAAGCCCGAG       1262
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Db   1351 TGCCTGCAGGCCCTGGGGGATGGCCCACGACCACCAGTTCCATCTACCTGGTGAAGCCCGAG       1410

Qy   1263 AACACCAACCGCCTCATGCAGGTGTGTGCGACCAGACACGACCCCCGGGGGGGCTGGACC         1322
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Db   1411 AACACCAACCGCCTCATGCAGGTGTGTGCGACCAGACACGACCCCCGGGGGGGCTGGACC         1470

Qy   1323 GTCATCCAGAGACGCCCTGGATGGCTCTTCTTAACTTCTTCAGGAACTGGGAGACGGTACAAG       1382
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Db   1531 CAAGGGTTTGGGAACATTGACGGCGCGAATACTGGCTGGGCCTGGAGAACACATTTACTGGCTG      1590

Qy   1443 ACGAACCAAGGCAAACTACAAACTTCCTTGTGACATGAGGACTGGGTCCGGGCCGAAAGTC         1502
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Db   1591 ACGAACCAAGGCAAACTACAAACTTCCTTGTGACATGAGGACTGGGTCCGGGCCGAAAGTC         1650

Qy   1503 TTTGCAGAATACGCCCAGTTCCCGCCCTTGAGAGCGCGAGTATTATTAAGCTGCGGCTG           1562
          ||||||||||||||||||||||||||||||||||||||||||
Db   1651 TTTGCAGAATACGCCCAGTTCCCGCCCTGAGAGCGCGAGTATTATTAAGCTGCGGCTG           1710

Qy   1563 GGGCGCTACCATGGCAATGCGGGTGACTCCTTTACATGGGACCAAGGCAAGCAGTTCACC          1622
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Db   1711 GGGCGCTACCATGGCAATGCGGGTGACTCCTTTACATGGGACCAAGGCAAGCAGTTCACC          1770

Qy   1623 ACCCTGGACAGAGGATCATGATGTCTACACAGAGAAACTGTGCCCACTACCAGAGAGGGGC         1682
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Db   1771 ACCCTGGACAGAGGATCATGATGTCTACACAGAGAAACTGTGCCCACTACCAGAGAGGGGC         1830

Qy   1683 TGGTGGTTATAAGCCGTCTCTGGTACGCGGGTACCGGAGGCAGGCCAT                  1742
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Db   1831 TGGTGGTTATAAGCCGTCTCTGGTACGCGGGTACCGGAGGCAGGCCAT                  1890

Qy   1743 TACCGGAGCAGCGGCTACAGGACGGAGTCTACTGGGGCTGAGTTCGCGAGGAGAGGCTCTTACTCA     1802
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Db   1891 TACCGGAGCCGCCTACCAGGACGGAGTCTACTGGGGCTGAGTTCCGAGGAGAGGCTCTTACTCA      1950

Qy   1803 CTCAGAAAAGTGGTGATGATGATCGGACCGGAACCGAACCCAACCCTTCCACTTCCAGAGCTCC      1862
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Db   1951 CTCAGAAAAGTGGTGATGATGATCGGACCGGAACCGAACCCAACCCTTCCACTTCCAGAGCTCC      2010

Qy   1863 CCCTCCTTGACCTTCTTCGTTGGCCCATTGCCAGGACCGCCACCCTGGTCAGCGTCGGCCACAGCAC   1922
          |||||||||||||||||||||||||||||||||||||||||
Db   2011 CCCTCCTTGACCTTCTTCGTTGGCCCATTGCCAGGACCGCCACCCTGGTCAGCGTCGGCCACAGCAC   2070

Qy   1923 AAAGAACAAACTCCTCACCCACAGTTCATCCTGAGGCTGGGGAGCTGGGAGGACCCGGAGTTCTGT    1982
          |||||||||||||||||||||||||||||||||||||||||
Db   2071 AAAGAACAAACTCCTCACCCACAGTTCATCCTGAGGCTGGGGAGCTGGGAGGACCCGGAGTTCTGT    2130

Qy   1983 TTTCCGAAGTCACTGCAGCGGATGATGGAACTGAATCGTGATAGCGGTGTGTTTTTTCTGTCCCTCC   2042
          |||||||||||||||||||||||||||||||||||||||||
Db   2131 TTTCCGAAGTCACTGCAGCGGATGATGGAACTGAATCGTGATAGCGGTGTGTTTTTTCTGTCCCTCC   2190

Qy   2043 TACTTTCCTTCACACCAGACAGCCCCTCATGTCTCCAGGACAGGAGGACTACAGACAA           2102
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Db   2191 TACTTTCCTTCACACCAGACAGCCCCTCATGTCTCCAGGACAGGAGGACTACAGACAA           2250

Qy   2103 CTCTTTCTTTAAATAAAATTAAGTCTCTACAATAAAAACA                          2141
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Db   2251 CTCTTTCTTTAAATAAAATTAAGTCTCTACAATAAAAAA                           2289
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RESULT 12

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LOCUS       AX403648                2290 bp    DNA     linear   PAT 14-JUN-2002
DEFINITION  Sequence 3 from Patent WO0077037.
ACCESSION   AX403648
VERSION     AX403648.1  GI:21437109
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Ashkenazi,A., Baker,K., Botstein,D., Desnoyers,L., Eaton,D.L.,
            Ferrara,N., Fong,S., Gao,W.Q., Gerber,H., Gerritsen,M.E.,
            Goddard,A., Godowski,P., Gurney,A., Kljavin,I.J., Mather,J.,
            Napier,M., Pan,J., Pacni,N., Roy,M., Tumas,D., Watanabe,C.,
            Williams,P.M., Wood,W.I. and Zhang,Z.
  TITLE     Secreted and transmembrane polypeptides and nucleic acids encoding
            the same
  JOURNAL   Patent: WO 0077037-A 3 21-DEC-2000;
            Genentech Inc. (US)
FEATURES             Location/Qualifiers
     source          1..2290
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

Query Match             98.1%;  Score 2132.6;  DB 6;  Length 2290;
Best Local Similarity   99.8%;  Pred. No. 0;
Matches  2135;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;
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Qy      3 AAATGAGGCTCGTCGCGGACGGGCCTGAGGATGAAACCCCAAGCCCTGCCGACGGACCGGTG   62
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    151 AAATGAGGCTCGTCGCGGACGGGCCTGAGGATGAAACCCCAAGCCCTGCCGACCTGAGGGTG  210

Qy     63 GCACTGAGGCACGGGGCTGACCGGCTACGTGGAGGGAAGAAGGTTGTGAGCAGGAGGGTG    122
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    211 GCACTGAGGCACGGGGCTGACCGGCTACGTGGAGGGAAGAAGGTTGTGAGCAGGAGG      270

Qy    123 ACCCCTGGCCAGCCCTGGCCCCAGCCCTCTGCGGGAGCCCTCTGTGTGGAGGCAGGAGCCAGTG  182
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    271 ACCCCTGGCCAGCCCTTGCCCCAGCCCTCTGCGGGAGCCCTCGTGTGAGGGCAGAGCCAGTG  330

Qy    183 GAGCCCAGTGAGGCAGGGCTGCTTGGCGCACCGGCGCTGCAACTCAGGAAACCCCTCCAG   242
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Db      1 ...
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RESULT 13

(The remainder of the page is a DNA sequence alignment between a Query (Qy) and Database (Db) sequence, presented in paired rows with match bars and flanking base-position numbers, running from positions ~243 through ~2289.)

TITLE   Secreted and transmembrane polypeptides and nucleic acids encoding same

JOURNAL   Patent: WO 0140466-A 267 07-JUN-2001;
           Genentech Inc. (US)

FEATURES
     source   1..2290
              Location/Qualifiers
              /organism="Homo sapiens"
              /mol_type="unassigned DNA"
              /db_xref="taxon:9606"

ORIGIN

Query Match   98.1%;   Score 2132.6;   DB 6;   Length 2290;
Best Local Similarity   99.8%;   Pred. No. 0;
Matches 2135;   Conservative   0;   Mismatches   4;   Indels   0;   Gaps   0;

(DNA sequence alignment between Query (Qy) and Database (Db) sequences, positions 3–2011 / 843–2011)

Qy 2071 AAAGAACAAACTCCTCACCAGTTCATCCTGAGGCTGGCAGGGACGGGACCGGGATTCTGT 2130

Qy 1983 TTTCCGAAGTCACTGCACGGGATGAGGAACTGAAATCGATACCGGTGTTTTTCGTCCCTCC 2042

Db 2131 TTTCCGAAGTCACTGCACGCGGATGAGATGGAACTGAATACGGTGTTTTCGTCCCTCC 2190

Qy 2043 TACTTTCCTTCACCAGCACGCGCCCCCCCATGTGTCTCAGGACAGGACAGGACTACAGACAA 2102

Db 2191 TACTTTCCTTCACCAGCACGCGCCCCCCATGTGTCTCAGGACAGGACAGGACTACAGACAA 2250

Qy 2103 CTCTTTCTTTAAATAAATTAAGTCTCTACAATAAAAAACA 2141

Db 2251 CTCTTTCTTTAAATAAATTAAGTCTCTACAATAAAAAA 2289

RESULT 14
BD076338

LOCUS   BD076338   2290 bp   DNA   linear   PAT 27-AUG-2002
DEFINITION Ligand homolog.
ACCESSION   BD076338
VERSION   BD076338.1 GI:22621941
KEYWORDS   JP 2001517437-A/1.
SOURCE   Homo sapiens (human)
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 2290)
  AUTHORS   Godowski,P.J., Gurney,A.L., Hillan,K., Botstein,D., Goddard,A.,
            Roy,M., Ferrara,N., Tumas,D. and Schwall,R.
  TITLE   Ligand homolog
  JOURNAL   Patent: JP 2001517437-A 1 09-OCT-2001;
            GENENTECH INC
COMMENT   OS Homo sapiens (human)
            PN JP 2001517437-A/1
            PD 09-OCT-2001
            PF 14-SEP-1998 JP 2000512945
            PR 19-SEP-1997 US 08/933821 29-OCT-1997 US 08/960507 PI
            PF 14-SEP-1997 US 08/933821,29-OCT-1997 US 08/960507 PI
            PA PAUL J GODOWSKI,AUSTIN L GURNEY,KENNETH HILLAN,DAVID BOISTEIN, PI
            AUDLEY GODDARD,MARGARET ROY,NAPOLEONE FERRARA,DANIEL TUMAS, PI
            RALPH SCHWALL
            PC C12N15/09,A61K38/00,A61K39/395,A61K39/44,A61P35/00,C07K14/515,
            PC C07K16/18,
            PC C12N15/00,A61K37/02,C12N5/00
            PC C12N1/15,C12N1/19,C12N1/21,C12N5/10,C12Q1/68,G01N33/53//C12P21/ PC
            08,
FEATURES   Location/Qualifiers
     source   1..2290
                     /organism="Homo sapiens"
                     FH   Key   Location/Qualifiers
     source   1..2290
                     /organism="Homo sapiens (human)"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"

ORIGIN

Query Match   98.1%; Score 2132.6; DB 6; Length 2290;
Best Local Similarity   99.8%; Pred. No. 0;
Matches 2135; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy   3 AAATGAGGCTGTGCGGACGGGGCCTGAGGATGAAACCCAAGCCCTGACCTGCCGAGCGTG 62

Qy   63 GCACTGAGGCACGGGCTGACCGGTACTGTGAGGGAAAAGAAGGTTGTGAGCGAGCCCGCAGG 122

Db   211 GCACTGAGGCACGGGCTGACCGTACTGTGAGGGAAAGAAGGTTGTGAGCAGCCCGCAGG 270

Qy   123 ACCCCTGGCCAGCCCTGCCCCCCAGCCTTCGCGGGAGGGACCCTCGTTGTGGGAGGGAGGCCAGTG 182

Db   271 ACCCCCTGGCCAGCCCTGGGCCCCCAGCCCTTCTGTGTGGGAGGGCAGAGAGCCAGTG 330

Qy   151 AAATGAGGCTGCTGCGGGACGGGGCCTGAGGATGAACCCCAAGCCCTGACCTGCCGAGCGTG 210

Qy   183 GAGGCCCAGTGAGGCAGAGGGGTGCTTGGCACTGCTTGCCGCAACTCAGGAGAACCCTCCAG 242

Db   331 GAGCCCAGTGAGGCAGAGGGGTGCTTGGGCACGGCAGGCCGCAACTCAGGAGAACCCTCCAG 390

Qy   243 AGGGCCATGGACAGGCTGCCCGCCCTGACGCGCCTGAAGCAATGACATCAGCGCCGCCGGG 302

Db   391 AGGGCCATGGACAGGCTGCCCGGCCCTGACGCGCCTGAAGCATTGAGCAGCGCCGCCGGG 450

Qy   303 AGCCAGGCAGGGGAAGAGGCCTTTCAAGAGATTCTATTCACAAAGAATAAACACCATTTT 362

Db   451 AGCCAAGCAGGGGAAGAGGCCTTTCAATAGATTCTATTCACAAAGAATAAACACCATTTT 510

Qy   363 GCAAAGACCAATGAGGGCCACTGTGCCTGACATGCTGGGTCGGGCTGGCCAGGAGAG 422

Db   511 GCAAGGACCAATGAGGGCCACTGTGCCTGACAATGCTGGGTCGGCTCGGGGACTGCTGGG 570

Qy   423 GGAGCTGGTTGCAGGGCCCAGGAGGACCGGTTTTGAGGGCACTGAAGGCTCGCCACTACACC 482

Db   571 GGAGCTGGTTGCAGGGCCCAGGAGGACCGGTTTTGAGGGCACTGAAGGCTCGCCAAGGAG 630

Qy   483 TTCATTTTACCTAAAACAGGTACAAAGCGCGGGGGGGCCCAGTCCCAGGACAAGTGCACTC 542

Db   631 TTCATTTACCTAAACAGGTACAAAGCGGGGGGGCCCAGTCCCAGGACAAGTGCACTC 690

Qy   543 TTCATTGTGCCCAGCAGCGGGGTCACGGGTGCCATCGTCGTCAACTCCCAAGGAGCCTGAG 602

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Qy   603 GTGCTTCTGGAGAACCGGAGTGCATAAGGAGGAGCTAGAGTGGCTCAACTCAACAATGAGGTGCTC 662

Db   751 GTGCTTCTGGAGAACCGGAGTGCATAAGGCAGGAGCTAGAGTGGCTCAACAATGAGGTGCTC 810

Qy   663 AAGCAGAAAGGGGCACGATCAGACACGCTGCAACGTGGTGAAAGGTGACCGGCCATTGTG 722

Db   811 AAGCAGGAAGCGGCACGATCGAGAGCTTGCAACGTGGTGGAAGGTGACCGGCCATTGTG 870

Qy   723 AGCGGAGGTGAAGCTCGCTGCGGTCGGCAAGGAGGAGCGGCGCAACATGAACTCGGCGGCTC 782

Db   871 AGCGGAGGTGAAGCTCGCTGCGGTCGGCAAGGAGCGGCGCAACATGAACTCGGCGGTCACGCGAGCTC 930

Qy   783 TACATGCAGCTCTCTGCCACGGAGATCAATCCGGAAGGGGACAAACGGGGTTGGAGCTCTCCCAG 842

Db   931 TACATGCAGCTCTCCTGCCACGGAGATCATCCCGGAAGGGGACAAACGGGGTTGGAGCTCTCCCAG 990

Qy   843 CTGGAGAAACAGGATCCTGAACCAGCAGCCGACATGGCTCGAGCTGGCCAGCAAGTACAAG 902

Db   991 CTGGAGGAACAGGATCCTGAACCAGCAGCCGACATGGCTCGCTGGCCAGCAAGTACAAG 1050

Qy   903 GACCTGGAGCACAAGTACCAGAGTGACACGCCCCAACTCCAACAATCAGAGATCATC 962

Db   1051 GACCTGGAGCACAAGTACCAGCACCTGGCCCAACTGGCCCAACAATCAGAGATCATC 1110

Qy   963 GCGCAGAGCTTGAGGGAGCACTGCCCAAGGGTGCCCCTCGGCCAGCCCCAGCCACCC 1022

Db   1111 GCGCAGACTTGAGGAGCACTGCCCAGGGTGCCCCTCGGCCAGCCCCAGCCACCC 1170

Qy   1023 CCCGGCTGCCCCGCGCCCCGGGTCTACCGAACCACCAACCCTACAACCCATCACCCAGATC 1082

Db   1171 CCCGGCTGCCCCGCGCCCCGGGTTCTACCGAACCACCCATCATCAACCAGATC 1230

Qy   1083 TCTACCGAACGAGATCCAGAGTGACCAGAACCTGAAGGTGCTGCCACCCCCCCACT 1142

Db   1231 TCTACCAACGAGATCCAGAGTGACCAGAACCTGCCACCCCACCCCCCTGCCCACT 1290

Qy   1143 ATGCCCACTCTCACCAGGCTCCCATCTTCCACCGACAACCCGTCGGGCATGGAGGAGAGAC 1202

Db   1291 ATGCCCACTCTCACCAGCCTCCCATCTTCCACCGACAACCCGTCGGGCATGGAGGAGAGAC 1350

Qy   1203 TGCCTGCCAGGCCCTGGAGGATGGGCCACGACACAGTCTCATCTCACCTGGTTGAAGCCGGGAG 1262

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Qy   271 ACCCCCTGGCCAGCCCTGCCCCCCAGCCTTCTGTGTGGGAGGGCAGAGAGCCAGTG 330

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LOCUS       AY358274                2290 bp    mRNA    linear   PRI 03-OCT-2003
DEFINITION  Homo sapiens clone DNA22779 NL1 (UNQ170) mRNA, complete cds.
ACCESSION   AY358274
VERSION     AY358274.1  GI:37181667
KEYWORDS    FLI_CDNA.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 2290)
  AUTHORS   Clark,H.F., Gurney,A.L., Abaya,E., Baker,K., Baldwin,D., Brush,J.,
            Chen,J., Chow,B., Chui,C., Crowley,C., Currell,B., Deue,B.,
            Dowd,P., Eaton,D., Foster,J., Grimaldi,C., Gu,Q., Hass,P.E.,
            Heldens,S., Huang,A., Kim,H.S., Klimowski,L., Jin,Y., Johnson,S.,
            Lee,J., Lewis,L., Liao,D., Mark,M., Robbie,E., Sanchez,C.,
            Schoenfeld,J., Seshagiri,S., Simmons,L., Singh,J., Smith,V.,
            Stinson,J., Vagts,A., Vandlen,R., Watanabe,C., Wieand,D., Woods,K.,
            Xie,M.H., Yansura,D., Yi,S., Yu,G., Yuan,J., Zhang,M., Zhang,Z.,
            Goddard,A., Wood,W.I. and Godowski,P.
  TITLE     The Secreted Protein Discovery Initiative (SPDI), a Large-Scale
            Effort to Identify Novel Human Secreted and Transmembrane Proteins:
            A Bioinformatics Assessment
  JOURNAL   Genome Res. 13 (10), 2265-2270 (2003)
   PUBMED   12975309
REFERENCE   2  (bases 1 to 2290)
  AUTHORS   Clark,H.F.
  TITLE     Direct Submission
  JOURNAL   Submitted (01-AUG-2003) Department of Bioinformatics, Genentech,
            Inc., 1 DNA Way, South San Francisco, CA 94080, USA
FEATURES             Location/Qualifiers
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ORIGIN
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Query Match             98.1%;  Score 2132.6;  DB 9;  Length 2290;
Best Local Similarity   99.8%;
Matches 2135;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

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Db       1411 AACACCAACCGCCTCATGCAGTGTGGTGGTGGCCAGAGACACGAACCCGGGGGGGCTGGGACC 1470

Qy       1323 GTCATCCAGAGACGCGCTGGATGGGCTCGTGTAACTCTTCTTCAGGAACTGGGAGAGCGTACAAG 1382
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Db       1471 GTCATCCAGAGACGCCTGGATGGGCTCGTGTTAACTTCTTCAGGAACTGGGAGAGCGTACAAG 1530

Qy       1383 CAAGGGTTGGGAACATTGACGGGGATAACTACGGGTCTGGGGCGTGGGCCTGGGAACATTTACGGCTG 1442
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Search completed: August 6, 2004, 16:43:20
Job time : 8388 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 6, 2004, 13:57:38 ; Search time 161 Seconds (without alignments) 7490.114 Million cell updates/sec

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Perfect score: 2173
Sequence: 1 gaaaatgaggctgctgcgga............aaaaaaaaaaaaaaaaaa 2173
Scoring table: IDENTITY_NUC
Gapop 10-0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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9	2132.6	98.1	2290	4	US-09-333-077-1	Sequence 1, Appli
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ALIGNMENTS

RESULT 1
US-08-933-821-1
Sequence 1, Application US/08933821
Patent No. 5972338
GENERAL INFORMATION:
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
TITLE OF INVENTION: Tie Ligands
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
CURRENT APPLICATION NUMBER: US/08/933,821
APPLICATION NUMBER: US/08/933,821
FILING DATE:
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Dreger, Ginger R.
REGISTRATION NUMBER: 33,055
REFERENCE/DOCKET NUMBER: P1130
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-3216
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2290 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
US-08-933-821-1

Query Match 98.1%; Score 2132.6; DB 2; Length 2290;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 2135; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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[sequence alignment continues — Qy/Db paired rows with position numbers, DNA sequence data]

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;  TITLE OF INVENTION:  Tie Ligands
;  NUMBER OF SEQUENCES:  24
;  CORRESPONDENCE ADDRESS:
;  ADDRESSEE:  Genentech, Inc.
;  STREET:  1 DNA Way
;  CITY:  South San Francisco
;  STATE:  California
;  COUNTRY:  USA
;  ZIP:  94080
;  COMPUTER READABLE FORM:
;  MEDIUM TYPE:  3.5 inch, 1.44 Mb floppy disk
;  COMPUTER:  IBM PC compatible
;  OPERATING SYSTEM:  PC-DOS/MS-DOS
;  SOFTWARE:  WinPatin (Genentech)
;  CURRENT APPLICATION DATA:
;  APPLICATION NUMBER:  US/08/960,507
;  FILING DATE:
;  CLASSIFICATION:  536
;  ATTORNEY/AGENT INFORMATION:
;  NAME:  Dreger, Ginger R.
;  REGISTRATION NUMBER:  33,055
;  REFERENCE/DOCKET NUMBER:  P1130p1
;  TELECOMMUNICATION INFORMATION:
;  TELEPHONE:  650/225-3216
;  TELEFAX:  650/952-9881
;  INFORMATION FOR SEQ ID NO:  1:
;  SEQUENCE CHARACTERISTICS:
;  LENGTH:  2290 base pairs
;  TYPE:  Nucleic Acid
;  STRANDEDNESS:  Single
;  TOPOLOGY:  Linear
US-08-960-507-1

Query Match    98.1%;  Score 2132.6;  DB 3;  Length 2290;
Best Local Similarity   99.8%;  Pred. No. 0;
Matches 2135;  Conservative   0;  Mismatches   4;  Indels   0;  Gaps   0;
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Qy   1203 TGCCTGCAGGCCCTGGAGGAGGGCCACGACACCAGTGTCACTTCTTGGTAAAGCGGGAG  1262
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1351 TGCCTGCAGGCCCTGGAGGAGGGCCACGACACCAGTGTCACTTCTTGGTAAAGCGGGAG  1410

Qy   1263 AACACAACCGCCATCATGCAGTGTGGTGCGACGACAGAGACACGACCCCGGGGGGGCCTGGACC  1322
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1411 AACACAACCGCCCTCATGCAGTGTGGTGCGACCAGAGACACGACCCCGGGGGGGCCTGGACC  1470

Qy   1323 GTCATCCAGAGACGCCTGGATGGCTCTGTTAACTTTCTTCAGGAACTGGGAGACGTACAAG  1382
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1471 GTCATCAGAGAGCGCCTGGATGGCTCTGTTAACTTTCTTCAGGAACTGGGAGACGTACAAG  1530

Qy   1383 CAAGGGGTTTGGGAAACATTGACGGGCGAATACTTGGCTGGGCCTGGAGGAACATTTACTGGCTG  1442
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1531 CAAGGGGTTTGGGAAACATTGACGGGCGAATACTTGGCTGGGCCTGGAGGAACATTTACTGGCTG  1590

Qy   1443 ACGAAACCAAGGCAAACTACAACTCCTGGTGACCATGGAGGACTGGTCGCGGGCCAAAGTC  1502
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1591 ACGAAACCAAGGCAAACTACAACTCCTGGTGACCATGGAGGACTGGTTCGCGGGCCAAAGTC  1650

Qy   1503 TTTGCAGAATACGCCAGTTTCCGCGTTGAGGAGCGACGAGTTATATAAGCTGCGGGGCTG  1562
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1651 TTTGCAGAATACGCCAGTTTCCGCGTTGAGGAGCGAGTTATATAAGCTGCGGGGCTG  1710

Qy   1563 GGGCGCTTACCATGGGCAAATGCGGGTGACTCCTTTACATGGCACAACGGCACAAGCCAGTTCACC  1622
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1711 GGGCGCTTACCATGGGCAAATGCGGGTGACTCCTTTACATGGCACAACGGCACAAGCCAGTTCACC  1770

Qy   1623 ACCCTGGACAGGAGGATCATGATGTCTACACAGGAAACTGTGCCCACTACCAGAGAGGGAGGGC  1682
```

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Db         1771 ACCCTGGACAGAGATCATGATGTCTACACAGGAAACTGTGCCCACTACCAGAAGGGAGGC 1830

Qy         1683 TGGTGGTATAACGCCTGTGCCCACTCCAACCTCAACGGGGTCTGGTACCGCGGGGGCCAT 1742
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1831 TGGTGGTATAACGCCTGTGCCCACTCCAACCTCAACGGGGTCTGGTACCGCGGGGGCCAT 1890

Qy         1743 TACCGGAGCCGCTACCAGGACGGAGTCTACTGGGCTGAGTTCCGAGGAGGCTCTTACTCA 1802
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1891 TACCGGAGCCGCTACCAGGACGGAGTCTACTGGGCTGAGTTCCGAGGAGGCTCTTACTCA 1950

Qy         1803 CTCAAGAAAGTGGTGATGATGATCCGACCGAACCCCAACACCTTCCACTAAGCCAGCTCC 1862
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1951 CTCAAGAAAGTGGTGATGATGATCCGACCGAACCCCAACACCTTCCACTAAGCCAGCTCC 2010

Qy         1863 CCCTCCTGACCTCTCGTGGCCATTGCCAGGAGCCCACCCTGGTCACGCTGGCCACAGCAC 1922
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         2011 CCCTCCTGACCTCTCGTGGCCATTGCCAGGAGCCCACCCTGGTCACGCTGGCCACAGCAC 2070

Qy         1923 AAAGAACAACTCCTCACCAGTTCATCCTGAGGCTGGGAGGACCGGGATGCTGGATTCTGT 1982
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         2071 AAAGAACAACTCCTCACCAGTTCATCCTGAGGCTGGGAGGACCGGGATGCTGGATTCTGT 2130

Qy         1983 TTTCCGAAGTCACTGCAGCGGATGATGGAACTGAATCGATACGGTGTTTTCTGTCCCTCC 2042
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Db         2131 TTTCCGAAGTCACTGCAGCGGATGATGGAACTGAATCGATACGGTGTTTTCTGTCCCTCC 2190

Qy         2043 TACTTTCCTTCACACCAGACAGCCCCTCATGTCTCCAGGACAGGACAGGACTACAGACAA 2102
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Db         2191 TACTTTCCTTCACACCAGACAGCCCCTCATGTCTCCAGGACAGGACAGGACTACAGACAA 2250

Qy         2103 CTCTTTCTTTAAATAAATTAAGTCTCTACAATAAAAACA 2141
                ||||||||||||||||||||||||||||||||||||| |
Db         2251 CTCTTTCTTTAAATAAATTAAGTCTCTACAATAAAAAAA 2289

RESULT 3
US-09-136-828-1
; Sequence 1, Application US/09136828
; Patent No. 6350450
;  GENERAL INFORMATION:
;    APPLICANT:  Godowski, Paul J.
;    APPLICANT:  Gurney, Austin L.
;    TITLE OF INVENTION:  Tie Ligands
;    NUMBER OF SEQUENCES:  17
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genentech, Inc.
;      STREET:  1 DNA Way
;      CITY:  South San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94080
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 inch, 1.44 Mb floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WinPatin (Genentech)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/136,828
;      FILING DATE:
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Dreger, Ginger R.
;      REGISTRATION NUMBER:  33,055
;      REFERENCE/DOCKET NUMBER:  P1130R1A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  650/225-3216
;      TELEFAX:  650/952-9881
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2290 base pairs
;      TYPE:  Nucleic Acid
;      STRANDEDNESS:  Single
;      TOPOLOGY:  Linear
US-09-136-828-1

  Query Match             98.1%;  Score 2132.6;  DB 4;  Length 2290;
  Best Local Similarity   99.8%;  Pred. No. 0;
  Matches 2135;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy            3 AAATGAGGCTGCTGCGGACGGCCTGAGGATGAACCCCAAGCCCTGGACCTGCCGAGCGTG 62
                ||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db          151 AAATGAGGCTGCTGCGGACGGCCTGAGGATGGACCCCAAGCCCTGGACCTGCCGAGCGTG 210

Qy           63 GCACTGAGGCAGCGGCTGACGCTACTGTGAGGGAAAGAAGGTTGTGAGCAGCCCCGCAGG 122
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          211 GCACTGAGGCAGCGGCTGACGCTACTGTGAGGGAAAGAAGGTTGTGAGCAGCCCCGCAGG 270

Qy          123 ACCCCTGGCCAGCCCTGGCCCCAGCCTCTGCCGGAGCCCTCTGTGGAGGCAGAGCCAGTG 182
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          271 ACCCCTGGCCAGCCCTGGCCCCAGCCTCTGCCGGAGCCCTCTGTGGAGGCAGAGCCAGTG 330

Qy          183 GAGCCCAGTGAGGCAGGGCTGCTTGGCAGCCACCGGCCTGCAACTCAGGAACCCCTCCAG 242
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Db          331 GAGCCCAGTGAGGCAGGGCTGCTTGGCAGCCACCGGCCTGCAACTCAGGAACCCCTCCAG 390

Qy          243 AGGCCATGGACAGGCTGCCCCGCTGACGGCCAGGGTGAAGCATGTGAGGAGCCGCCCCGG 302
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          391 AGGCCATGGACAGGCTGCCCCGCTGACGGCCAGGGTGAAGCATGTGAGGAGCCGCCCCGG 450

Qy          303 AGCCAAGCAGGAGGGAAGAGGCTTTCATAGATTCTATTCACAAAGAATAACCACCATTTT 362
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          451 AGCCAAGCAGGAGGGAAGAGGCTTTCATAGATTCTATTCACAAAGAATAACCACCATTTT 510

Qy          363 GCAAAGACCATGAGGCCACTGTGCGTGACATGCTGGTGGCTCGGACTGCTGGCTGCCATG 422
                |||| |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          511 GCAAGGACCATGAGGCCACTGTGCGTGACATGCTGGTGGCTCGGACTGCTGGCTGCCATG 570

Qy          423 GGAGCTGTTGCAGGCCAGGAGGACGGTTTTGAGGGCACTGAGGAGGGCTCGCCAAGAGAG 482
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Db          571 GGAGCTGTTGCAGGCCAGGAGGACGGTTTTGAGGGCACTGAGGAGGGCTCGCCAAGAGAG 630

Qy          483 TTCATTTACCTAAACAGGTACAAGCGGGCGGGCGAGTCCCAGGACAAGTGCACCTACACC 542
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          631 TTCATTTACCTAAACAGGTACAAGCGGGCGGGCGAGTCCCAGGACAAGTGCACCTACACC 690

Qy          543 TTCATTGTGCCCCAGCAGCGGGTCACGGGTGCCATCTGCGTCAACTCCAAGGAGCCTGAG 602
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          691 TTCATTGTGCCCCAGCAGCGGGTCACGGGTGCCATCTGCGTCAACTCCAAGGAGCCTGAG 750

Qy          603 GTGCTTCTGGAGAACCGAGTGCATAAGCAGGAGCTAGAGCTGCTCAACAATGAGCTGCTC 662
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          751 GTGCTTCTGGAGAACCGAGTGCATAAGCAGGAGCTAGAGCTGCTCAACAATGAGCTGCTC 810

Qy          663 AAGCAGAAGCGGCAGATCGAGACGCTGCAGCAGCTGGTGAAGGTGGACGGCGGCATTGTG 722
                ||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db          811 AAGCAGAAGCGGCAGATCGAGACGCTGCAGCAGCTGGTGGAGGTGGACGGCGGCATTGTG 870

Qy          723 AGCGAGGTGAAGCTGCTGCGCAAGGAGAGCCGCAACATGAACTCGCGGGTCACGCAGCTC 782
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          871 AGCGAGGTGAAGCTGCTGCGCAAGGAGAGCCGCAACATGAACTCGCGGGTCACGCAGCTC 930

Qy          783 TACATGCAGCTCCTGCACGAGATCATCCGCAAGCGGGACAACGCGTTGGAGCTCTCCCAG 842
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          931 TACATGCAGCTCCTGCACGAGATCATCCGCAAGCGGGACAACGCGTTGGAGCTCTCCCAG 990

Qy          843 CTGGAGAACAGGATCCTGAACCAGACAGCCGACATGCTGCAGCTGGCCAGCAAGTACAAG 902
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          991 CTGGAGAACAGGATCCTGAACCAGACAGCCGACATGCTGCAGCTGGCCAGCAAGTACAAG 1050

Qy          903 GACCTGGAGCACAAGTACCAGCACCTGGCCACACTGGCCCACAACCAATCAGAGATCATC 962
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1051 GACCTGGAGCACAAGTACCAGCACCTGGCCACACTGGCCCACAACCAATCAGAGATCATC 1110

Qy          963 GCGCAGCTTGAGGAGCACTGCCAGAGGGTGCCCTCGGCCAGGCCCGTCCCCCAGCCACCC 1022
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RESULT 4
US-09-332-928A-1

; Sequence 1, Application US/09332928A
; Patent No. 6368853
; GENERAL INFORMATION:
; APPLICANT:
; Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; TITLE OF INVENTION: Tie Ligands
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/332,928A
; FILING DATE: 14-Jun-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/933,821
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Ginger R.
; REGISTRATION NUMBER: 33,055
; REFERENCE/DOCKET NUMBER: P1130
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-3216
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2290 base pairs
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-332-928A-1

Query Match 98.1%; Score 2132.6; DB 4; Length 2290;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 2135; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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Qy    3 AAATGAGGCTGCTGCGGACGGCCTGAGGATGAACCCAGCCTGGACCTGCCGAGCGTG   62
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Db  151 AAATGAGGCTGCTGCGGACGGCCTGAGGATGAACCCAGCCTGGACCTGCCGAGCGTG  210

Qy   63 GCACTGAGGCAGCGGCGCTGACCCTACTGTGAGGGAAAGAAGGTTGTTGCAGCCCCGCAGG  122
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Db  211 GCACTGAGGCAGCGGCGCTGACCCTACTGTGAGGGAAAGAAGGTTGTTGCAGCCCCGCAGG  270

Qy  123 ACCCCTGGCCAGCCTCGGCCCCCAGCCCTCTCCCGGAGCCCTTCTGTGGGAGGGCCAGTG  182
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Db  271 ACCCCTGGCCAGCCTCGGCCCCCAGCCCTCTGCCGGAGCCCTTCTGTGGGAGGGCCAGTG  330

Qy  183 GAGCCCCAGTGAGGCAGGCGTGCTTGGCCAGCCACCACCCAACTTCAGGAGAACCCCTTCCAG  242
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  331 GAGCCCCAGTGAGGCAGGCGTGCTTGGCCAGCCACCACCCAACTTCAGGAGAACCCCTTCCAG  390

Qy  243 AGGCCATGGACAGGCGCCCGCCCGAGCCAGGGTGAAGCCATGTGAGGAGGCCAGG  302
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  391 AGGCCATGGACAGGCTGCCCCGCTCACGGCCAGGGTGAAGCCATGTGAGGAGGCCGCCGG  450
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Qy 2103 CTCTTCTTTAAATAAAATTAAGTCTCTACAATAAAAAACA 2141
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Db 2251 CTCTTCTTTAAATAAAATTAAGTCTCTACAATAAAAAACA 2289
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Db 1171 CCCGGCTGCCCCCCCGGGTCTACCAACCACCACCACCGGCAATCATCAAACCAGATC 1230
Qy 1083 TCTACCAAGCAGAGATCAGAGTGACAGAACCTGAAGGTGCTGCCCACCCCCTCTGCCCACT 1142
Db 1231 TCTACCAAGCAGAGATCAGAGTGACAGAACCTGAAGGTGCTGCCCACCCCCTCTGCCCACT 1290
Qy 1143 ATGCCCACTCTCACCAGCCTCCCATCTTCCACGACGCAGAGCCCCATGGAGAGAC 1202
Db 1291 ATGCCCACTCTCACCAGCCTCCCATCTTCCACGACGCAGAGCCCCATGGAGAGAC 1350
Qy 1203 TGCCTGCAGGCCCCTGGAGGATGGCCACGACACCAGCTCCCATCTACCTGGTGAAGCCCGAG 1262
Db 1351 TGCCTGCAGGCCCCTGGAGGATGGCCACGACACCAGCTCCCATCTACCTGGTGAAGCCCGAG 1410
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Qy 1323 GTCATCCAGAGACGCCTGGGATGGCTCTGTTAACTTCTTCAGGAACTGGGAGACGTACAAG 1382
Db 1471 GTCATCCAGAGACGCCTGGGATGGCTCTGTTAACTTCTTCAGGAACTGGGAGACGTACAAG 1530
Qy 1383 CAAGGGTTTGGGAACATTGACGGGAATACTGGCTGGGCCCTGAGAGAACATTACTGGCTG 1442
Db 1531 CAAGGGTTTGGGAACATTGACGGGAATACTGGCTGGGCCCTGAGAGAACATTACTGGCTG 1590
Qy 1443 ACGAACCAGGCAAACTACAAACTCCTGGTGACCATGGGAGACTGGTGTTCCGGGCGCAAAGTC 1502
Db 1591 ACGAACCAGGCAAACTACAAACTCCTGGTGACCATGGGAGACTGGTGTTCCGGGCGCAAAGTC 1650
Qy 1503 TTTGCAGAATACGGCCAGTTTCCGCCTTGAGCGGTATTATATAAGCTGCGGCTG 1562
Db 1651 TTTGCAGAATACGGCCAGTTTCCGCCTTGAGCGGTATTATATAAGCTGCGGCTG 1710
Qy 1563 GGGCGCTACCATGGCAATGCGGGTGACTCCTTTACATGGCACAAACGGCAAGCAGTTCACC 1622
Db 1711 GGGCGCTACCATGGCAATGCGGGTGACTCCTTTACATGGCACAAACGGCAAGCAGTTCACC 1770
Qy 1623 ACCCTGGACAGAGATCAATGAGTCTACACAGGAAACTGTGCCCACTACCACGAAAGGGAGGC 1682
Db 1771 ACCCTGGACAGAGATCAATGAGTCTACACAGGAAACTGTGCCCACTACCACGAAAGGGAGGC 1830
Qy 1683 TGGTGGTATACGCCTGCCCACTCAACCTCACACGGGGTTGGTTACCGCGGGGGGCCAT 1742
Db 1831 TGGTGGTATACGCCTGCCCACTCAACCTCAACGGGGTTGGTTACCGCGGGGGGCCAT 1890
Qy 1743 TACCGGAGCCCTACCAGGAGAGTCTACTGGGCTTCGGAGTTCCGGAGGCTCTTACTCA 1802
Db 1891 TACCGGAGCCCTACCAGGAGAGTCTACTGGGCTTCGGAGTTCCGGAGGCTCTTACTCA 1950
Qy 1803 CTCAAGAAAGTGGTGATGATGCCGACCCAACACCTTCCACTAAGCCAGCTCC 1862
Db 1951 CTCAAGAAAGTGGTGATGATGCCGACCCAACACCTTCCACTAAGCCAGCTCC 2010
Qy 1863 CCCTCCTGACCTCTGGCCATTGCCAGGAGCCCACAGCAC 1922
Db 2011 CCCTCCTGACCTCTGGCCATTGCCAGGAGCCCACAGCAC 2070
Qy 1923 AAAGAACAAACTCCTCACCAGTTCATCTGAGGCTGGGAGAACCGGGATTCTGT 1982
Db 2071 AAAGAACAAACTCCTCACCAGTTCATCTGAGGCTGGGAGAACCGGGATTCTGT 2130
Qy 1983 TTTCCGGAAGTCACTGACGGACTGAATCGATACGGTGTTTTCTGTGCCCTCC 2042
Db 2131 TTTCCGGAAGTCACTGACGGACTGAATCGATACGGTGTTTTCTGTGCCCTCC 2190
Qy 2043 TACTTTCCTTCACACAGACGACCCCTCATGTCTCCAGGACAGGACTACAGACAA 2102
Db 2191 TACTTTCCTTCACACAGACGACCCCTCATGTCTCCAGGACAGGACTACAGACAA 2250
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Qy    303  AGCCAAGCAGCAGGAGGGAAGAGAGAGGCTTCATGATTCTATTCACAAAGAATAACCACCATTTT 362
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Db   1531  AGCCAAGCAGGAGGGAAGAGAGGCTTCATGATTCTATTCACAAAGAATAACCACCATTTT 1590

Qy   1383  CAAGGGTTTGGGAACATTGACGGCGGACCGGAATACTGGGCTGGGAGGGGCCTGGAGAGAACATTTACTGGGCTG 1442
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1531  CAAGGGTTTGGGAACATTGACGGCGGAATACTGGGCTGGGGCCTGGGCCGGAAAAGTC 1590
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;   STATE: California
;   COUNTRY: USA
;   ZIP: 94080
COMPUTER READABLE FORM:
;   MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/09/136,801
;   FILING DATE:
;   CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
;   NAME: Dreger, Ginger R.
;   REGISTRATION NUMBER: 33,055
;   REFERENCE/DOCKET NUMBER: P1130P2
TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 650/225-3216
;   TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
;   LENGTH: 2290 base pairs
;   TYPE: Nucleic Acid
;   STRANDEDNESS: Single
;   TOPOLOGY: Linear
US-09-136-801-1
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Query Match          98.1%;  Score 2132.6;  DB 4;  Length 2290;
Best Local Similarity 99.8%;  Pred. No. 0;  Mismatches 4;  Indels 0;  Gaps 0;
Matches 2135;  Conservative 0;  Mismatches 4;  Indels 0;  Gaps 0;
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(Nucleotide alignment block — Query (Qy) vs Database (Db), positions 3–1890)

RESULT 6
US-09-332-929-1
Sequence 1, Application US/09332929
Patent No. 6420542
GENERAL INFORMATION:
  APPLICANT: Godowski, Paul J.
  APPLICANT: Gurney, Austin L.
  TITLE OF INVENTION: Tie Ligands
  NUMBER OF SEQUENCES: 17
  CORRESPONDENCE ADDRESS:
  ADDRESSEE: Genentech, Inc.
  STREET: 1 DNA Way
  CITY: South San Francisco
  STATE: California
  COUNTRY: USA
  ZIP: 94080
  COMPUTER READABLE FORM:
  MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
  COMPUTER: IBM PC compatible
  OPERATING SYSTEM: PC-DOS/MS-DOS
  SOFTWARE: WinPatin (Genentech)
  CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/09/332,929
  FILING DATE:
  CLASSIFICATION:
  PRIOR APPLICATION DATA:
  APPLICATION NUMBER: 08/933,821
  FILING DATE:
  ATTORNEY/AGENT INFORMATION:
  NAME: Dreger, Ginger R.
  REGISTRATION NUMBER: 33,055
  REFERENCE/DOCKET NUMBER: P1130
  TELECOMMUNICATION INFORMATION:
  TELEPHONE: 650/225-3216
  TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 1:
  SEQUENCE CHARACTERISTICS:
  LENGTH: 2290 base pairs
  TYPE: Nucleic Acid
  STRANDEDNESS: Single
  TOPOLOGY: Linear
US-09-332-929-1

Query Match   98.1%;   Score 2132.6;   DB 4;   Length 2290;
Best Local Similarity   99.8%;   Pred. No. 0;
Matches 2135;   Conservative   0;   Mismatches   4;   Indels   0;   Gaps   0;

(The remainder of the page consists of a dense nucleic-acid sequence alignment between Query (Qy) and Database (Db) strands, with flanking coordinate numbers. Representative coordinate-paired alignment lines are reproduced below.)

Qy   3 AAATGAGGCTTGCTTGCGGAGCAGGACCGGTTCGCGGACCGGACCCCAAGCCCTGGACCTGCCGAGCGTG 62
Db   1 AAATGAGGCTGGCTGCGGACCGGACCCCAAGCCCTGGACCTGCCGAGCGTG 62
Qy   63 GCACTGAGGCAGCGGCGGCCTGAGCCTACTGTGAGGGAAAGAAGGTTGTGAGCAGCCCCGCAGG 122
Db   151 ... 210
Qy   123 ... 182
Db   211 ... 270
Qy   183 GAGCCCAGTGAGGCAGGGCTGCTTGGCGTGGCGGCCACCCGGCCTGCAACTCAGCACCCTCCAG 242
Qy   243 AGGGCCATGGACAGGCGTGCCCGGCCCGGGTGAGCAGTGCCACCTACACC 302
Qy   303 AGCCAGCACAGGAGGGAAGAGGCCTTTCAATAGATTCTTATTCACAAAGAAATAACCACCATTTT 362
Qy   423 GGAGCTCGTTGCAGGCACGGAGGACCGGTTTGAGGGCCACTGAGGAGCTGCCAAGGAG 482
Qy   543 TTCATTGTGCCCCAGCAGGGGTGCCCATCTGCCCTCAACTCCAGGAGCCTGAG 602
Qy   663 AAGCAGAAAGCGGCACGATCGAGCGTGCAGCAGCTGGGTGAAGGTGGACGGCGCCATTGTG 722
Qy   783 TACATGCAGCTTCTGCGACGAGGATCATCCGACGAGCGGGACAACGCGGTTGGAGCTCTCCAG 842
Qy   903 GACCTGGAGCACAAGTACCAGGACCCTGGCCACACTGGCCAGCCAAACCAATCAGAGATCATC 962
Qy   1023 CCCGGCTGCCCCCGGGGTTACCAACCACCACTACAACGGCATCATCAACCAGATC 1082

Db   1891 TACGGGAGCCGCGTTACCAGGACGGAGTCTACTGGGCTGAGTTCCGAGGAGGAGGGCTCTTACTCA 1950
Qy   1743 TACGGGACCGCTACCAGGACGGACGGAGTCACTGGGCTGAGTTCCGAGGAGGAGGGCTCTTACTCA 1802
Db   1951 CTCAAGAAAGTGGTGATGATCGATCCGACCACCGAACCACCACTTTCACTAAGCCACGCTCC 2010
Qy   1803 CTCAAGAAAGTCGTGATGATCGATCCGACCACCGAACCACCACCTTTCACTAAGCCACGCTCC 1862
Db   2251 CTCTTCTTTAAATAAAATTAAGTCTCTACAATAAAAAAA 2289
Qy   2103 CTCTTCTTTAAATAAAATTAAGTCTCTACAATAAAAAAACA 2141

Db   2251 CTCTTTCTTTAAATAAATTAAGTCTCACAATAAAAAAA 2289

RESULT 7
US-09-333-075-1
; Sequence 1, Application US/09333075
; Patent No. 6492331
; GENERAL INFORMATION:
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; TITLE OF INVENTION: Tie Ligands
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Genentech, Inc.
;   STREET: 1 DNA Way
;   CITY: South San Francisco
;   STATE: California
;   COUNTRY: USA
;   ZIP: 94080
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: WinPatin (Genentech)
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/09/333,075
;   FILING DATE:
;   CLASSIFICATION:
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 08/933,821
;   FILING DATE:
; ATTORNEY/AGENT INFORMATION:
;   NAME: Dreger, Ginger R.
;   REGISTRATION NUMBER: 33,055
;   REFERENCE/DOCKET NUMBER: P1130
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 650/225-3216
;   TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 2290 base pairs
;   TYPE: Nucleic Acid
;   STRANDEDNESS: Single
;   TOPOLOGY: Linear
US-09-333-075-1

Query Match   98.1%; Score 2132.6; DB 4; Length 2290;
Best Local Similarity   99.8%; Pred. No. 0;
Matches 2135; Conservative   0; Mismatches   4; Indels   0; Gaps   0;

Qy   3 AAATGAGGCTGCTGCCGGCACGGCCCTGAGGATGAACCCCAAGCCCTGACCTGCCGAGCGTG 62
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   151 AAATGAGGCTGCTGCCGGCACGGCCCTGAGGATGAACCCCAAGCCCTGACCTGCCGAGCGTG 210

Qy   63 GCACTGAGGCACGGGCTTGACGCTACTGTGAGGAAAGAAGGTTTGTGAGCGACCCCCGCAGG 122
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   211 GCACTGAGGCACGGGCTTGACGCTACTGTGAGGAAAGAAGGTTTGTGAGCGACCCCCGCAGG 270

Qy   123 ACCCCTGGCCAGCCCCTGGGCCCCAGCCTCTGCGGGAGCCCCTTGTGTGGAGGACAGAGCAGTG 182
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   271 ACCCCTGGCCAGCCCCTGGGCCCCAGCCTCTGCGGGAGCCCCTTGTGTGGAGGACAGAGCAGTG 330

Qy   183 GAGCCCCAGTGAGGCAGGGCTGCTTGGCCAGCCCACCGGCCTGCGAACTCAGGAACCCCTTCCAG 242
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   331 GAGCCCCAGTGAGGCAGGGCTGCTTGGCCAGCCCACCGGCCTGCGAACTCAGGAACCCCTTCCAG 390

Qy   243 AGGCCCATGGACAGGGCTGCCCCGCGCTGACGGCCAGGGTGAAGCCATGTGAGGAGGCCCCCGG 302
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   391 AGGCCCATGGACAGGGCTGCCCCGCGCTGACGGCCAGGGTGAAGCCATGTGAGGAGGCCCCCGG 450

Qy   303 AGCCAGCAGAGAGGGGAGGAGAGAGGGCTTTCATAGAGTTCTATTCACAAAGAATAAGGCCCG 362
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   451 AGCCAGCAGAGAGGGGAGGAGAGAGGGCTTTCATAGAGTTCTATTCACAAAGAATAACCACAATTTT 510

The page contains DNA sequence alignment data presented in Query (Qy) and Database (Db) paired rows with position numbers. The alignment spans positions 363 through 2289.

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; ORGANISM: Homo Sapiens
US-09-202-088A-1

Query Match        98.1%;  Score 2132.6;  DB 4;  Length 2290;
Best Local Similarity   99.8%;  Pred. No. 0;  Mismatches 0;
Matches 2135;  Conservative  0;  Mismatches  4;  Indels  0;  Gaps  0;
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Qy  2103 CTCTTTCTTTAAATAAATTAAGTCTCTTACACAATTAAAAAACA 2141
         |||||||||||||||||||||||||||||||||||||||||||
Db  2251 CTCTTTCTTTAAATAAATTAAGTCTCTTACACAATTAAAAAAAA 2289
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RESULT 9
US-09-333-077-1
Sequence 1, Application US/09333077
Patent No. 6586397
GENERAL INFORMATION:
  APPLICANT: Godowski, Paul J.
  APPLICANT: Gurney, Austin L.
  TITLE OF INVENTION: Tie Ligands
  NUMBER OF SEQUENCES: 17
  CORRESPONDENCE ADDRESS:
    ADDRESSEE: Genentech, Inc.
    STREET: 1 DNA Way
    CITY: South San Francisco
    STATE: California
    COUNTRY: USA
    ZIP: 94080
  COMPUTER READABLE FORM:
    MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
    COMPUTER: IBM PC compatible
    OPERATING SYSTEM: PC-DOS/MS-DOS
    SOFTWARE: WinPatin (Genentech)
  CURRENT APPLICATION DATA:
    APPLICATION NUMBER: US/09/333,077
    FILING DATE:
    CLASSIFICATION:
  PRIOR APPLICATION DATA:
    APPLICATION NUMBER: 08/933,821
    FILING DATE:
  ATTORNEY/AGENT INFORMATION:
    NAME: Dreger, Ginger R.
    REGISTRATION NUMBER: 33,055
    REFERENCE/DOCKET NUMBER: P1130
  TELECOMMUNICATION INFORMATION:
    TELEPHONE: 650/225-3216
    TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 1:
  SEQUENCE CHARACTERISTICS:
    LENGTH: 2290 base pairs
    TYPE: Nucleic Acid
    STRANDEDNESS: Single
    TOPOLOGY: Linear

US-09-333-077-1

Query Match   98.1%; Score 2132.6; DB 4; Length 2290;
Best Local Similarity 99.8%; Pred. No. 0; Mismatches 4; Indels 0; Gaps 0;
Matches 2135; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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Qy     3 AAATGAGGCGTGCTGCCGGACGGACGGCTGAGGATGAACCCCAAGCCCTGGACCTGCCGAGCGGTG 62
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   151 AAATGAGGCGTGCTGCCGGACGGACGGCTGAGGATGAACCCCAAGCCCTGGACCTGCCGAGCGGTG 210

Qy    63 GCACTGAGGCAGCGGCGGCTGACGCTACTGTGAGGGAAAGAAGGTTGTGAGCGAGCCGGCGCCGAGG 122
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   211 GCACTGAGGCAGCGGCGGCTACGCTACTGTGAGGGAAAGAAGGTTGTGAGCAGCCCCGGCGCAGG 270

Qy   123 ACCCCTGGCCAGCCCCCAGCCCTGCCGGAGCGCCCTCGTGGAGGCAGAGCCAGTG 182
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   271 ACCCCTGGCCAGCCCCCAGCCCTCTGCCACTCGTGGAGGCAGAGCCAGTG 330

Qy   183 GAGCCCAGTGAGGCAGGCGCTGCTTGCAGCTGAGGAGGAACCCCTCCAG 242
         |||||||||||||||||||||||||||||||||||||||||||||||||
Db   331 GAGCCCAGTGAGGCAGGCGCTGCTTGCAGCTGAGGAGGAACCCCTCCAG 390

Qy   243 AGGCCATGGACACAGCCTGCCCCGCTGACCGGCCAGGTGAAGCAGTGAGAGCCGCCCCGG 302
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   391 AGGCCATGGACACAGCCTGCCCCGCTGACCGGCCAGGTGAAGCAGTGAGAGCCGCCCCGG 450
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Qy   303 AGCCAAGCAGGAGGAGGAAGAGAGAGCCTTTCATAGAGATTCTATTCACAAAGAATAACCACCATTTT 362
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   451 AGCCAAGCAGGAGGAGGAAGAGAGAGCCTTTCATAGAGATTCTATTCACAAAGAATAACCACCATTTT 510

Qy   363 GCAAAGAACCATGAGCCCACTGTGCGTGCCGGGAGTGCCCGGACTGCTTGGCGTGCCCATG 422
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   511 GCAAGGACCATGAGCCCACTGTGCGTGCCGGGAGTGCCCGGACTGCTTGGCGTGCCCATG 570

Qy   423 GGAGCTGTTGCAGGCGCCAGGAGGACCGGTTTGAGGGCCACTGGCCGAGAGGAG 482
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   571 GGAGCTGTTGCAGGCGCCAGGAGGACCGGTTTGAGGGCCACTGGCCGAGAGGAG 630

Qy   483 TTCATTTACCTTAAACAGGTTACAAGCGCGGGGGGCGGTCCCAGGAGTGCCACCTACACC 542
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   631 TTCATTTACCTTAAACAGGTTACAAGCGCGGGGGGCGGTCCCAGGAGTGCCACCTACACC 690

Qy   543 TTCATTGTGCCCCAGCAGCGGGTCAGGGGTGCCATCTGCGGTCAACTCCAAGGAGGCCTGAG 602
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   691 TTCATTGTGCCCCAGCAGCGGGTCAGGGGTGCCATCTGCGGTCAACTCCAAGGAGGCCTGAG 750

Qy   603 GTGCTTCTGGAGAACCGAGTGCATAAGCAGGAGCTAGAGTGCTCAAACAATGAGCTGCTC 662
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   751 GTGCTTCTGGAGAACCGAGTGCATAAGCAGGAGCTAGAGTGCTCAAACAATGAGCTGCTC 810

Qy   663 AAGCACAAGCGGGCAGATCGACGCGCTGCACCAGCGTGTGAAGGTTGGACGGCCATTGTG 722
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   811 AAGCACAAGCGGGCAGATCGACGCGCTGCACCAGCGTGTGAAGGTTGGACGGCCATTGTG 870

Qy   723 AGCGAGGTGAAGCTGCTGCGCCAAGGAGACGCGCAACAATGAAACTCGGCCAGTCACCCAGCTC 782
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   871 AGCGAGGTGAAGCTGCTGCGCCAAGGAGACGCGCAACAATGAAACTCGGCCAGTCACCCAGCTC 930

Qy   783 TACATTCCAGCTCCTGACGAGATCATCCGCAAGGGGGAACAAGCTCTCCCAG 842
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   931 TACATTCCAGCTCCTGACGAGATCATCCGCAAGGGGGAACAAGCTCTCCCAG 990

Qy   843 CTGGAGAACAGGATCCTTGAACCAGACCAGCCGACATGGCCAGCAGCAAGTACAAG 902
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   991 CTGGAGAACAGGATCCTTGAACCAGACCAGCCGACATGGCCAGCAGCAAGTACAAG 1050

Qy   903 GACCTGGAGCACAGTTACCAGCACCTTGGCCGCCACACCAAATCAGAGAATCATC 962
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1051 GACCTGGAGCACAGTTACCAGCACCTTGGCCGCCACACCAAATCAGAGAATCATC 1110

Qy   963 GCGCAGCTTGAGGAGGAACTGCCCAGAGGTCCCCTGCAGGGTCCCCCAGCCACCC 1022
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1111 GCGCAGCTTGAGGAGGAACTGCCCAGAGGGTCCCCTGCAGGGTCCCCCAGCCACCC 1170

Qy  1023 CCGGCTGCCCCGCCCCGGGGGTCTACCACCACCACTACTCAAACCCACCGATCATCAACCAGATC 1082
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1171 CCGGCTGCCCCGCCCCGGGGGTTACCGCACCAACCACCACTCAACCCGATCATCAACCAGATC 1230

Qy  1083 TCTACCAAACGAGATCCAGAGTGACCAGAACCTGAAGGTTGCTCAACCCCTCTGCCCACT 1142
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1231 TCTACCAAACGAGATCCAGAGTGACCAGAACCTGAAGGTTGCTCAACCCCTCTGCCCACT 1290

Qy  1143 ATGCCCACTCTCACCAGCCTCCACTTTCCACACGGAAGCGCGTCGCCGGTCGGGCGGAGAC 1202
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1291 ATGCCCACTCTCACCAGCCTCCACTTTCCACACGGAAGCGCGTCGCCGGTCGGGCGGAGAC 1350

Qy  1203 TGCCTGGACAGCCCCTGGAGGATGGCCACGACGACACGGAGTCATCTCATCTACCTGGTGAAGCCGGAG 1262
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1351 TGCCTGCAGGCCCTGGAGGATGGCCACGACACGGAGTCCATCTCATCTACCTGGTGAAGCGGGAG 1410

Qy  1263 AACACCAAACCCGCCTCATGCAGGTGTGGTGGCCACGACGACCAGTGGCTTGGACC 1322
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1411 AACACCAAACCCGCCTCATGCAGGTGTGGTGGCCACGACGACCAGTGGCTTGGACC 1470

Qy  1323 GTCATCCAGAGACGCGCTGGAGTGGCTCTGTTGTTAACTTCTTCAGGAACTGGGAGACGTACAAG 1382
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1471 GTCATCCAGAGACGCGCTGGATGGCTCTGTTGTTAACTTCTTCAGGAACTGGGAGACGTACAAG 1530

Qy  1383 CAAGGGTTTGGGAACAATTGACGGCGAATACTGGGCTGGAGAACAATTACTGGCTG 1442
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1531 CAAGGGTTTGGGAACAATTGACGGCGAATACTGGGCTGGAGAACAATTACTGGCTG 1590
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RESULT 10
US-08-933-821-3
Sequence 3, Application US/08933821
Patent No. 597338
GENERAL INFORMATION:
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; TITLE OF INVENTION: Tie Ligands
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatin (Genentech)

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/933,821
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Ginger R.
; REGISTRATION NUMBER: 33,055
; REFERENCE/DOCKET NUMBER: P1130
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-3216
; TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3355 base pairs
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
US-08-933-821-3

Query Match   22.6%;   Score 491.8;   DB 2;   Length 3355;
Best Local Similarity   62.9%;   Pred. No. 1e-105;
Matches 836;   Conservative 0;   Mismatches 472;   Indels 21;   Gaps 4;

Qy   526 ACAAGTCACCTACACCTTCATTGTCCCAGCAGCGGGGTCACGGGGTCCAATCTGCGTCA 585
Db   588 AGAAATGTGCAATACACATTCCTGGGTACCTGAACAACAAAGAATAACAGGGCCAATCTGTGTCA 647

Qy   586 ACTCCAAGGAGGCCTGAGGTGCTTC---TGGAGAACGGAGTGCATAAGACAGGAGAGC 642
Db   648 ACACCAAGGGCGCAAGATGCAAGTACCATTAAAGACAATGATGACCAGAATGGAACCTTGAAA 707

Qy   643 TGCTCAACAATGAGCTGCTCAAGCAGAAGAGCCGGCAGATCGAGAGCGCTCAGCTTGGTGA 702
Db   708 ACCTGAAGGATGTGCTCTCCAGGCGCAGAAAGGCCGGAGATAGAGTTCTGCAACTGGGTGG 767

Qy   703 AGGTGGACGGCGCGCCCATTGTGAGCGAGGTGAAGCTGCGTCGCGGAAGGAGAGCGCAACATGA 762
Db   768 ATGTAGATGGAAACATTGTGAATGAGGTAAAGCTGGAGAAGGAAAAGCCGTACATGA 827

Qy   763 ACTCCGCGGGTCACGCAGCCTTCATACAGTCCTGCAGCGCGACGGAGATCATCCCGCAAGCGGGACA 822
Db   828 ACTCTCGTGTTCACTCAAACTCTATAGCAATTATTCACATGAAGAGGGAATA 887

Qy   823 ACGCGTTGGAGCTCTCCCAGTGTGGGAACAGGATCTGACCAGACAGACGCCGACATGCTGC 882
Db   888 ATTCACTTGAACTTTCCCAACTGGAAAAAACAAAATCCTCAATGTCACCACAGAAATGTTGA 947

Qy   883 AGCTCGCCACGAAGTACAAGAACAAGACTGGAGACAACAAGTACCAGCACACTGGGCACATGA 942
Db   948 AGATGGCAACAAGATTACAGGGAACTAGAGGTGAAATACGCTTCCTTGACTGATCTGTCA 1007

Qy   943 ACAACCAAATCAGAGATCATCCGCAGCTTGAGGGAGGCACTGCCAGAGAGGGTGCCCTCGGCCA 1002
Db   1008 ATAACCAAATCTTGTGAGATCACTTTGTTGGAAGAACAGTGCTTGAGGGATTATTTTCCGAC 1067

Qy   1003 GGCCCGGTCCCCAGCCACCCCCGCGCTGCCCCG------CCCGGGGTCTACCAACCACCC 1055
Db   1068 AAGACACCCAGTGTCTCCCCACTTGTCCCAGGTGGTGCCACAACATATTCCTTACAGACC 1127

Qy   1056 ACCTACAAACGGCATCATCAACCAGATCTCTACCACGAGATCCAGAGTGACCAGAACCTG 1115
Db   1128 AACAGTATACTCCTGGTCTGGCTGGAGGTAACGAGAGATTCAGAGGGATCCAGGTTATCCCA 1187

Qy   1116 AAGG------TGCTGCACCCCTCTTGCCCACTATGCCCACTCTCACCAGCCTC------C 1164
Db   1188 GAGATTTAATCCCACCACCTGATCTCGGCAACTTCTCCCACCAAAAAGCCCTTTTCAAGATAC 1247

Qy   1165 CATCTTCCACGGACAAGCGCGTCGGGCCCATGGAGAGAGGACTGCCCTGCAGGCCCTGGAGGATG 1224
Db   1248 CACCGGTAACTTTCATCAATGAAGGACCAATTCAAAGACTGTCAGCAAGCAAAGAAGCTG 1307

Qy   1225 GCCACGACACCAGCTCCATCTACCTGGTGAAGGCCGGAGACACCAACCGCGCCTCATGCAGG 1284

Db   1531 CAAGGGTTTGGGAAACAATTGACGGCGGAATACTGGGCTGGGCCTGGGAGAACATTACTGGCTG 1590
Qy   1443 ACGAACCAAGGCAACTACAACAACTCCTGGTGACCATGGAAGGAGGACTGGTTCCGGCCGCAAAGTC 1502
Db   1591 ACGAACCAAGGCAACTACAAACTCCTGGTGACCATGGAAGGAGGACTGGTTCCGGCCGCAAAGTC 1650
Qy   1503 TTTGCAGAATACGGCCAGTTTCGCCTGGAACCTGAGAGCGATATTATAAGCTGCGGCTG 1562
Db   1651 TTTGCAGAATACGGCCAGTTTCGCCTGGAACCTGAGAGCGATATTATAAGCTGCGGCTG 1710
Qy   1563 GGGGCGCTACCATGGCAATGCGGGTGACTCCTTCCTTTACATGGCAACGCAACGAGTTCACC 1622
Db   1711 GGGGCGCTACCATGGCAATGCGGGTGACTCCTTTTACATGGCAACGGGCAAGCAGTTCACC 1770
Qy   1623 ACCCTGGACACAGAGATCATGATGTCTACACAGAGAAACTGTGCCCACTACCAGAAGGGAGGC 1682
Db   1771 ACCCTGACACAGAGATCATGATGTCTACACAGAGAAACTGTGCCCACTACCAGAAGGGAGGC 1830
Qy   1683 TGGTGGTATAACGCCCTGTGCCCACTCGAACCTCAACCTTCACAGGCCGCCGCGGGGGCCCAT 1742
Db   1831 TGGTGGTATAACGGCCTGTGCCCACTCAAACCTCAACGGGTCTGGTGTTACCGCGGGGGGCCAT 1890
Qy   1743 TACCGGAGCCGCTACCAGGAGCGTCTACTGGCTGAGTTCCGAGAGGAGGGCTCTACTCA 1802
Db   1891 TACCGGAGCCGGCGCTACCAGGAGCGGTCTACTGGCTGAGTTCCGAGAGGAGGGCTCTTACTCA 1950
Qy   1803 CTCAAGAAAGTGGTGATGAATCCACCGGAACCCCAAACACCTTCACTAGCTCACTAGCTCC 1862
Db   1951 CTCAAGAAAGTGGTGATGAATCCGGACCAGGCAGATACCATTAAACACAGCTGGTCGCTGCC 2010
Qy   1863 CCCTCCTGAACCTCTCGTGGGCCCATTGCCAGAGACGCCCACCCTGGTCTGCCACCCAGCAC 1922
Db   2011 CCCTCCTGACCTCTCGTGTGGGCCCATTGCCAGAGAGGCCCACCCTGGTCTGCCACCAGCAC 1922
Qy   1923 AAAGAACAACTCCTCACCAGTTCATCCTGAGCGTGGGAGAGCTGCTGGAGTTCTGGTGT 1982
Db   2071 AAAGAACAACTCCTCACCAGTTCATCCTGGAGGACACCGGGGATGCTGGGAATTCTGT 2130
Qy   1983 TTTCCGAAGTCACTGCAGCGGAATGAATCGATACGGGTGGTGTTTTTCCTGTCCCTCC 2042
Db   2131 TTTCCGAAGTCACTGCAGCGGAATCGATACGGGTGGTGTTTTTCCTGTCCCTCC 2190
Qy   2043 TACTTTTCCTTCACACAGACACCCCTCAGGACAGGACCCATGTCTCTCAGGACAGACTACAGACAA 2102
Db   2191 TACTTTCCCTTCACACAGACACCCCTCATGTCTCCAGGACAGGACTACACGACAA 2250
Qy   2103 CTCTTTCTTTAAATAAAATTAAGTCTCTTACAATTACAAAAAAACA 2141
Db   2251 CTCTTTCTTTAAATAAAATTAAGTCTCTTACAATAAAAAAAA 2289

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Db       1308 GGCATTCGGTCAGTGGGATTTATATGATTAAACCTGAAAACAGCAATGGACCAATGCAGT 1367

Qy       1285 TGTGGTGCGACCAGAGACACGACCCCGGGGGCTGGACCGTCATCCAGAGACGCCTGGATG 1344
              | ||||| ||  | ||    ||||| ||||| ||||| || || |||| | |    || |
Db       1368 TATGGTGTGAAAACAGTTTGGACCCTGGGGGTTGGACTGTTATTCAGAAAAGAACAGACG 1427

Qy       1345 GCTCTGTTAACTTCTTCAGGAACTGGGAGACGTACAAGCAAGGGTTTGGGAACATTGACG 1404
              ||||||| |||||||||| || ||||| |  || ||| ||||||||| ||||||||||
Db       1428 GCTCTGTCAACTTCTTCAGAAATTGGGAAAATTATAAGAAAGGGTTTGGAAACATTGACG 1487

Qy       1405 GCGAATACTGGCTGGGCCTGGAGAACATTTACTGGCTGACGAACCAAGGCAACTACAAAC 1464
              | ||||||||||| || |||| || || || |   ||| |  || ||||  || |||||
Db       1488 GAGAATACTGGCTTGGACTGGAAAATATCTATATGCTTAGCAATCAAGATAATTACAAGT 1547

Qy       1465 TCCTGGTGACCATGGAGGACTGGTCCGGCCGCAAAGTCTTTGCAGAATACGCCAGTTTCC 1524
              |  || |     |  | ||||||   |     ||||||| ||||||||||  ||| || |
Db       1548 TATTGATTGAATTAGAAGACTGGAGTGATAAAAAAGTCTATGCAGAATACAGCAGCTTTC 1607

Qy       1525 GCCTGGAACCTGAGAGCGAGTATTATAAGCTGCGGCTGGGGCGCTACCATGGCAATGCGG 1584
              | ||||||||||| || || |  ||||  ||||| |||||    ||||| || ||||| |
Db       1608 GTCTGGAACCTGAAAGTGAATTCTATAGACTGCGCCTGGGAACTTACCAGGGAAATGCAG 1667

Qy       1585 GTGACTCCTTTACATGGCACAACGGCAAGCAGTTCACCACCCTGGACAGAGATCATGATG 1644
              | || ||  | |  ||||| || || || || |||||||| ||||||||||||| | |||
Db       1668 GGGATTCTATGATGTGGCATAATGGTAAACAATTCACCACACTGGACAGAGATAAAGATA 1727

Qy       1645 TCTACACAGGAAACTGTGCCCACTACCAGAAGGGAGGCTGGTGGTATAACGCCTGTGCCC 1704
              | ||  |||||||||| |||||||  || || ||||||||||||||| || |||||||| |
Db       1728 TGTATGCAGGAAACTGCGCCCACTTTCATAAAGGAGGCTGGTGGTACAATGCCTGTGCAC 1787

Qy       1705 ACTCCAACCTCAACGGGGTCTGGTACCGCGGGGGCCATTACCGGAGCCGCTACCAGGACG 1764
              | || ||||| || || || |||||| | || |||||||||| | |||    |||| || |
Db       1788 ATTCTAACCTAAATGGAGTATGGTACAGAGGAGGCCATTACAGAAGCAAGCACCAAGATG 1847

Qy       1765 GAGTCTACTGGGCTGAGTTCCGAGGAGGCTCTTACTCACTCAAGAAAGTGGTGATGATGA 1824
              || | | ||||||| || | | |||| || || |||||  | |    |||   ||||||||
Db       1848 GAATTTTCTGGGCCGAATACAGAGGCGGGTCATACTCCTTAAGAGCAGTTCAGATGATGA 1907

Qy       1825 TCCGACCGA 1833
              ||   ||  |
Db       1908 TCAAGCCTA 1916

RESULT 11
US-08-960-507-3
; Sequence 3, Application US/08960507
; Patent No. 6057435
;  GENERAL INFORMATION:
;    APPLICANT:  Godowski, Paul J.
;    APPLICANT:  Gurney, Austin L.
;    TITLE OF INVENTION:  Tie Ligands
;    NUMBER OF SEQUENCES:  24
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genentech, Inc.
;      STREET:  1 DNA Way
;      CITY:  South San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94080
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 inch, 1.44 Mb floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WinPatin (Genentech)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/960,507
;      FILING DATE:
;      CLASSIFICATION:  536
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Dreger, Ginger R.
;      REGISTRATION NUMBER:  33,055
;      REFERENCE/DOCKET NUMBER:  P1130p1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  650/225-3216
;      TELEFAX:  650/952-9881
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  3355 base pairs
;      TYPE:  Nucleic Acid
;      STRANDEDNESS:  Single
;      TOPOLOGY:  Linear
US-08-960-507-3

  Query Match             22.6%;  Score 491.8;  DB 3;  Length 3355;
  Best Local Similarity   62.9%;  Pred. No. 1e-105;
  Matches  836;  Conservative    0;  Mismatches  472;  Indels   21;  Gaps    4;

Qy        526 ACAAGTGCACCTACACCTTCATTGTGCCCCAGCAGCGGGTCACGGGTGCCATCTGCGTCA 585
              | || ||  | ||||| ||| | || ||  | ||  |  | || ||  | ||||| ||||
Db        588 AGAAATGTGCATACACATTCCTGGTACCTGAACAAAGAATAACAGGGCCAATCTGTGTCA 647

Qy        586 ACTCCAAGGAGCCTGAGGTGCTTC---TGGAGAACCGAGTGCATAAGCAGGAGCTAGAGC 642
              || |||||| ||  || |    |    ||  ||    |    | | ||| || ||
Db        648 ACACCAAGGGGCAAGATGCAAGTACCATTAAAGACATGATCACCAGGATGGACCTTGAAA 707

Qy        643 TGCTCAACAATGAGCTGCTCAAGCAGAAGCGGCAGATCGAGACGCTGCAGCAGCTGGTGA 702
                || ||  ||| |||   || |||||||||| |||| ||    ||||| | | |||||
Db        708 ACCTGAAGGATGTGCTCTCCAGGCAGAAGCGGGAGATAGATGTTCTGCAACTGGTGGTGG 767

Qy        703 AGGTGGACGGCGGCATTGTGAGCGAGGTGAAGCTGCTGCGCAAGGAGAGCCGCAACATGA 762
              | || || ||   |||||||||  ||||| |||||||||| | ||||| ||||| || |||||||
Db        768 ATGTAGATGGAAACATTGTGAATGAGGTAAAGCTGCTGAGAAAGGAAAGCCGTAACATGA 827

Qy        763 ACTCGCGGGTCACGCAGCTCTACATGCAGCTCCTGCACGAGATCATCCGCAAGCGGGACA 822
              |||| || || || || ||||| |||||  |  | || ||||| ||||| ||| |||| |
Db        828 ACTCTCGTGTTACTCAACTCTATATGCAATTATTACATGAGATTATCCGTAAGAGGGATA 887

Qy        823 ACGCGTTGGAGCTCTCCCAGCTGGAGAACAGGATCCTGAACCAGACAGCCGACATGCTGC 882
              |  |  | || || ||||| ||||| ||||  ||||| ||    ||  | || ||| ||
Db        888 ATTCACTTGAACTTTCCCAACTGGAAAACAAAATCCTCAATGTCACCACAGAAATGTTGA 947

Qy        883 AGCTGGCCAGCAAGTACAAGGACCTGGAGCACAAGTACCAGCACCTGGCCACACTGGCCC 942
              || |||| |  |  |||| ||| || ||| |||   || |||     |||| |    || | |
Db        948 AGATGGCAACAAGATACAGGGAACTAGAGGTGAAATACGCTTCCTTGACTGATCTTGTCA 1007

Qy        943 ACAACCAATCAGAGATCATCGCGCAGCTTGAGGAGCACTGCCAGAGGGTGCCCTCGGCCA 1002
              | |||||||| | ||| ||| |   | | || || || ||  |||| |    ||
Db       1008 ATAACCAATCTGTGATGATCACTTTGTTGGAAGAACAGTGCTTGAGGATATTTTCCCGAC 1067

Qy       1003 GGCCCGTCCCCCAGCCACCCCCCGCTGCCCCG-------CCCCGGGTCTACCAACCACCC 1055
                  |  ||    | | |||||   || ||  |       | |    | | || | || ||
Db       1068 AAGACACCCATGTGTCTCCCCCACTTGTCCAGGTGGTGCCACAACATATTCCTAACAGCC 1127

Qy       1056 ACCTACAACCGCATCATCAACCAGATCTCTACCAACGAGATCCAGAGTGACCAGAACCTG 1115
              | |   |  | | |  ||  |  |      || |     |    ||   |    | ||
Db       1128 AACAGTATACTCCTGGTCTGCTGGGAGGTAACGAGATTCAGAGGGATCCAGGTTATCCCA 1187

Qy       1116 AAGG-----TGCTGCCACCCCCTCTGCCCACTATGCCCACTCTCACCAGCCTC------C 1164
               ||      |||  |||||   |||| | |||   |||||    | |     ||      |
Db       1188 GAGATTTAATGCCACCACCTGATCTGGCAACTTCTCCCACCAAAAGCCCTTTCAAGATAC 1247

Qy       1165 CATCTTCCACCGACAAGCCGTCGGGCCCATGGAGAGACTGCCTGCAGGCCCTGGAGGATG 1224
              || |    ||   ||        || ||||  | |||||| | ||| ||    || | ||
Db       1248 CACCGGTAACTTTCATCAATGAAGGACCATTCAAAGACTGTCAGCAAGCAAAAGAAGCTG 1307

Qy       1225 GCCACGACACCAGCTCCATCTACCTGGTGAAGCCGGAGAACACCAACCGCCTCATGCAGG 1284
              | ||      |||    || ||  || | || || || ||| |||  | |  ||||||
Db       1308 GGCATTCGGTCAGTGGGATTTATATGATTAAACCTGAAAACAGCAATGGACCAATGCAGT 1367

Qy       1285 TGTGGTGCGACCAGAGACACGACCCCGGGGGCTGGACCGTCATCCAGAGACGCCTGGATG 1344
              | ||||| ||  | ||    ||||| ||||| ||||| || || |||| | |    || |
Db       1368 TATGGTGTGAAAACAGTTTGGACCCTGGGGGTTGGACTGTTATTCAGAAAAGAACAGACG 1427

Qy       1345 GCTCTGTTAACTTCTTCAGGAACTGGGAGACGTACAAGCAAGGGTTTGGGAACATTGACG 1404
              ||||||| |||||||||| || ||||| |  || ||| ||||||||| ||||||||||
Db       1428 GCTCTGTCAACTTCTTCAGAAATTGGGAAAATTATAAGAAAGGGTTTGGAAACATTGACG 1487
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;
;
; US-09-136-828-3
; Sequence 3, Application US/0913682B
; Patent No. 6350450
; GENERAL INFORMATION:
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; TITLE OF INVENTION: Tie Ligands
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/136,828
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Ginger R.
; REGISTRATION NUMBER: 33,055
; REFERENCE/DOCKET NUMBER: P1130R1A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-3216
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3355 base pairs
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
US-09-136-828-3
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RESULT 12
US-09-136-828-3

Query Match    22.6%;   Score 491.8;  DB 4;  Length 3355;
Best Local Similarity   62.9%;  Pred. No. 1e-105;
Matches 836;  Conservative 0;  Mismatches 472;  Indels 21;  Gaps 4;

Qy   526 ACAAGTGCACCTACACCTTCATTGTGCCCAGCAGCGGGGTCACGGGTGCCAATCTCGGTCA 585
                 ||||| |  |  |||  || || || ||||  |  ||||    ||  |||| | |||
Db   588 AGAAAGTGCATACACATTCCTTGGTACCTGAACAAAGAATAACAGGGCCAATCTGTGTCA 647

Qy   586 ACTCCAAGGAGGCCTGAAGGGTGCTTC---TGGAGAACGGAGTGCATAAGCAGGAGGGAGC 642
                 |||||| |||   | |||   || |     ||||  |||| |  ||| ||||  ||
Db   648 ACACCAAGGGCCAAGATGCAAGTACCATTAAAGACATGATCACCGGATGGACCTTGAA  707

Qy   643 TGCTCAACAATGAGCTGCTCAAGCAGAAGTGGCAGACTCGAGAAGCGGCGCACACTGA 702
                 |||||  ||||| |  ||  ||| |  ||||  ||  |||| |  ||| | |||||
Db   708 ACCTGAAGGAGTGCTCTCCAGGCGAAGCGGGAGAATAGAGTTCTGAACTGGTCGGGTGG 767

Qy   703 AGGTGGACGGGCGGGGCATTGTGAGCGAGGTGAAGCTGCTGCGCAAGGAGAGCGGACACGA 762
                 || |  |  |  ||||  | || || | ||||  | ||   ||| |||  || | ||
Db   768 ATGTAGGATGGAAACATTGTGAATGAGGTAAAGCTGCTGAGAGAAGAAAGCCGTAACATGA 827

Qy   763 ACTCGCGGGGTCACGCAGCGCTCACACGCCTGCCCATCACCCGCAAGCCGGACA 822
                 ||| | | |  || |||   ||  | |||| |  |||||  ||| | ||| || |
Db   828 ACTCTCGTGTTACTCAACTCTATATCCAATTATTACATGAGTATCCGTAACGAAG 887

Qy   823 ACGCGTTGGAGACTTCTCCCAGCTGGAGAACAAGGATCCGAACGAAATGCTGC 882
                 || | ||||| ||  |||||| ||||| |||| |  |  | || | ||| |
Db   888 ATTCACTTGAACTTTCCCAACTGGAAAAACACAAAAATCCTCAATGTCACCACAGAAAAGTTGA 947

Qy   883 AGCTGGCCAGCAAGTACACTGGAGACCTGGAGCACAAGTACCACCAGCCCC 942
                 |  | || | || || |  ||| ||  ||| | |  |||| | |  ||| ||
Db   948 AGATGGCAACAAAGATACAGGGAACAGAGCATGAAATACGGCTCCTTGACTGATCTTGTCA 1007

Qy   943 ACAACCAAATCAGAGATCATGCGCAGCCTTGAGGACGACACTGCCGAGGGTGCCCCTGGCCA 1002
                 |||||  | |||||  ||| ||||  |||||| |  | ||| | |||||| | | ||||
Db  1008 ATAACCAAATCTGTGATGAATCACTTTGTTGGGAAGAACAGGCTTGAGGAGATATTTCCGGAC 1067

Qy  1003 GGCCGCGTCCCCAGCCACCCCCCCGCTGCCCCG------CCCCCGGTCTACCAACCCACCC 1055
                 | || |  || | || || ||  || ||  ||       ||  || |  |||||||| |
Db  1068 AAGACACCCATGTGCTCCCCACTTGTCCACAACATATTCCTAACAGCC 1127

Qy  1056 ACCTACACCACGGCATCATCAACCCAGATCTCTACCAGAATCCGAGTGACCAGAACCTG 1115
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Db  1128 AACAGTAATACTTCCCTGGTCTCTGTCTGGGAGAAGGTAACGACGATTCCAGGTTATCCCA 1187

Qy  1116 AAGG----TCCTGCCACCCCCTCTGCCCACTATGCCCACTACTCTCACCCAGCCTC 1164
                 |        | |  ||||    |||| | || |  | || |  ||| | |  |
Db  1188 GAGATTTAATGCCACCAACCTGATCTGGCAAACTTCTCCCCACCAAAAAGCCCTTTCAAGATAC 1247

Qy  1165 CATCTTCACCGACAAGCCGTCGGGGCCCATGGAGAGACTGCCTCAGGCCCTGGAGGATG 1224
                 ||| ||  |  |  |||  | ||  || || |||| || | ||  | ||| |||| || |
Db  1248 CACCGGTAACTTTCATCAATGAAGGGACCAATTCAAGACTGTCAGCAAGCAGAAAGAAGCTG 1307

Qy  1225 GCCACGACGACCAGCTCCATCTACTCTGGGATGGATTTATATGA 1284
                 || | ||||| || | ||||  | ||||  |  |||  |||| |
Db  1308 GGCAATCGGTCAGTGGGGATTTATATAAACCTGAAACCAATGCAGT 1367

Qy  1285 TGTGGTGCGACCAGGACACGGACCCCGCGGGGGGCTGGACCGGTCACAGCGACCCTGGAATG 1344
                 |  | |   ||| | || ||  || | ||||| | |  |||| | | |  | | || ||
Db  1368 TATGGTGTGAAAACAGTTTGGACCCTGGGGTTGGAACTGCAT 1427

Qy  1345 GCTCTGTTAACTTCTTCAGGAACTGGGAGACGTACAGAGGAAGGGTTTGGGGAACATTGACG 1404
                 ||| | | | |||| | ||| |  | | | | ||| || ||  ||||| || | |||||||
Db  1428 GCTCGTCAACTTCTTCAGAAAATGGAAAATTATAAGAAGGTTTGAAACANTGACG 1487

Qy  1405 GCGAATACTGGCTGGGCCTGGGGAACATTTACTGGCTGACGAACCAAGGCAACTACAAAC 1464
                 || |||||||||| ||  ||||| || | |  |||||||||   || |  ||||| |||
Db  1488 GAGAATACTGGCTTGGACTGGGAAAATCTATATGCTTAGCAATCAAGATAATTACAAGT 1547

Qy  1465 TCCTGGTGACCAATGGAGGAC ... TTCC 1524
Db  1548 TATTGATTGAATTAGAAGAC ... TTTC 1607

Qy  1525 GCCTGGAAACCGAGAGCGGAG ... GGG 1584
Db  1608 GTCCTGGAACCTGAAAGTGAAT ... CAG 1667

Qy  1585 GTGACTCCTTTACATGGCACAACG ... GATG 1644
Db  1668 GGGATTCTTATGAGTGGCATAAAG ... AGATA 1727

Qy  1645 TCTACACAGGAAAACTGTGCCCAC ... CTGTGCCC 1704
Db  1728 TGTATGCAGGAGAACTGCGGCCCA ... GGCAC 1787

Qy  1705 ACTCCAAGCTCAAGCGGGGGTTCTGTGTACCG ... GTACCAGGACG 1764
Db  1788 ATTCTAACCTAAATGGAGTAATGGGTACAGA ... GGGATA 1847

Qy  1765 GAGTCTACTCTGGCTGAGTTCCCGAGGAGGCTCTTACTCACTCAAGAAAGTGGTGATGATGA 1824
Db  1848 GAATTTTCTGGGCCGAATACAGAGCCGGGTCATACTCCTTAAGAGCAGTTCAGATGATGA 1907

Qy  1825 TCCGACCGA 1833
Db  1908 TCAAGCCTA 1916
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RESULT 13
US-09-332-928A-3
Sequence 3, Application US/09332928A
Patent No. 6368853
GENERAL INFORMATION:
  APPLICANT: Godowski, Paul J.
           Gurney, Austin L.
  TITLE OF INVENTION: Tie Ligands
  NUMBER OF SEQUENCES: 17
  CORRESPONDENCE ADDRESS:
    ADDRESSEE: Genentech, Inc.
    STREET: 1 DNA Way
    CITY: South San Francisco
    STATE: California
    COUNTRY: USA
    ZIP: 94080
  COMPUTER READABLE FORM:
    MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
    COMPUTER: IBM PC compatible
    OPERATING SYSTEM: PC-DOS/MS-DOS
    SOFTWARE: WinPatin (Genentech)
  CURRENT APPLICATION DATA:
    APPLICATION NUMBER: US/09/332,928A
    FILING DATE: 14-Jun-1999
    CLASSIFICATION: <Unknown>
  PRIOR APPLICATION DATA:
    APPLICATION NUMBER: 08/933,821
    FILING DATE: <Unknown>
    CLASSIFICATION: <Unknown>
  ATTORNEY/AGENT INFORMATION:
    NAME: Dreger, Ginger R.
    REGISTRATION NUMBER: 33,055
    REFERENCE/DOCKET NUMBER: P1130
  TELECOMMUNICATION INFORMATION:
    TELEPHONE: 650/225-3216
    TELEFAX: 650/952-9881
  INFORMATION FOR SEQ ID NO: 3:
    SEQUENCE CHARACTERISTICS:
      LENGTH: 3355 base pairs
      TYPE: Nucleic Acid
      STRANDEDNESS: Single
      TOPOLOGY: Linear
    SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-332-928A-3

Query Match   22.6%;
Best Local Similarity   62.9%;
Matches   836;   Conservative   0;   Mismatches   472;   Indels   21;   Gaps   4;
Score 491.8; DB 4; Length 3355;
Pred. No. 1e-105;

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Qy  1525 GCCTGGAACCTGAGAGGGAGGGTATTATTAAGCTGGCGGCGCTGGGGGGCGGCTGGGGGCTTGGGCGCTTACCCATGGCAATGCGG 1584
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  526  ACAAGTGCACTACACCACCTTCATTGTCGTTGTCCGGCAGCGCGGGGTCGACGGCTGCCACGGTGCCATCTGCGTCA 585

Qy  1608 GTCTGGAACCTGAAAGTGAATTCTATAGACTGCGCGCTGGGAACTTACCAGGAAATGCAG 1667
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  588  AGAAAGTGCATACACATTCCTGGTGACTGACCAAACAAAGAATAACAGGGCCAAATCTGGTGTCA 647

Qy  1585 GTGACTCCTTTACATGGCACAACGGCAAGCAGTTCACCACCCTGGACAGAGATCATGGATG 1644
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  586  ACTCCAAGAGAGCCTGAGGTGCTTC---TSGAGAACCGAGTGCATAAGAGAAGGAGCTAGAGC 642

Qy  1668 GGGATTCTATGATGTGGCATAATGGTAAACAATTCACCACTGGACAGCATAAAGATA 1727
         |||||||||||||||||||||||||||||||||||||||||||||||||||
Db  648  ACACCAAGGCGGCAAGATGCAAGGTACCATTGAAGTGCTGATGGTGGCCTTGAAA 707

Qy  1645 TCTACACAGAGAAACTGTGCCCACTACCGAGAGAGGAGCTGGGTGGTAAACGGCCTGTGCCC 1704
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  643  TGCTGACAATGAGCTGCTTCAAGCAGCGAGGAAGAAGGGCAGGATTCAGCAGCTGTGA 702

Qy  1668 TGTATGCAGGAGAAACTGCGCCCCACTTTCATTAAAGGAGGAGCGGGTACAATGCCTGGGG 1727
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Db  708  ACCTGAAGAGATGTGCTCTCCAGGCGAGCGAGAAGCGGGAGTAGAGTTCTGCAACTGGTGG 767

Qy  1705 ACTCCAACCTCAACGGGGTCTGGTACCGCGCGGGGGGGGCCATTACCGGCGCTACCAGCACG 1764
         |||||||||||||||||||||||||||||||||||||||||||||||
Db  768  ATGTAGAGTCCAAACATTGTAGATGAGGTAAAGCTGACTGAGAAGGAAAGCCGTAACATGA 827

Qy  1728 ATTCTAACCTAAATGGGAGTATGGGTACAGAGGAGGGCCATTACAACCAGTTTGCATAG 1787
         ||||||||||||||||||||||||||||||||||||||||||
Db  828  ACTTCTGTGTTACTCAACTCCTATATGCAATTATTACACAGAGATTATCCGTAAGAGGGATA 887

Qy  1765 GAGTCTACTCGGGCTGAGTTCCGAGGAGGCTCTTACTCACTCAAGAAAAGTGGTTGAAGATGA 1824
         |||||||||||||||||||||||||||||||||||||||||||
Db  828  ACTTCTGTGTTACTCAACTCCTATATGCAATTATTACACAGAGATTATCCGTAAGAGGGATA 887

Qy  1848 GAATTTTCTGGGCCCGAATACAGAGGCGGGTCATACTCCTTAAGAGCAGTTCAGATGATGA 1907
         |||||||||||||||||||||||||||||||||||||||||||||
Db  768  ATGTAGAGTCCAAACATTGTAGATGAGGTAAAGCTGACTGAGAAGGAAAGCCGTAACATGA 827

Qy  1825 TCCGACCGA 1833
         |||||||||
Db  1908 TCAAGCCTA 1916
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Db 526 ACAAGTGCACTACACCACCTTCATTGTCGTTGTCCGGCAGCGCGGGGTCGACGGCTGCCACGGTGCCATCTGCGTCA 585
Qy 588 AGAAAGTGCATACACATTCCTGGTGACTGACCAAACAAAGAATAACAGGGCCAAATCTGGTGTCA 647
Db 586 ACTCCAAGAGAGCCTGAGGTGCTTC---TSGAGAACCGAGTGCATAAGAGAAGGAGCTAGAGC 642
Qy 648 ACACCAAGGCGGCAAGATGCAAGGTACCATTGAAGTGCTGATGGTGGCCTTGAAA 707
Db 586 ACTCCAAGAGAGCCTGAGGTGCTTC---TSGAGAACCGAGTGCATAAGAGAAGGAGCTAGAGC 642
Qy 648 ACACCAAGGCGGCAAGATGCAAGGTACCATTGAAGTGCTGATGGTGGCCTTGAAA 707
Db 643 TGCTGACAATGAGCTGCTTCAAGCAGCGAGGAAGAAGGGCAGGATTCAGCAGCTGTGA 702
Qy 708 ACCTGAAGAGATGTGCTCTCCAGGCGAGCGAGAAGCGGGAGTAGAGTTCTGCAACTGGTGG 767
Db 763 ACTCCGGGTCACGCAGCTCCTACAATGCAGGTCCTGCACGAGATCATCCGCAAGGGGACA 822
Qy 768 ATGTAGAGTCCAAACATTGTAGATGAGGTAAAGCTGACTGAGAAGGAAAGCCGTAACATGA 827
Db 823 ACGCGGTTGGAGCTCTCCCACTGACTGGGAACCAGGATCCTGAGAACAGAGCCGACACATGCTGC 882
Qy 828 ACTTCTGTGTTACTCAACTCCTATATGCAATTATTACACAGAGATTATCCGTAAGAGGGATA 887
Db 883 AGCTCGGCCAGCGAAGTACAAGGAGACCTGGAGGACACAGTGACACACCTGGGCACTGGGCC 942
Qy 888 ATTCACTTGAACTTTCCCAACTGGAAAAAATCCTCAAATGTACCACCAGAGAAATGTTGA 947
Db 943 ACAACCAATCAGAGAGATCAATGCGCAGCAGCTTGAAGAGAAGCACTGCCAGCAGGGGTTGGCCTTCGGGCCA 1002
Qy 948 AGATGGCAACAAGATACAGGGAACCTAGAGGTGAAAATACCGCTTCCTTGACTGATCTTGTCA 1007
Db 1003 GGCCCCGTCCCCACGCACCCCCGGTTGCCCCG------CCCGGGGTCTTACCCAACCACCC 1055
Qy 1008 ATAACCAATCTGTGATCGATTGAATCACTTTGGTTGGAGAACGAGGTGGCCAGAGGGGCCA 1067
Db 1056 AACGACACCCATGTGTCTCCCCACTTGTTCCAGGTGGTGTCCACAACATATTCCTTAACAGCC 1115
Qy 1068 AAGACACCCATGTGTCTCCCCACTTGTTCCAGGTGGTGTCCACAACATATTCCTTAACAGCC 1127
Db 1116 AAGG------TGCTGCCACCCCCCTCTGCCCCACTTATGCCCACTCACCAGCCTC------C 1164
Qy 1128 AACAGTATACTACCTCGGTCTGCGCTGGGAGGTAACGAGATCAGAGTGACAGAGAACCTG 1187
Db 1056 AACGACACCCATGTGTCTCCCCACTTGTTCCAGGTGGTGTCCACAACATATTCCTTAACAGCC 1115
Qy 1165 CATCTTCACCGACAAGCCGTCGGCGCCCATGGAACTTCTCCCACCAAAGCCCTTTCAAGATAC 1224
Db 1188 GAGATTTAAGTCCACCACCTGATCTGCCAACTTCTCCCACCAAAGCCCTTTCAAGATAC 1247
Qy 1225 GCCAGACAACCAGCTCCATCTACCTGGTGAAGCCGGAGAACAACCGGCCTCATGCAGG 1284
Db 1248 CACCGGTAACTTTCATCAATCGAAGGACAATTCAAAGCAATCAAAGAAGCTG 1307
Qy 1285 TGTGGTCCGACCAGAGACACGACAGCCTGGACCGTCATCCAGAGGACGCCTGGATG 1344
Db 1308 GGCATTCGGTCAGTGGGGATTTATATGACTTAAAAATCAGCAGCAAATGCAGT 1367
Qy 1345 GCTCTGTCTTTACTTCTTCTCAGAAATTGGAACCTGGGGAGACGTACAACAGAGGGTTTTGGGAACATTGACG 1404
Db 1368 TATGGTGTGAAAAACAGTTTGGACACCCTGGGGTTGGACTGTTATTCAGAAAAGGAACGACG 1427
Qy 1405 GCGAATACTTGGCTGGCTGGGCCCTGGAGAGAACAGTTTTACTTGGCTGACTGGGAAAAGGAACTACAAAAC 1464
Db 1428 GCTCTGTCAACTTCTTCAGAAATTGGGAAAATTATAGAGAAACAATTGACG 1487
Qy 1465 TCCTGGGTGACCATGGAGACTGGTTCCGGCGCCGCAAAGCTTTTTGCGAGAATACGGCAGTTTCC 1524
Db 1488 GAGAATACTGCCTTGACTGGAAAATATCTTAGCCTGGAGAATAACGGCGAGT 1547
Qy 1525 GCCTGGAACCTGAGAGCGGAGTATTATTAAGCTGGCGGCGCTGGGGGCGGCTGGGGGCTGGGGCCAATGCGG 1584
Db 1548 TATTGATTGAATTAGAAGAGAACTGGAGTGATAAAAAGTCATGCGAATACAGCAGCTTTC 1607
Qy 1585 GTGACTCCTTTACATGGCACAACGGCAAGCAGTTCACCACCCTGGACAGAGATCATGGATG 1644
Db 1608 GTCTGGAACCTGAAAGTGAATTCTATAGACTGCGCGCTGGGAACTTACCAGGAAATGCAG 1667

RESULT 14
US-09-136-801-3
Sequence 3, Application US/09136801
Patent No. 6413770
GENERAL INFORMATION:
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin
APPLICANT: Hillan, Kenneth
APPLICANT: Botstein, David
APPLICANT: Goddard, Audrey
APPLICANT: Roy, Margaret
APPLICANT: Ferrara, Napoleone
APPLICANT: Tumas, Daniel
APPLICANT: Schwall, Ralph
TITLE OF INVENTION: Tie Ligand Homologues
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/136,801
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Dreger, Ginger R.
REGISTRATION NUMBER: 33,055
REFERENCE/DOCKET NUMBER: P1130P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-3216
TELEFAX: 650/952-9981
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 3355 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
US-09-136-801-3

Query Match 22.6%; Score 491.8; DB 4; Length 3355;
Best Local Similarity 62.9%; Pred. No. 1e-105;
Matches 836; Conservative 0; Mismatches 472; Indels 21; Gaps 4;

Qy   526 ACAAGTGCACCTACACCTTCATTGTGCCCAGCAGCGGGGTCACGGGTGCCATCTCGGTCA 585
          ||||||| |||| || |||| ||||||||||||||||||||||||||||| ||||| ||||
Db   1668 GGGATTCTTATGATGTGGGCATAATTGGTAAAACAATTCACCACACTTGGACAGAGAGATAAAGATA 1727

Db   588 AGAAATGTGCATACACATTCCTTGGGTACCTGAACAGAAGAATAACAGGGCCAATCTGTGTCA 647
Qy   586 ACTCCAAGGAGGCCTGAGGGTGCTTC---TGGAGAACCGAGTGGCATAAGGACAGGGGCTAGAGC 642
Db   648 ACACCAAGGGGCAAGATGCAAGTACCATTAAAGACAATGACCACCAGATGGACCTTGAA 707
Qy   643 TGCTCAACATGAGCTGCTCAAGCAGAAGAGCGGGAGCGCTGCAAGCAGCTGGCTGA 702
Db   708 ACCTGAAGGAGTGTGCTCTCCAGGCACCAGAAGCGGGAGGAGGAGGAGATAGAGATGTTCTGCAACTGGCTGTGG 767
Qy   703 AGGTGGACGGGCGGGGCATTGTGACGAGGAGGTGAGGAGCTGCGCGAAGGAGGGCCCAACATGA 762
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Qy   823 ACGCGGTTGGAGCTTCCCCACTGGAAAAACAAAATCCTCAAGTGTCACCACACAGAAAATGTTGA 882
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Qy   943 ACAAACCAAATCAGAATCATCGCGCACTTGAGGACGACACTGCCAGAGGTGCCTCGGCCA 1002
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Qy   1003 GGCCGGTGCCCCAGCCACCCCCGGCGTGCCCCG------CCCGCGGGTCTACCCAACCACCC 1055
Db   1008 ATAACCAAATCTGTGATGATCAACTTGTTGGAAGACAACAGTGCCTTGAGGAATATTTCCCGAC 1067
Qy   1056 ACCTACAACGGCATCATCAACCAGATCTCTACCAACGAGATCCAGAGCGTGACCAGAACCTG 1115
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Qy   1116 AAGG-----TGCTGCCACCCCCTTGCCCACTATGCCCACTCTCACCAGCCTC------C 1164
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Qy   1165 CATCTTCACCGACAAGCCGTCGGGCGCCCATGGAGACACTGGCCTGCAGGCCTGGGAGATG 1224
Db   1188 GAGATTTAATGCCACACACTGGATCGGCGACTTCTCCCACCAAAAGCCCTTTCAGATAC 1247
Qy   1225 GCCACACACAGCTCCATCTTACCTGGTGAAGCCGGAGACACACAACGGCTCAGCAGG 1284
Db   1248 CACCGGTAACTTTCATCAAATGAAGGACCAATTCAAAGAGACTGTTCAGCAAGCAAAAGAAGCTG 1307
Qy   1285 TGTGGTTGCGACCAGAGACACCGAACCCCGGGGGGGGGCTGACCGGTCATCCGACGAGGGATG 1344
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Qy   1645 TCTACACAGGAAACTGTCCCCACTACCAGAGAAGGGAGGGGCTGGGTGGGTTATAACGGCTTGTCCC 1704
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RESULT 15
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; Sequence 3, Application US/09332929
; Patent No. 6420542
; GENERAL INFORMATION:
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; TITLE OF INVENTION: Tie Ligands
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/332,929
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/933,821
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Ginger R.
; REGISTRATION NUMBER: 33,055
; REFERENCE/DOCKET NUMBER: P1130
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-3216
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3355 base pairs
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
US-09-332-929-3

Query Match   22.6%; Score 491.8; DB 4; Length 3355;
Best Local Similarity   62.9%; Pred. No. 1e-105;
Matches 836; Conservative   0; Mismatches 472; Indels 21; Gaps 4;

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Qy  1825  TCCGACCGA  1833
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Db  1908  TCAAGCCTA  1916
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Search completed: August 6, 2004, 18:18:56
Job time : 172 secs

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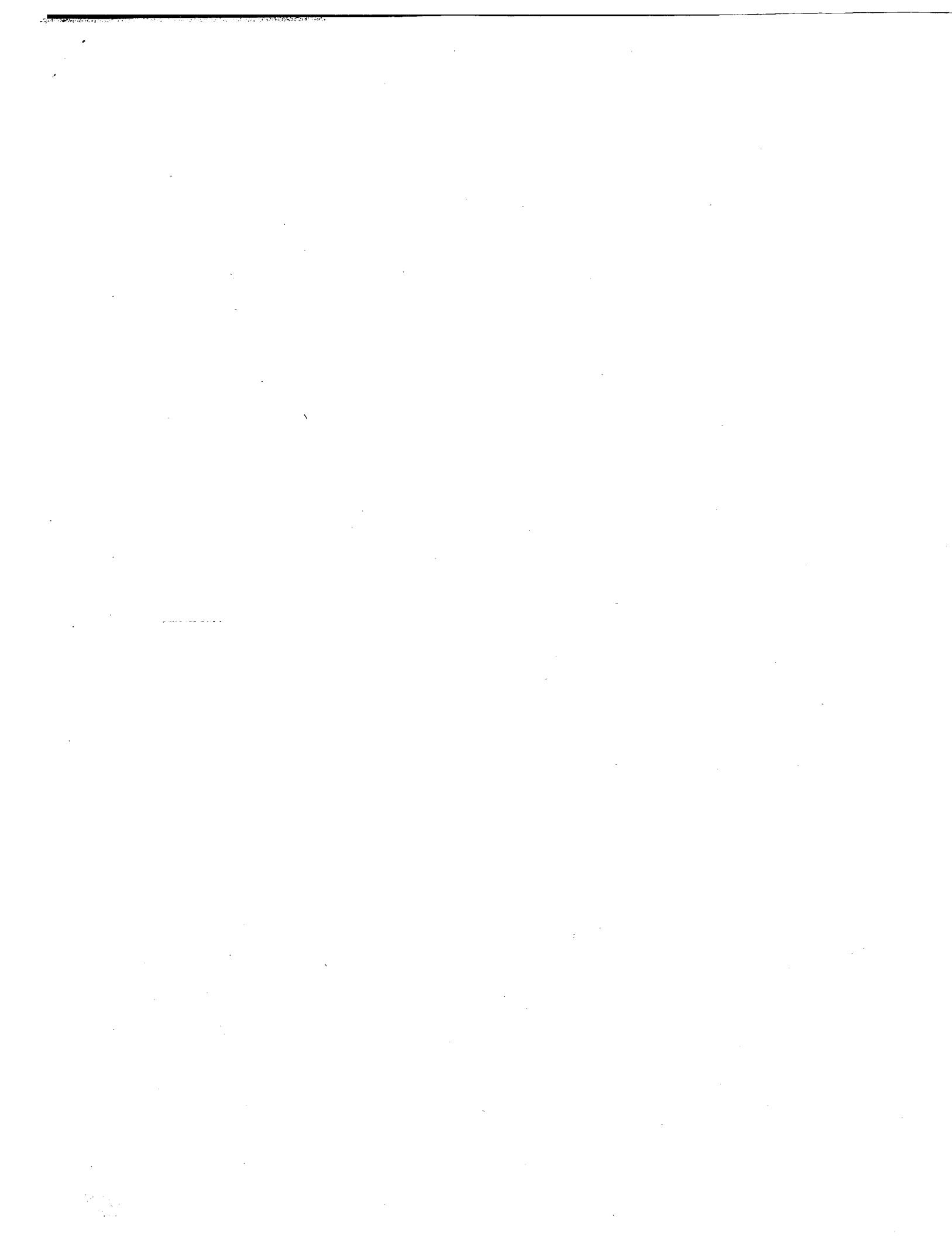
                         GenCore version 5.1.6
                         Copyright (c) 1993 - 2004 Compugen Ltd.

Run on:         August   6, 2004, 16:43:28 ; Search time 976 Seconds
                                            (without alignments)
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Title:          US-10-018-386-1
Perfect score:  2173
Sequence:       1 gaaatgaggctgctgcgga.................aaaaaaaaaaaaaaaaaa 2173

Scoring table:  IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched:       3222919 seqs, 2451570024 residues

Total number of hits satisfying chosen parameters:         6445838

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

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SUMMARIES

Result No.	Score	% Query Match	Length	DB ID	Description
1	2146.2	98.8	2288	9	US-09-818-143-11	Sequence 11, Appl
2	2132.6	98.1	2290	13	US-10-147-493-267	Sequence 267, App
3	2132.6	98.1	2290	13	US-10-145-127-267	Sequence 267, App
4	2132.6	98.1	2290	13	US-10-160-503-267	Sequence 267, App
5	2132.6	98.1	2290	13	US-10-143-118-267	Sequence 267, App
6	2132.6	98.1	2290	13	US-10-144-993-267	Sequence 267, App
7	2132.6	98.1	2290	13	US-10-158-787-267	Sequence 267, App
8	2132.6	98.1	2290	13	US-10-140-024-267	Sequence 267, App
9	2132.6	98.1	2290	13	US-10-140-808-267	Sequence 267, App
10	2132.6	98.1	2290	13	US-10-152-405-267	Sequence 267, App
11	2132.6	98.1	2290	13	US-10-127-852A-267	Sequence 267, App
12	2132.6	98.1	2290	13	US-10-127-000A-267	Sequence 267, App
13	2132.6	98.1	2290	13	US-10-128-685A-267	Sequence 267, App
14	2132.6	98.1	2290	13	US-10-131-820A-267	Sequence 267, App

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

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15   2132.6   98.1   2290   13   US-10-142-886-267    Sequence 267, App
16   2132.6   98.1   2290   13   US-10-146-728-267    Sequence 267, App
17   2132.6   98.1   2290   13   US-10-146-786-267    Sequence 267, App
18   2132.6   98.1   2290   13   US-10-147-499-267    Sequence 267, App
19   2132.6   98.1   2290   13   US-10-157-798-267    Sequence 267, App
20   2132.6   98.1   2290   14   US-10-066-500-3      Sequence 3, Appli
21   2132.6   98.1   2290   15   US-10-028-072-267    Sequence 267, App
22   2132.6   98.1   2290   15   US-10-121-049-267    Sequence 267, App
23   2132.6   98.1   2290   15   US-10-123-904-267    Sequence 267, App
24   2132.6   98.1   2290   15   US-10-140-470-267    Sequence 267, App
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29   2132.6   98.1   2290   15   US-10-066-273-3      Sequence 3, Appli
30   2132.6   98.1   2290   15   US-10-066-494-3      Sequence 3, Appli
31   2132.6   98.1   2290   15   US-10-137-865-267    Sequence 267, App
32   2132.6   98.1   2290   15   US-10-142-431-267    Sequence 267, App
33   2132.6   98.1   2290   15   US-10-140-474-267    Sequence 267, App
34   2132.6   98.1   2290   15   US-10-143-114-267    Sequence 267, App
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37   2132.6   98.1   2290   15   US-10-066-211-3      Sequence 3, Appli
38   2132.6   98.1   2290   15   US-10-066-193-3      Sequence 3, Appli
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40   2132.6   98.1   2290   15   US-10-123-262-267    Sequence 267, App
41   2132.6   98.1   2290   15   US-10-142-423-267    Sequence 267, App
42   2132.6   98.1   2290   15   US-10-121-050-267    Sequence 267, App
43   2132.6   98.1   2290   15   US-10-121-755-267    Sequence 267, App
44   2132.6   98.1   2290   15   US-10-143-032-267    Sequence 267, App
45   2132.6   98.1   2290   15   US-10-123-108-267    Sequence 267, App
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ALIGNMENTS

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US-09-818-143-11
; Sequence 11, Application US/09818143
; Patent No. US2002019000A1
; GENERAL INFORMATION:
;  APPLICANT: Walker, Michael G.
;  APPLICANT: Volkmuth, Wayne
;  APPLICANT: Klingler, Tod M.
;  TITLE OF INVENTION: POLYNUCLEOTIDES COEXPRESSED WITH MATRIX-REMODELING GENES
;  FILE REFERENCE: PB-0004 CIP
;  CURRENT APPLICATION NUMBER: US/09/818,143
;  CURRENT FILING DATE: 2001-03-26
;  NUMBER OF SEQ ID NOS: 23
;  SOFTWARE: PERL Program
; SEQ ID NO 11
;  LENGTH: 2288
;  TYPE: DNA
;  ORGANISM: Homo sapiens
;  FEATURE:
;  OTHER INFORMATION: 2268890CB1
US-09-818-143-11

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  Best Local Similarity   99.4%;
  Matches 2154;  Conservative   0;  Mismatches  13;  Indels  0;  Gaps  0;

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Qy    243 AGGCCCATGGACAGGCCTGCCCGCTGACCGGCCAGGGTGAAGCATGTGAGGAGGCGCGGCCCGG 302
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Qy   2163 AAAAAAA 2169
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APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin

TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C345
CURRENT APPLICATION NUMBER: US/10/147,493
CURRENT FILING DATE: 2002-05-17
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 550

SEQ ID NO 267
LENGTH: 2290
TYPE: DNA
ORGANISM: Homo Sapien
US-10-147-493-267

Query Match   98.1%;   Score 2112.6;   DB 13;   Length 2290;
Best Local Similarity   99.8%;   Pred. No. 0;   Mismatches 4;   Indels 0;   Gaps 0;
Matches 2135;   Conservative 0;   Mismatches 0;

[Sequence alignment data between Query (Qy) and Database (Db) nucleotide sequences, positions 3 through 2135]

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Qy   1863 CCCTCCTGACCCCTCGTTGGGCCATTGTCCAGAGAGCCCACGCTGGGCACAGCAC 1922
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Db   2011 CCCTCCTGACCCTCGTTGGGCCATTGTCCAGAGAGCCCACGCTGGGCACAGCAC 2070

Qy   1923 AAAGAACAAACTCCTCACCAGTTCATCCTGAGGCTGGGAGACCCGGAGATGGTGGATTCTGT 1982
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; Sequence 267, Application US/10145127
; Publication No. US20040033558A1
; GENERAL INFORMATION:
;  APPLICANT: Baker,Kevin P.
;  APPLICANT: Beresini,Maureen
;  APPLICANT: DeForge,Laura
;  APPLICANT: Desnoyers,Luc
;  APPLICANT: Filvaroff,Ellen
;  APPLICANT: Gao,Wei-Qiang
;  APPLICANT: Gerritsen,Mary E.
;  APPLICANT: Goddard,Audrey
;  APPLICANT: Godowski,Paul J.
;  APPLICANT: Gurney,Austin L.
;  APPLICANT: Sherwood,Steven
;  APPLICANT: Stewart,Timothy A.
;  APPLICANT: Smith,Victoria
;  APPLICANT: Tumas,Daniel
;  APPLICANT: Watanabe,Colin K
;  APPLICANT: Wood,William
;  APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330R1C252
; CURRENT APPLICATION NUMBER: US/10/145,127
; CURRENT FILING DATE: 2002-05-13
; PRIOR APPLICATION: Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 267
;  LENGTH: 2290
;  TYPE: DNA
;  ORGANISM: Homo Sapien
US-10-145-127-267

  Query Match       98.1%;  Score 2132.6;  DB 13;  Length 2290;
  Best Local Similarity  99.8%;  Pred. No. 0;
  Matches 2135;  Conservative  0;  Mismatches  4;  Indels  0;  Gaps  0;

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Qy    123 ACCCCTGGCCACCCTGGCCCCGAGGCTCTGCGGGGAGGGACCAGCCTCC 182
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Db    271 ACCCCTGGCCCACCCTGGCCCCGAGGCTCTGCGGGGAGGGACCAGCCAGTG 330

Qy    183 GAGCCCAGTGAGGCAGGGGCGTTGGCAGCCACCGGCGCCGCCTCAAGCCCCTCCAG 242
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    331 GAGCCCAGTGAGGCAGGGGCGCTCGTTGGCAGCCACCGGCGCCGCAAACCCCTCCAG 390

Qy    243 AGGCCCATGGACAGGGCTGCCCGGGTCAGGGCCAGGGTGAAGCATGTGAGGCGCCCCCGG 302
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    391 AGGCCCATGGACAGGGCTGCCCGGGTCAGGGCCAGGGTGAAGCATGTGAGGCGCCCCCGG 450

Qy    303 AGCCAGGCAGGAGGGAAGAGGCTTTCATAGATTCTATTCACAAAGAATAACCACCATTTT 362
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    451 AGCCAGGCAGGAGGGAAGAGGCTTTCATAGATTCTATTCACAAAGAATAACCACCATTTT 510

Qy    363 GCAAAGACCATGAGGGCCACCATGTGGCTGGCTGGTGGCTGCTGGTGGCTGCCATG 422
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Db    511 GCAAGACCATGAGGGCCACCATGTGGCTGGCTGGTGGCTGCTGGTGGCTGCCATG 570

Qy    423 GGAGCTGTTGCAGGGCCAGGAGGACCGGTTTTGAGGGGCCACTGAGGATGCAAGAGAG 482
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    571 GGAGCTGTTGCAGGGCCAGGAGGACCGGTTTTGAGGGGCACTGAGGATGCAAGAGAG 630

Qy    483 TTCATTTACCTTAAACAGGTACAAAGGGGGGGGGGGGAGTCCCAGGACAGAGTGCAACTACACC 542
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    631 TTCATTTACCTTAAACAGGTACAAAGGGGGGGGGGGAGTCCCAGGACAAGTGCAACTACACC 690

Qy    543 TTCATTGTGCCCCACCAGCCGCGGTGTGCATCTCGTCAAACTCCAAGGAGGCCCTGAG 602
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    691 TTCATTGTGCCCCAGCAGCCGCGGTGTGCATCTCGTCAAACTCCAAGGAGGCCCTGAG 750

Qy    603 GTGGCTTCTGGAGAACCGAGTGCAATAAGCAGGAGGTGCTGCTCAACAAATGAGCTGCTC 662
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    751 GTGGCTTCTGGAGAACCGAGTGCATAAGCAGGAGGTGCTGCTCAACAAATGAGCTGCTC 810

Qy    663 AAGCAGAAGCGGGCAGATCGAGACCGCTCGACGCCGCTGGTGGAAGTGGAAGTGGCCATTGTG 722
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    811 AAGCAGAAGCGGGCAGATCGAGACCGCTCGACGCCGCTGGTGGAGGTGGAAGTGGCCATTGTG 870

Qy    723 AGCGAGGTGAAGCTGCTGCGCAAGGAGAGGCCGAACATGAACTCGGCGCCAGCTC 782
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    871 AGCGAGGTGAAGCTGCTGCGCAAGGAGAGGCCGAACATGAACTCGGCGCCAGCTC 930

Qy    783 TACATGCAGCTCCTGCCACGAGATCATCCGCAGGGAGGGGGACCAACGCGTTGGAGTCTCCCAG 842
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    931 TACATGCAGCTCCTGCCACGAGATCATCCGCAGGGAGGGGGACCAACGCGTTGGAGTCTCCCAG 990

Qy    843 CTGGGAGAACAGGATCCTGAACCAGCAGCCGACATGCTGCAGTGGCGTCAGCCAAGCTACAAG 902
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    991 CTGGGAGAACAGGATCCTGAACCAGCAGCCGACATGCTGCAGTGGCGTCAGCCAAGCTACAAG 1050

Qy    903 GACCTGGAGCACAAGTACCAGCACCTGGCCACACTGGCCCACAACAAATCAGAGATCATC 962
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1051 GACCTGGAGCACAAGTACCAGCACCTGGCCACACTGGCCCACAACAAATCAGAGATCATC 1110

Qy    963 GCGCAGCTTGAGGAGCACATGCCAGAGGGTGCCCTCGGCCACCCGTCCCCAGCCACCC 1022
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1111 GCGCAGCTTGAGGAGCACACTGCCAGAGGGTGCCCTCGGCCACCCGTCCCCAGCCACCC 1170

Qy   1023 CCCGCTGCCCCGCCCGGGTTCACCAACCACCACCTACAACCGCATCATCACAGATC 1082
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1171 CCCGCGCTGCCCCGCCCGGGTTCTACCACCACCACCTACAACCGCATCATCACAGATC 1230

Qy   1083 TCTACCAACGAGATCCAGAGTGACCAGAACCTGAAGGTGCTGCCACCCCCCTTGCCCACT 1142
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1231 TCTACCAACGAGATCCAGAGTGACCAGAACCTGAAGGTGCTGCCACCCCCCTTGCCCACT 1290

Qy   1143 ATGCCCACTCACCAGCCTCCCCATCTTCACGGACAAGCCGTCGGGGCCCCATGGAGAGAC 1202
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1143 ATGCCCACTCACCAGCCTCCCCATCTTCACGGACAAGCCGTCGGGGCCCCATGGAGAGAC 1202
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RESULT 4
US-10-160-503-267
Sequence 267, Application US/10160503
; Publication No. US20040035590A1
; GENERAL INFORMATION:

; APPLICANT: Baker,Kevin P.
; APPLICANT: Beresini,Maureen
; APPLICANT: DeForge,Laura
; APPLICANT: Desnoyers,Luc
; APPLICANT: Filvaroff,Ellen
; APPLICANT: Gao,Wei-Qiang
; APPLICANT: Gerritsen,Mary E.
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Gurney,Austin L.
; APPLICANT: Sherwood,Steven
; APPLICANT: Smith,Victoria
; APPLICANT: Stewart,Timothy A.
; APPLICANT: Tumas,Daniel
; APPLICANT: Watanabe,Colin K
; APPLICANT: Wood,William
; APPLICANT: Zhang,Zemin

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330R1C446
; CURRENT APPLICATION NUMBER: US/10/160,503
; CURRENT FILING DATE: 2002-05-30
; NUMBER OF SEQ ID NOS: 550
SEQ ID NO 267
; LENGTH: 2290
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-160-503-267

Query Match   98.1%; Score 2132.6; DB 13; Length 2290;
Best Local Similarity 99.8%;
Matches 2135; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy   3 AAATGAGGCTGCTGCCGGACGCGGCCCTGAGGATGAACCCAAGCCCTGGCAGGGTG   62
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   151 AAATGAGGCTGCTGCCGGACGCGGCCCTGAGGATGAACCCAAGCCCTGGCAGGGTG 210

Qy   63 GCACTGAGGCACGGCGGCTGACGCTACTGTGAGGGAAAGAAGGTTGTGGACGAGCC 122
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   211 GCACTGAGGCACGGCGGCTGACGCTACTCTGAGGGAAAGAAGGTTGTGGACGAGCC 270

Qy   123 ACCCCTGGCCACCGCCCTGGGCCCTGGGCTGCTTCCTGCGCGAGCCCCTCTGTGGA 182
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   271 ACCCCTGGCCACCGCCCTGGGCCCTGGGCTGCTTCCTGCGCGAGCCCCTCTGTGGA 330

Qy   183 GAGCCCAGTGAGGCACGGGCTCTCTTGGCCAGCCACCGGCCTGCAACTCAGGAAC   242
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   331 GAGCCCAGTGAGGCACGGGCTCTCTTGGCCAGCCACCGGCCTGCAACTCAGGAAC   390

Qy   243 AGGCCATGGACAGGCGCTGCCCCGCTGACGGCGCAGGGTGAAGCAGTGAGGAGCC 302
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   391 AGGCCATGGACAGGCTGCCCCGCTGACGGCGCCAGGGTGAAGCAGTGAGGAGCC   450

Qy   303 AGCCAAGCAGAGGGAAGAGGCTTTCATAGATTCTATTCACAAAGATTAACCACAT 362
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   451 AGCCAAGCAGAGGGAAGAGGCTTTCATAGATTCTATTCACAAAGATTAACCACATTTT 510

Qy   363 GCAAAGACCATCAGGCGCCACTGTTGCGTCACATGCTGGTCGGACTGCTGGCTGCCATG 422
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   511 GCAAGGACCATCAGGCGCCACTGTTGCGTCACATGCTGGTCGGACTGCTGGCTGCCATG 570

Qy   423 GGAGCTGTTGCAGGCGCCAGGGACCAGGGCGGGCTCCAAGAGG   482
            |||||||||||||||||||||||||||||||||||||||
Db   571 GGAGCTGTTGCAGGCGCCAGGGACCAGGGTTTTGAGGGGCTCGCCAAGAGG   630

Qy   483 TTCATTTACCTAAACAGGTACAAGCGGGGGCGGGGAGTCCCAGGACAAGTGACCTACACC 542
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Db   631 TTCATTTACCTAAACAGGTACAAGCGGGGGCGGGGAGTCCCAGGACAAGTGACCTACACC 690

Qy   543 TTCATTGTGCCCCAGCAGCGGGGTCACGGGTGCCCATCTGCGTCAACTCCAAGGAGGCCTGAG 602
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   691 TTCATTGTGCCCCAGCAGCGGGGTCAGGGGTGCCCATCTGCGTCAACTCCAAGGAGGCCTGAG 750

Db   1291 ATGCCCACTCTCACCAAGCCTCCCAICTTCCACCGACAAGCCGTCGGGCCCCATGGGAGAGAC 1350
            |||||||||||||||||| |||||||||||| ||||||||||||||||||||||||||||||
Qy   1203 TGCCTGCAGCCCCTGGAGATGGGCCACGAGCCAGCCACACGGACCTCCATCCATCGAGAAGGG 1262

Db   1351 TGCCTGCAGCCCCTGGAGGATGGGCCACGACACCACCAGCTCAICTACCTGGTGAACCCGGAG 1410
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Qy   1263 AACACCACCGCCTCACTGCAGGTTGTGGTGCCACCAGAGACACCGACCCCCGGGGGCTGGACC 1322

Db   1411 AACACCAACCGCCTTCATGCAGGTGTTGGTGCCGACACCAGAGACACCGACCCCCGGGGGCTGGACC 1470
            |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1323 GTCATCCAGAGACGCCCTGGATGGCTCGTCTGTTAACTTCTTCAGGAATGGGGAGGACGTACAAG 1382

Db   1471 GTCATCCAGAGACGCCCTGGATGGCTCTGTTAACTTCTTCAGGAATGGGGAGGACGTACAAG 1530
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1383 CAAGGGTTTGGGAACATTGACGGGGGAAATACTGGCGTGGGCTGGGGGCTGAGAGAACATTTACTGGGCTG 1442

Db   1531 CAAGGGTTTGGGAACATTGACGGGCGGGAAATACTGGCGTGGGCTGGGGGCTGAGAGAACATTTACTGGGCTG 1590
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1443 ACGAACCAAGGCAACTACACAAACTCCTGGTTGTACACAGAGAAGAGACTGGTCCGGCGCCCAAAGTC 1502

Db   1591 ACGAACCAAGGCAACTACAAACTCCTGGTTGTACACAGAGAAGAGACTGGTCCGGCGCCCAAAGTC 1650
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1503 TTTGCAGAATACCCCAGTTTCCCCTGGAACCTGAGAGAGCGGAGTATTATTAAGTCTGCGGCTG 1562

Db   1651 TTTGCAGAATACCCCAGTTTCCGGCCTGAACCTGAGGCGGAGTATTATTAAGTCTGCGGCTG 1710
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Qy   1563 GGGCGGCTACCATGGGCAATGCGGGTGAACTGCTTTTACARTGGCACAACGGGGCAAGCAGTTCACC 1622

Db   1711 GGGCGGCTACCATGGGCAATGCGGGTGAACTGCTTTTACARTGGCACAACGGGGCAAGCAGTTCACC 1770
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1623 ACCCTGGACAGAGGATCATGAGTGTCTACACGGGAAACTGTGCCCACTACCACAGAGAAGGGAGGC 1682

Db   1771 ACCCTGGACAGAGGATCATGAGTGTCTACACAGGAAACTGTGCCCACTACACAGAGAAGGGAGGC 1830
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1683 TGGTGGTTATAAGCCCTGTGCCCACTCAACCTCAACGGGTTGGTACGGCGGGGTACCGGGCCCAT 1742

Db   1831 TGGTGGTTATAAGCCCTGTGCCCACTCAACCTCAACGGGTTGGTACGGCGGGGTACCGGGCCCAT 1890
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1743 TACCGGACGGACCGGTACTCACCGAGAACGGGAGTTTCGATCTGAGTTCGAGGAGGCCTCTTACTCA 1802

Db   1891 TACCGGACGGACCGGTACTCACCGAGAACGGGAGTTTCGAGTTCGAGGAGGCCTCTTACTCA 1950
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1803 CTCAAGGAAAGTGGTGATGATGATGACCGGAGACGGGAGTGTTACTGGGCTGGGGCTCGACTGCTCC 1862

Db   1951 CTCAAGGAAAGTGGTGATGATGATGACCGGAGACGGGAGTGTTACTGGGCTGGGGCTCGACTGCTCC 2010
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1863 CCCTCCTCGACCTCTCGTGGCCATTGCCAGGAGCCACCCACCCTGGTCATCGGCCTGGCCCACAGCAC 1922

Db   2011 CCCTCCTCGACCTCTCGTGGCCATTGCCAGGAGCCACCCACCCTGGTCATCGGCCTGGCCCACAGCAC 2070
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1923 AAAGAACAACTCCTCACCAGTTCATCCTGAGGCTGGGAGGACCGGGGATGCTGGATTCTGT 1982

Db   2071 AAAGAACAACTCCTCACCAGTTCATCCTGAGGCTGGGAGGACCGGGGATGCTGGATTCTGT 2130
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1983 TTTCCGGAAGTCACTGCAGCCGAGTGAAGTCAGTATCAGTAGCATCGTGTTTTCTGTCCCTCC 2042

Db   2131 TTTCCGGAAGTCACTGCAGCCGAGTGAAGTCAGTATCAGTAGCATCGTGTTTTCTGTCCCTCC 2190
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   2043 TACTTTCCTTCACCAGACACCCCTTCATGTCTCAGGACACGAGGACAGGGACTACACAGACAA 2102

Db   2191 TACTTTCCTTCACCAGACACCCCTTCATGTCTCAGGACACGAGGACAGGGACTACACAGACAA 2250
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   2103 CTCTTTCTTTAAATAAATTAAGTCTCTACAATAAAAACA 2141

Db   2251 CTCTTTCTTTAAATAAATTAAGTCTCTACAATAAAAAAA 2289

Qy 603 GTGCTTCTTGGGAGAACCGAGTGCATAAGGCAGGTAGAGAGGTAGAGCTAGAGCTGCTC 662
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 751 GTGCTTCTTGGGAGAACCGAGTGCATAAGGCAGGTAGAGAGGTAGAGCTGCTCAACACAATGAGCTGCTC 810

Qy 663 AAGCAGAAGCGGCGAGATCGGACGCTCGAGCAGCTCGGTGGAGTGGACGGGCGCATTGTG 722
Db 811 AAGCAGAAGCGGCGAGATCGGACGCTCGAGCAGCTCGGTGGAGTGGACGGGCGGCATTGTG 870

Qy 723 AGGGAGGTGAAGCTGCTGCGCAAGGAGCAGCCCAAACATGAACTCGGGGGTTCACGCAGCTC 782
Db 871 AGGGAGGTGAAGCTGCTGCGCAAGGAGCAGCCCAAACATGAACTCGGGGGTTCACGCAGCTC 930

Qy 783 TACATGCAGCTCCTGCACGGAGATCATCGGCAAGCGGCGCAAGCGGGCAGGGGGTTGGGAGCTC 842
Db 931 TACATGCAGCTCCTGCACGGAGATCATCGGCAAGCGGCGCAAGCGGGCAGGGGGTTGGGAGCTC 990

Qy 843 CTGGAGAACAGGATCCTGAACAGAGACAGCGGCAGCGACGGACAAGTAGCAGGTACAAG 902
Db 991 CTGGAGAACAGGATCCTGAACAGAGACAGCGGCAGCGACGGACAAGTAGCAGGTACAAG 1050

Qy 903 GACCTGGAGCACAAGTACCAGCACACCTGGCCCACCTGGGCCCACAAACCAATCAGGATCATC 962
Db 1051 GACCTGGAGCACAAGTACCAGCACACCTGGCCCACCTGGGCCCACAAACCAATCAGGATCATC 1110

Qy 963 GCCGAGCTTGAGGAGCACAGCTGCCAGAGGCCGGGTGCCCTCGGCGGGCCGGTGTCCCAGCCACCC 1022
Db 1111 GCCGAGCTTGAGGAGCACAGCTGCCAGAGGCCGGGTGCCCTCGGCGGGCCGGTGTCCCAGCCACCC 1170

Qy 1023 CCCGCTGCCCCGCGCCCGGGGTCTACCAAACCGCAGTCATCAAACCAGATC 1082
Db 1171 CCCGCTGCCCCGCGCCCGGGGTCTACCAAACCGCAGTCATCAAACCAGATC 1230

Db 1231 TCTACCAACGAGATCCAGAGTGACGAGAACCTGAAAGGTGCTCCCACCCCTCTGCCCACT 1290

Qy 1083 TCTACCAACGAGATCCAGAGTGACGAGAACCTGAAAGGTTGCTGCCACCCCTCTGCCCACT 1142

Qy 1143 ATGCCCACTCTCACCAGCCTCCCATCTTCCACCGACAAGCCGTGGGCCCCCATGGAGAGAC 1202
Db 1291 ATGCCCACTCTCACCAGCCTCCCATCTTCCACCGACAAGCCGTGGGCCCCCATGGAGAGAC 1350

Qy 1203 TGCCCTGCAGGCCCTGGACGATGGCCCAGACTCCATCTACCTGGTGAAGCCGGAG 1262
Db 1351 TGCCCTGCAGGCCCTGGACGATGGCCCAGACTCCATCTACCTGGTGAAGCCGGAG 1410

Qy 1263 AACACCAACCGCCTCATGCAAGGGTGTGGTGCGGACCACCACCCCGGGGGGCTGGACC 1322
Db 1411 AACACCAACCGCCTCATGCAAGGGTGTGGTGCGGACCACCACCCCGGGGGGCTGGACC 1470

Qy 1323 GTCATCCAGAGACGGCTGGATGGCTCGTTAACTTCTTCAGGAACTGGGAGACGGTACAAG 1382
Db 1471 GTCATCCAGAGACGGCTGGATGGCTCGTTAACTTCTTCAGGAACTGGGAGACGGTACAAG 1530

Db 1531 CAAGGGTTTGGGAACATTGACGGGCGGCGAAATACTGGCCTGCGTGGGCCTGGAGAAACATTTACTGGCTG 1590

Qy 1383 CAAGGGTTTGGGAACATTGACGGGCGGGAAATACTGGCGTGGGCCTGGAGAAACATTTACTGGCTG 1442

Qy 1443 ACGAACCAAGGCACTACAAAACTCCTGGTTGACCATGGAGGACTGGGTCCGGCCCGCAAAGTC 1502
Db 1591 ACGAACCAAGGCACTACAAAACTCCTGGTTGACCATGGAGGACTGGGTCCGGCCCGCAAAGTC 1650

Qy 1503 TTTGCAGAATACGCCAGTTTCCGCCTGGAACCTGAGACGGGTATTATAAGCTGCGGGTG 1562
Db 1651 TTTGCAGAATACGCCAGTTTCCGCCTGGAACCTGAGACGGGTATTATAAGCTGCGGGTG 1710

Qy 1563 GGGGCGCCTACCATGGCAATGGGGGTGACTCTTTTACATGCCACAACGGGCAAGCAGTTCACC 1622
Db 1711 GGGGCGCCTACCATGGCAATGGGGGTGACTCTTTTACATGCCACAACGGGCAAGCAGTTCACC 1770

Qy 1623 ACCCTTGGACAGAGATCATGAGTGCTTCTACAGGAGAAAACTGTTGCCACTACCAGAGAGGAGC 1682
Db 1771 ACCCTTGGACAGAGATCATGAGTGCTTCTACAGGAGAAAACTGTTGCCACTACCAGAGAGGAGC 1830

Qy 1683 TGGTGGTATAACGCCTGTGCCCACTCAACGGGGTCTGGTACCGGGGGGGCCAT 1742
Db 1831 TGGTGGTATAACGCCTGTGCCCACTCAACGGGGTCTGGTACCGGGGGGGCCAT 1890

Db 1743 TACCGGAGCCCGCCTACCAGGGACGGAGTCTACTGGGGTTCCGAGGAGGCTCTTACTCA 1802

Db 1891 TACCGGAGCCCGCCTACCAGGGACGGAGTCTACTGGGGTTCCGAGGAGGCTCTTACTCA 1950

Db 1803 CTCAAGAAAGTGGTGATGATGATCCGACCGGAAGCCCCAACCACCTTCCACTAAGCCAGCTCC 1862

Db 1951 CTCAAGAAAGTGGTGATGATGATCCGACCGGAAGCCCCAACCACCTTCCACTAAGCCAGCTCC 2010

Db 1863 CCCTCCTGACCCTCTCGGTTGCCGGCCATTGCCAGGAGCCGCCACCCCTGGGTCACGGCTGGCCACGAGCAC 1922

Db 2011 CCCTCCTGACCCTCTCGGTTGCCGGCCATTGCCAGGAGCCGCCACCCCTGGGTCACGGCTGGCCACGAGCAC 2070

Qy 1923 AAAGAACAACTCCTCACCAGTTCATCCTGAGGCTGGAGGCCCACCCCTGGGTGACGCTGGCCACGAGCAC 1982

Db 2071 AAAGAACAACTCCTCACCAGTTCATCCTGAGGCTGGAGGCCCACCCCTGGGTGACGCTGGCCACGAGCAC 2130

Qy 1983 TTTCCGAAGTCACTCGCAGCGGATGAATGGAACTGAATCGAATGGACGGCTGGGAGGGATTCTGT 2042

Db 2131 TTTCCGAAGTCACTCGCAGCGGATGAATGGAACTGAATCGAATGGACGGCTGGGAGGGATTCTGT 2190

Qy 2043 TACTTTCCTTCACACCAGACAGCAGCCCCTCATGTCTCCAGGACAGGAGGACTACAGACAA 2102

Db 2191 TACTTTCCTTCACACCAGACAGCAGCCCCTCATGTCTCCAGGACAGGAGGACTACAGACAA 2250

Qy 2103 CTCTTTCTTTAAATAAAATTAAGTCTCTACAAATAAAAACA 2141

Db 2251 CTCTTTCTTTAAATAAAATTAAGTCTCTACAATAAAAAAA 2289

Query Match   98.1%; Score 2132.6; DB 13; Length 2290;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 2135; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 3 AAATGAGGCTGCTGTGCGGGATGAACCCAAGCCCTGGACCTGCGAGGGTG 62

Publication No. US20040038336A1

GENERAL INFORMATION:

APPLICANT: Baker,Kevin P.
APPLICANT: Beresini,Maureen
APPLICANT: DeForge,Laura
APPLICANT: Desnoyers,Luc
APPLICANT: Filvaroff,Ellen
APPLICANT: Gao,Wei-Qiang
APPLICANT: Gerritsen,Mary E.
APPLICANT: Goddard,Audrey
APPLICANT: Godowski,Paul J.
APPLICANT: Gurney,Austin L.
APPLICANT: Sherwood,Steven
APPLICANT: Smith,Victoria
APPLICANT: Stewart,Timothy A.
APPLICANT: Tumas,Daniel
APPLICANT: Watanabe,Colin K
APPLICANT: Wood,William
APPLICANT: Zhang,Zemin

TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME

SEQ ID NO 267
LENGTH: 2290
TYPE: DNA
ORGANISM: Homo Sapien
US-10-144-993-267

Query Match   98.1%;   Score 2132.6;   DB 13;   Length 2290;
Best Local Similarity   99.8%;   Pred. No. 0;
Matches 2135;   Conservative 0;   Mismatches 4;   Indels 0;   Gaps 0;

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Qy      3 AAATGAGGAGGCTGCTTCCGGACGGGCCTTGAGGATGAACCCAAGCCCTTGGGACCTGAGG      62
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    151 AAATGAGGAGGCTGCTTCCGGACGGGCCTTGAGGATGAACCCAAGCCCTTGGGACCTGAGG     210

Qy     63 GCACTGAGGCGAGCGCGGCTGACGCTACTGTGTGAGGAAAAGAAGGTTGTGACGAGCCAGG     122
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    211 GCACTGAGGCGAGCGCGGCTGACGCTACTGTGTGAGGAAAAGAAGGTTGTGACGAGCCAGG     270

Qy    123 ACCCCTGGCCGCCAGCCCTGGCCCCCAGCCCTTCGTGGGAGGCAAGCCAGTG     182
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    271 ACCCCTGGCCGCCAGCCCTGGCCCCCAGCCCTTCGTGGGAGGCAAGCCAGTG     330

Qy    183 GAGCCCAGTGAGCGCAGGGGTGCTTGGCAGCCCACGCGGCCCTGCAACTCAGGAACCCCTTCCAG     242
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    331 GAGCCCAGTGAGCGCAGGGGCTGCTTGGCAGCCCACGCGGCCCTGCAACTCAGGAACCCCTTCCAG     390

Qy    243 AGGCCCATGGACAGGCGTGCCCCGCTGACGGCCAGGGTGAAGCATGTGACGAGCCGCCGG     302
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    391 AGGCCCATGGACAGGCGTGCCCCGCTGACGGCCAGGGTGAAGCATGTGACGAGCCGCCGG     450

Qy    303 AGCCAAGCAGGAGGGAAGAGGCTTTCATAGATTCTATTCACAAAAGAATAACCACCATTTT     362
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    451 AGCCAAGCAGGAGGGAAGAGGCTTTCATAGATTCTATTCACAAAAGAATAACCACCATTTT     510

Qy    363 GCAAAGACCATGAGCCCACTGTGTGCCGTGACATGCTGGTGGTCCGCGAAAGTC     422
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Db    511 GCAAGGACCATGAGCCCACTGTGTGCCGTGACATGCTGGTGGTCCGCGAAAGTC     570

Qy    423 GGAGCTGTTGCAGGCGCAGGAGGACCCTTTGAGGGGCTCGCCCAAGAGAG     482
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db    571 GGAGCTGTTGCAGGCGCAGGAGGACGCTTTGAGGGGCTCGCCCAAGAGAG     630

Qy    483 TTCATTTACCTAAACACAGGTACAAAGCGGGGGGGGGGGAGTCCCAGGACACAAGTGCACCTACACC     542
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    631 TTCATTTACCTAAACAGGTACAAGCGGGGGGGGGAGTCCCAGGACAAGTGCACCTACACC     690

Qy    543 TTCAATGTGCCCCAGCAGCGGGGTGCCATCCTGCGTCAACTCCAAGGAGCCCTACAGC     602
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    631 TTCAATTTACCTAAACAGGTACAAGCGGGGGGGGGAGTCCCAGGACAAGTGCACCTACACC     690
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Db    691 TTCATTGTTGCCCCAGCAGCGGGGTGCCATCCTGCGTCAACTCCAAGGAGCCCTGAG     750

Qy    603 GTGCTTCTTGGAGAATCCGGAGTGCAAGCAGGAGGCTGCTTCAACCTTCCAAGCTCTC     662
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    751 GTGCTTCTTGGAGAATCCGGAGTGCAAGCAGGAGGCTGCTTCAACCTTCCAAGCTCTC     810

Qy    663 AAGCAGGAAAGCGGGCAGAATCGAGACGCTGCAGCAGGAGCTTGAAGGCGGCATTGTG     722
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    811 AAGCAGGAAAGCGGGCAGAATCGAGACGCTGCAGCAGGAGCTTGAAGGCGGCATTGTG     870

Qy    723 ACGGAGGTGAAGCTGCTCCGCAAGGAAGAGCAGGCCCCAACATGAACTCGCAGCAGCTC     782
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    871 ACGGAGGTGAAGCTGCTCCGCAAGGAAGAGCAGGCCCCAACATGAACTCGCAGCAGCTC     930

Qy    783 TACATGCAGCTCCTGCACGAGATCATCCGCAAGGGGGAGCAACACGCGTTGGAGCTTCTCCCAG     842
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    931 TACATGCAGCTCCTGCACGAGATCATCCGCAAGGGGGAGCAACACGCGTTGGAGCTTCTCCCAG     990

Qy    843 CTTGGAGAACAGGATTCCTGAACCAGACCAGCCGACATGCTGCAGCTGGCCAGCAAGTACAAG     902
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    991 CTTGGAGAACAGGATTCCTGAACCAGACCAGCCGACATGCTGCAGCTGGCCAGCAAGTACAAG     1050

Qy    903 GACCTGGAGCACAAGTACCAGCACCTGCCCACACTGGCCCAAACCAATCAGATCATC     962
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1051 GACCTGGAGCACAAGTACCAGCACCTGCCCACACTGGCCCAAACCAATCAGATCATC     1110

Qy    963 GCGCAGCTTGAGGAGCACTGCCAGGAGGTGCCCTCGCCCAGGCCCCAGCCACCC     1022
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1111 GCGCAGCTTGAGGAGCACTGCCAGGAGGTGCCCTCGCCCAGGCCCCAGCCACCC     1170

Qy   1023 CCGGCTTGCCCCGCCCGGGTCTTACCACCACCACTTACAACAGATC     1082
          ||||||||||||||||||||||||||||||||||||||||||||||
Db   1171 CCCGGCTGCCCCGCCCGGGTTCTTACCACCACTTACAACAGATC     1230

Qy   1083 TCTACCAACGAGATCCAGAGTGACCAGAAACCTGAAGGTGCTGCCCACCCCCTTCCCCACT     1142
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1231 TCTACCAACGAGATCCAGAGTGACCAGAAACCTGAAGGTGCTGCCCACCCCCTTCCCCACT     1290

Qy   1143 ATGCCCACTCTCACCAGCCTCCCAATCTTCACCGACAAGCGGTCGGGCCAGGAGGAGAC     1202
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1291 ATGCCCACTCTCACCAGCCTCCCAATCTTCACCGACAAGCGGTCGGGCCATGGAGGAGAC     1350

Qy   1203 TGCCTGCAGCGCCCTGGAGGATGCCACAGACACCAGTCCATCTACCTTGGTGAAGCCGGAG     1262
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1351 TGCCTGCAGCGCCCTGGAGGATGGCCACAGACACCAGTCCATCTACCTTGGTGAAGCCGGAG     1410

Qy   1263 AACACCAACCGCCTCATGCAGTGTGGTCGGACCACAGACACAGACACC     1322
          ||||||||||||||||||||||||||||||||||||||||||||||||
Db   1411 AACACCAACCGCCTCATGCAGTGTGGTCGGACCACAGACACAGACACC     1470

Qy   1323 GTCAATCCAGAGACGCCCTGGATGGCTGTTAACTTCTTCAGGAGACACAGTACAAG     1382
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1471 GTCATCCAGAGACGCCTGGATGGCTGTTAACTTCTTCAGGAGACACGTACAAG     1530

Qy   1383 CAAGGGTTTGGGAACATTGACGGGAATACTGGGCCTGGAGAACATTTACTCGGCTG     1442
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1531 CAAGGGTTTGGGAACATTGACGGGAATACTGGGCCTGGAGAACATTTACTCGGCTG     1590

Qy   1443 ACGAACCAAGGCAACTACAAACTCCTGGGTGACCATGGAGGACCGTCCGGCCAAAGTC     1502
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1591 ACGAACCAAGGCAACTACAAACTCCTGGGTGACCATGGAGGACGTCCGGCCAAAGTC     1650

Qy   1503 TTTGCAGAATACCCACAGTTTCCGCCTGAGCCTGAGCAGGAGTCGGGCTG     1562
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1651 TTTGCAGAATACCCACAGTTTCCGCCTGGGAACCTGAGCCTGGGCTG     1710

Qy   1563 GGGCGCGCTACCATGGCAATGGCGGTGACTCCTTTACACATGGCAACGGCAGTTCACC     1622
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1711 GGGCGCGCTACCATGGCAATGGCGGTGACTCCTTTACACATGGCAACGGCAGTTCACC     1770

Qy   1623 ACCCTGGACAGGAGATCATGAGTTCTACACAGGAAACTGTGCCCACTACCGAAAGGGAGGC     1682
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db  1771 ACCCTGGACGAGAGATCATGATGTCTACACAGGAAACTGTGCCCACTACCAGAAGGAGGC 1830
Qy  1683 TGGTGGTATAAACGCCTGTGTGCCCACTCCAACCTCAAACCGGGTTCTTGGTACCGGGCCCAT 1742
Db  1831 TGGTGGTATAACGCCTGTGCCCACTCCAACCTCAAACGGGGTTGGTACCGGGCGGGGGGCCAT 1890
Qy  1743 TACCGGAGCCGCTACCAGGAGGAGGAGTCTTACTGGGCTGAGTTCGGAGGAGGCTTCTTACTCA 1802
Db  1891 TACCGGAGCCGCTACCAGGACGGAGTCTTACTGGGGTGAGTTCCGGAGGAGGCTCTTACTCA 1950
Qy  1803 CTCAAGAAAGTGGTGATGATGATGATCCGACCGAACCCCACACCCTTCCACTAAGCCAGCTCC 1862
Db  1951 CTCAAGAAAGTGGTGATGATGATCCGACCGAACCCCACACCCTTCCACTAAGCCAGCTCC 2010
Qy  1863 CCCTCCCTGACCCTCCGTGGCCATTGCCAGGAGCCCACCCCCCTGGTCACCCTGGGCCACACGAC 1922
Db  2011 CCCTCCCTGACCCTCCGTGGCCATTGCCAGGAGCCCACCCCCCTGGTCACCCTGGGCCACACGAC 2070
Qy  1923 AAAGAACAACTCCTCACCCAGTTCATCCTCTGAGGCTGGGGGAGGACCGGGGATTGGGATTCTGT 1982
Db  2071 AAAGAACAACTCCTCACCCAGTTCATCCTCTGAGGCTGGGGGAGGACCGGGGATTGGGATTCTGT 2130
Qy  1983 TTTCCGGAAGTCACTGCACCGCGGATGGAACTGAAATCGAATCAGGTGTTTTTCTGTCCCTCC 2042
Db  2131 TTTCCGGAAGTCACTGCACCGCGGATGGAACTGAAATCGAATCAGGTGTTTTTCTGTCCCTCC 2190
Qy  2043 TACTTTCCTTCACACCAGACAGCAGCCCCTCCATGTCTCCAGGACACAGGACACTACAGACAA 2102
Db  2191 TACTTTCCTTCACACCAGACAGCAGCCCCTCATGTCTCCAGGACAGGACACTACAGACAA 2250
Qy  2103 CTCTTTCTTTAATATAAAATTAAGTCTCTACAATTAAAAAACA 2141
Db  2251 CTCTTTCTTTAATATAAAATTAAGTCTCTACAATTAAAAAAA 2289
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Query Match      98.1%;  Score 2132.6;  DB 13;  Length 2290;
Best Local Similarity   99.8%;  Pred. No. 0;
Matches 2135;  Conservative   0;  Mismatches   4;  Indels   0;  Gaps   0;

Qy     3 AAATGAGGCTGCTGCGGAGCGGGGCCTGAGGATGAACCCCAAAGCCTGGAGCCTGCCGAGGGTG 62
Db    151 AAATGAGGCTGCTGCGGACGGGGGCCTGAGGATGAACCCCAAAGCCTGGAGCCTGCCGAGGGTG 210
Qy    63 GCACTGAGGCAGCGGGGCGTTGCGTCACGTCTACTGTGAGGGAAAGAAAGGTTGTGAGCACATG 122
Db    211 GCACTGAGGCAGCGGGGCGTTGCGTCACGTCTACTGTGAGGGAAAGAAAGGTTGTGAGCACATG 270
Qy   123 ACCCCTGGCCCAGCCCTGCCCCAGCCCTTCTGCGGGAGCCCTGTGTGGAGGACAGACCCAGTG 182
Db   271 ACCCCTGGCCCAGCCCTGCCCCAGCCCTTCTGCGGGAGCCCTGTGTGGAGGACAGACCCAGTG 330
Qy   183 GAGCCCAGTGAGGCAGAGGGGCTGCTTGCCAGCCACCGGCCTGCAACTCAGGAACCCCTTCAG 242
Db   331 GAGCCCAGTGAGGCAGAGGGGCTGCTTGCCAGCCACCGGCCTGCAACTCAGGAACCCCTTCAG 390
Qy   243 AGGCCATGGACAGGGCTGCCCCGGCTCAGCGCCAGGGTTGAGCAGCATGTGAGGAGCCCCCGG 302
Db   391 AGGCCATGGACAGGGCTGCCCCGGCTCAGCGCCAGGGTCCATCTGCGGTCAACTCCAAGACCTG 450
Qy   303 AGCCAAGCCAGGCGAAGAGGGCGTTCATTAGGATTCTATTCACAAAAGAATTAACCACCATTT 362
Db   451 AGCCAAGCCAGGCGAAGAGGGCTTCATTAGGATTCTATTCACAAAAGAATTAACCACCATTT 510
Qy   363 GCAAAGACCATGAGGCCCACTGTTGCGTCACATGCTGGTGGCCTGGCTGGCCTGCCATG 422
Db   511 GCAAGGACCATGAGGCCCACTGTTGCGTCACATGCTGGTGGCCTGGCTGGCCTGCCATG 570
Qy   423 GGAGCTGTTGCAGGCCCAGGAGGACGGTTTGTTGAGGGCCACTGAGGGCTCCCCACAGAG 482
Db   571 GGAGCTGTTGCAGGCCCAGGAGGACGGTTTGTTGAGGGCCACTGAGGGCTCCCCAAGAGAG 630
Qy   483 TTCATTTACCTTAAACAGGTACAAGCCGGGGCGGGGCGGGAGTCCCAGGACAAAGTGACCTACACC 542
Db   631 TTCATTTACCTTAAACAGGTACAAGCCGGGGCGGGGCGGGAGTCCCAGGACAAAGTGACCTACACC 690
Qy   543 TTCATTGTGCCCAGCAGCCAGGGTGCCATCGGGTCAACTCCAAGGAGCCCTGAG 602
Db   691 TTCATTGTGCCCAGCAGCGGGTGCCATCTCAGGGTCAACTCCAAGGAGCCCTGAG 750
Qy   603 GTGGCTTCTGGAGAACCGAGTGCATAAGCAGCAGAGAGCTGCTCAACAATGAGTGCTC 662
Db   751 GTGGCTTCTGGAGAACCGAGTGCATAAGCAGCAGAGAGCTGCTCAACAATGAGTGCTC 810
Qy   663 AAGCAGAAGCGCAGATCGAGACGCTGCCAGCAGCTGGTGAAGGTGGACGGCGGCCAGTTGTG 722
Db   811 AAGCAGAAGCGCAGATCGAGACGCTGCCAGCAGCTGGTGAAGGTGGACGGCGGCCAGTTG 870
Qy   723 AGCGAGGTGAAGCTGCTGCGCAAAGAGAGACGCACACATGAACTCCGGCGTCACGCAGCTC 782
Db   871 AGCGAGGTGAAGCTGCTGCGCAAAGAGAGACGCCGCAACATGAACTCCGGCGTCACGCAGCTC 930
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Qy          783 TACATGCAGCTCCTGCACGAGATCATCCGCAAGCGGGACAACGCGTTGGAGCTCTCCCAG 842
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          931 TACATGCAGCTCCTGCACGAGATCATCCGCAAGCGGGACAACGCGTTGGAGCTCTCCCAG 990

Qy          843 CTGGAGAACAGGATCCTGAACCAGACAGCCGACATGCTGCAGCTGGCCAGCAAGTACAAG 902
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          991 CTGGAGAACAGGATCCTGAACCAGACAGCCGACATGCTGCAGCTGGCCAGCAAGTACAAG 1050

Qy          903 GACCTGGAGCACAAGTACCAGCACCTGGCCACACTGGCCCACAACCAATCAGAGATCATC 962
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1051 GACCTGGAGCACAAGTACCAGCACCTGGCCACACTGGCCCACAACCAATCAGAGATCATC 1110

Qy          963 GCGCAGCTTGAGGAGCACTGCCAGAGGGTGCCCTCGGCCAGGCCCGTCCCCCAGCCACCC 1022
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1111 GCGCAGCTTGAGGAGCACTGCCAGAGGGTGCCCTCGGCCAGGCCCGTCCCCCAGCCACCC 1170

Qy         1023 CCCGCTGCCCCGCCCCGGGTCTACCAACCACCCACCTACAACCGCATCATCAACCAGATC 1082
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1171 CCCGCTGCCCCGCCCCGGGTCTACCAACCACCCACCTACAACCGCATCATCAACCAGATC 1230

Qy         1083 TCTACCAACGAGATCCAGAGTGACCAGAACCTGAAGGTGCTGCCACCCCCTCTGCCCACT 1142
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1231 TCTACCAACGAGATCCAGAGTGACCAGAACCTGAAGGTGCTGCCACCCCCTCTGCCCACT 1290

Qy         1143 ATGCCCACTCTCACCAGCCTCCCATCTTCCACCGACAAGCCGTCGGGCCCATGGAGAGAC 1202
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1291 ATGCCCACTCTCACCAGCCTCCCATCTTCCACCGACAAGCCGTCGGGCCCATGGAGAGAC 1350

Qy         1203 TGCCTGCAGGCCCTGGAGGATGGCCACGACACCAGCTCCATCTACCTGGTGAAGCCGGAG 1262
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1351 TGCCTGCAGGCCCTGGAGGATGGCCACGACACCAGCTCCATCTACCTGGTGAAGCCGGAG 1410

Qy         1263 AACACCAACCGCCTCATGCAGGTGTGGTGCGACCAGAGACACGACCCCGGGGGCTGGACC 1322
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1411 AACACCAACCGCCTCATGCAGGTGTGGTGCGACCAGAGACACGACCCCGGGGGCTGGACC 1470

Qy         1323 GTCATCCAGAGACGCCTGGATGGCTCTGTTAACTTCTTCAGGAACTGGGAGACGTACAAG 1382
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1471 GTCATCCAGAGACGCCTGGATGGCTCTGTTAACTTCTTCAGGAACTGGGAGACGTACAAG 1530

Qy         1383 CAAGGGTTTGGGAACATTGACGGCGAATACTGGCTGGGCCTGGAGAACATTTACTGGCTG 1442
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1531 CAAGGGTTTGGGAACATTGACGGCGAATACTGGCTGGGCCTGGAGAACATTTACTGGCTG 1590

Qy         1443 ACGAACCAAGGCAACTACAAACTCCTGGTGACCATGGAGGACTGGTCCGGCCGCAAAGTC 1502
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1591 ACGAACCAAGGCAACTACAAACTCCTGGTGACCATGGAGGACTGGTCCGGCCGCAAAGTC 1650

Qy         1503 TTTGCAGAATACGCCAGTTTCCGCCTGGAACCTGAGAGCGAGTATTATAAGCTGCGGCTG 1562
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1651 TTTGCAGAATACGCCAGTTTCCGCCTGGAACCTGAGAGCGAGTATTATAAGCTGCGGCTG 1710

Qy         1563 GGGCGCTACCATGGCAATGCGGGTGACTCCTTTACATGGCACAACGGCAAGCAGTTCACC 1622
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1711 GGGCGCTACCATGGCAATGCGGGTGACTCCTTTACATGGCACAACGGCAAGCAGTTCACC 1770

Qy         1623 ACCCTGGACAGAGATCATGATGTCTACACAGGAAACTGTGCCCACTACCAGAAGGGAGGC 1682
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1771 ACCCTGGACAGAGATCATGATGTCTACACAGGAAACTGTGCCCACTACCAGAAGGGAGGC 1830

Qy         1683 TGGTGGTATAACGCCTGTGCCCACTCCAACCTCAACGGGGTCTGGTACCGCGGGGGCCAT 1742
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1831 TGGTGGTATAACGCCTGTGCCCACTCCAACCTCAACGGGGTCTGGTACCGCGGGGGCCAT 1890

Qy         1743 TACCGGAGCCGCTACCAGGACGGAGTCTACTGGGCTGAGTTCCGAGGAGGCTCTTACTCA 1802
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1891 TACCGGAGCCGCTACCAGGACGGAGTCTACTGGGCTGAGTTCCGAGGAGGCTCTTACTCA 1950

Qy         1803 CTCAAGAAAGTGGTGATGATGATCCGACCGAACCCCAACACCTTCCACTAAGCCAGCTCC 1862
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1951 CTCAAGAAAGTGGTGATGATGATCCGACCGAACCCCAACACCTTCCACTAAGCCAGCTCC 2010

Qy         1863 CCCTCCTGACCTCTCGTGGCCATTGCCAGGAGCCCACCCTGGTCACGCTGGCCACAGCAC 1922
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         2011 CCCTCCTGACCTCTCGTGGCCATTGCCAGGAGCCCACCCTGGTCACGCTGGCCACAGCAC 2070

Qy         1923 AAAGAACAACTCCTCACCAGTTCATCCTGAGGCTGGGAGGACCGGGATGCTGGATTCTGT 1982
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         2071 AAAGAACAACTCCTCACCAGTTCATCCTGAGGCTGGGAGGACCGGGATGCTGGATTCTGT 2130

Qy         1983 TTTCCGAAGTCACTGCAGCGGATGATGGAACTGAATCGATACGGTGTTTTCTGTCCCTCC 2042
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         2131 TTTCCGAAGTCACTGCAGCGGATGATGGAACTGAATCGATACGGTGTTTTCTGTCCCTCC 2190

Qy         2043 TACTTTCCTTCACACCAGACAGCCCCTCATGTCTCCAGGACAGGACAGGACTACAGACAA 2102
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         2191 TACTTTCCTTCACACCAGACAGCCCCTCATGTCTCCAGGACAGGACAGGACTACAGACAA 2250

Qy         2103 CTCTTTCTTTAAATAAATTAAGTCTCTACAATAAAAACA 2141
                ||||||||||||||||||||||||||||||||||||| |
Db         2251 CTCTTTCTTTAAATAAATTAAGTCTCTACAATAAAAAAA 2289

RESULT 8
US-10-140-024-267
; Sequence 267, Application US/10140024
; Publication No. US20040058424A1
; GENERAL INFORMATION:
;  APPLICANT: Baker,Kevin P.
;  APPLICANT:  Beresini,Maureen
;  APPLICANT:  DeForge,Laura
;  APPLICANT:  Desnoyers,Luc
;  APPLICANT:  Filvaroff,Ellen
;  APPLICANT:  Gao,Wei-Qiang
;  APPLICANT:  Gerritsen,Mary E.
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Sherwood,Steven
;  APPLICANT:  Smith,Victoria
;  APPLICANT:  Stewart,Timothy A.
;  APPLICANT:  Tumas,Daniel
;  APPLICANT:  Watanabe,Colin K
;  APPLICANT:  Wood,William
;  APPLICANT:  Zhang, Zemin
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P3330R1C69
;  CURRENT APPLICATION NUMBER: US/10/140,024
;  CURRENT FILING DATE:  2002-05-06
;  Prior Application removed - See Palm or File Wrapper
;  NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 267
;   LENGTH: 2290
;   TYPE: DNA
;   ORGANISM: Homo Sapien
US-10-140-024-267

  Query Match             98.1%;  Score 2132.6;  DB 13;  Length 2290;
  Best Local Similarity   99.8%;  Pred. No. 0;
  Matches 2135;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy            3 AAATGAGGCTGCTGCGGACGGCCTGAGGATGAACCCCAAGCCCTGGACCTGCCGAGCGTG 62
                ||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db          151 AAATGAGGCTGCTGCGGACGGCCTGAGGATGGACCCCAAGCCCTGGACCTGCCGAGCGTG 210

Qy           63 GCACTGAGGCAGCGGCTGACGCTACTGTGAGGGAAAGAAGGTTGTGAGCAGCCCCGCAGG 122
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          211 GCACTGAGGCAGCGGCTGACGCTACTGTGAGGGAAAGAAGGTTGTGAGCAGCCCCGCAGG 270

Qy          123 ACCCCTGGCCAGCCCTGGCCCCAGCCTCTGCCGGAGCCCTCTGTGGAGGCAGAGCCAGTG 182
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          271 ACCCCTGGCCAGCCCTGGCCCCAGCCTCTGCCGGAGCCCTCTGTGGAGGCAGAGCCAGTG 330

Qy          183 GAGCCCAGTGAGGCAGGGCTGCTTGGCAGCCACCGGCCTGCAACTCAGGAACCCCTCCAG 242
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C182
CURRENT APPLICATION NUMBER: US/10/140,808
CURRENT FILING DATE: 2002-05-07
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 267
LENGTH: 2290
TYPE: DNA
ORGANISM: Homo Sapien
US-10-140-808-267

Query Match 98.1%; Score 2132.6; DB 13; Length 2290;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 2135; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy   3 AAAATGAGGCTTGCTCCGGACAGGGCCCTGAGGATGAAGACCCCAAGCCTTGGACAGCTG   62
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   151 AAAATGAGGCTTGCTGGGGACGGGCCCTGAGGATGAAGACCCCAAGCCTTGGACAGCTG   210

Qy   63 GCACTGAGGCGAGCGCGGCTGAGCGCTACTGTGAGGGAAAGAAGGTTGTGAGGAGCCCGCAGG   122
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   211 GCACTGAGGCGAGCGCGGCTGAGCGCTACTGTGAGGGAAAGAAGGTTGTGAGGAGCCCCGCAGG   270

Qy   123 ACCCCTGGGCCAGCCCTGGCCCCAGCCTCTTCGCCGGAGCGGCAGGCAGTG   182
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   271 ACCCCTGGGCCAGCCCTGGCCCCAGCCTCTTCGCCGGAGGCGGCAGGCAGTG   330

Qy   183 GAGCCCAGTGAGGCAGGGTTGCTTGGCACGCACGCCTGCAACTCAGGAACCTCCAG   242
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   331 GAGCCCAGTGAGGCAGGGTTGCTTGGCACGCACGCCTGCAACTCAGGAACCTCCAG   390

Qy   243 AGGGCCATGACAGCGGCTGCCCCGGTGACGTGAGCATGTGAGGAGCCCGCAGG   302
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   391 AGGGCCATGACAGCGGCTGCCCCGGTGACGTGAGCATGTGAGGAGCCCGCAGG   450

Qy   303 AGCCAAGACAGCAGGGAGGAAGAGGCTTTCATAGATTCTATTCACAGAGAGAATAAACACACCATTTT   362
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   451 AGCCAAGCACAGGGAGGAAGAGGCTTTCATAGATTCTATTCACAAAGAGAATAAACACCATTTT   510

Qy   363 GCAAGAGACCATGAGGCCCACTGTGCGTGACATGCTGGTCTTGGGTGACTGCTGGGGCTGCCATG   422
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   511 GCAAGGACCACTGTGGGTGACATGCTGGTCTCGGACTGCTGTGGCTGCCATG   570

Qy   423 GGAGCTGTTCCAGGCGGCCAGGCCCGGTTTGAGGCGGCCATGAGCGGCTCGCGGAGAG   482
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   571 GGAGCTGTTTGCAGGCGGCCACTGAGGGGCACGGTTTTGAGGCACTGCTGTGGCTGGGAGTC   630

Qy   483 TTCATTTACCTAAACACAGGGTACAACGGGGTACAAGCTGCAATGGGCGGGGGG   542
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   631 TTCATTTACCTAAACACAGGGTGACAACAAGTGCAACTACACC   690

Qy   543 TTCAATTGTGCCCCAGCAGCAGGGGTCACGGGTGCCATCTGGGTCAACTCAAGGAGCCTGAG   602
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   691 TTCAATTGTGCCCCAGCAGCGGGGTCACGGGTGCCATCTGGGTCAACTCAAGGAGCCTGAG   750

Qy   603 GTGCTTCTCGGAGAACCGAGTGCATAAGACGAGGAGCTGCTCACGATGAGCTGCTC   662
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   751 GTGCTTCTCGGAGAACCGAGTGCATAAGACGAGGAGCTGCTCAACAATGAGCTGCTC   810

Qy   663 AAGAGAAGCGGGCAGATCAGAGACGCTGCAGCGACTTGGTGAAGGTTGGACGGGCGGCCATTGTG   722
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   811 AAGCAGAGAGCGGGCAGATCAGAGACGCTGCAGCAGCTGGTGGAGGTCGACGGGCGGCCATTGTG   870

Qy   723 AGCGAGGGTGAAGCTCTGCCCAAGGAGAGCGCAACAATGAACTGCGGGGTCACGCAGCTC   782
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   871 AGCGGAGGTGAAGCTGCTGTGCGCAAGGAGAGCGCGGCAACATGAACTCGCGGGGTCACGCAGCTC   930

Qy   783 TACATGCACGCTCCTGCACGGAGATCATCCGCAGCGGGCAGCAACGGCTTGGAGCTCTCCCAG   842
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   931 TACATGCAGCTCCTGCACGAGATCATCCGCAGCGGGCAGCAACGGCGTTGGAGCTCTCCCAG   990

Qy   843 CTGGAGAACAGAGATCCTGAACAGCAGCAGCGGCCAGCATGCTGCAGCTGCAGGAAGTACAAG   902
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   991 CTGGAGAACAGAGGATCCTGAACCAGCAGCCGGCGACCAGCATGCTGCAGCTGCAGGAAGTACAAG   1050

Qy   903 GACCTGAGCGACCAAGTACCAGCGACCTGCCCACACTGCCCCAACAGCGACCAATCATCAGACGATC   962
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1051 GACCTGAGCGACACGACTACCAGCACCTGGCCCACACTGCCCCACACAATGACGATCATC   1110

Qy   963 GGGCCAGACTTGAGGAGCACTGCCACAGGGTGCCCTCGCCGCGCCCTCCCCAGGCCACCC   1022
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1111 GGGCCAGACTTGAGGAGCACTGCCACAGGGTGCCCTCGCCGCGCCCTCCCCAGGCCACCC   1170

Qy 1023 CCCGGCTGCCCCCCCCGGGTCTTACCAACCACCCACCTACAAACGCCATCATCAAACCAGATC   1082
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1171 CCCGTCGCCCCCCCCCGGTCTACCAACCACCCACCTACAAACGCCATCATCAAACCAGATC   1230

Qy 1083 TCTACCAACGACGAGTCCAAGAGTGACCAGAAACCTGAAGGTGCTTGCCACCCCCTTGCCCACT   1142
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1231 TCTACCAACGACGAGTCCAAGAGTGACCAGAAACCTGAAGGTGCTTGCCACCCCCTTGCCCACT   1290

Qy 1143 ATGCCCACTCTCACCAGCCTCCCATCTTCCACCGACAAGCCGTCGGGGCCCATGAGGAGAC   1202
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1291 ATGCCCACTCTCACCAGCCTCCCATCTTCCACCGACAAGCCGTCGGGGCCCATGGGGAGAC   1350

Qy 1203 TGCCTGCAGGCCCTGGAGGATGGCCACGAGCACCCAGTCCATTGACGGCCTGGAGAGCCGGAG   1262
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1351 TGCCTGCAGGCCCTGGAGGATGGCCACGAGCACCCAGTTCCATCTGACGGCCCTGGGGAGAGCCGGAG   1410

Qy 1263 AACACCAACCACGCCCTCATGCAGGTGTTGGTGCGGACCACGAGAACAGCACGACCCCCGGGGACC   1322
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1411 AACACCAACCGCCCTCATGCAGGTGTGGTGGCGGACCACGAGGAACAGCACGACCCCGGGGACC   1470

Qy 1323 GTCATCAGAGACGCCTGGATGGCTGTGTTAACTTCTTCAGGAACTGGGAACGTACAAG   1382
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1471 GTCATCAGAGACGCGGTGAGGCTCTTGTTAACTTCTTCAGGAACGGGAACGTACAAG   1530

Qy 1383 CAAGGGGTTTGGGAACATTGACGGCGGAATACTGGCCTGGAGAACACATTACTGGCTG   1442
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1531 CAAGGGTTTGGGAACATTGACGGCGGAATACTGGCCCTGGGAACACATTACTGGCTG   1590

Qy 1443 ACGAACCAAGGCAAACTACAAACTCCTGTGACCAGAACTGGGGTCGCGCAAAGTC   1502
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1591 ACGAACCAAGGCAAACTACAAACTCCTGGTGACCAGGACTGGGTCCGGCGCAAAGTC   1650

Qy 1503 TTTGCCAGAATAGGCCCAGTTTCCGGCCCTGGGAAACCTGGAGCGGAGTGTAATTAAGGTTGCGCGTG   1562
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1651 TTTGCAGAATAGGCCCAGTTTCCGGCCCTGGGAAACCTGAGCGGAGTGTAATTATAAGGTTGCGCGTG   1710

Qy 1563 GGGCGCGTACCATCTGGCCAATGCGGGTGACTCCTTTACACAGGCCAACGCGCAAGCAGTTCACC   1622
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1711 GGGCGCGTACCATCTGGCCAATGCGGGTGACTCCTTTACACAGGCCAACGCGCAAGCAGTTCACC   1770

Qy 1623 ACCCTGGACACAGAGGATCATGAGTCTACACAGGAAACTGTGCCCCACTACCAGAAGGGAGGC   1682
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1771 ACCCTGGACACAGAGATCATGAGTCTCTACACAGGAAACTGTGCCCCACTACCAGAAGGGAGGC   1830

Qy 1683 TGGTGGTTATAACGCCCTGTGCCCACTCCAAACTCCAACGGGGTCTGGTTACCGGGGCCAT   1742
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1831 TGGTGGTTATAACGCCCTTGTGCCCACTCCAAACTCCAACGGGTCTTGGTTACCGGGGCCAT   1890

Qy 1743 TACCGGGAGGCCGCTACCAGGACGGGAGTCACTTTGGGAGTTCCGAGGACGGGCTCTTACTCA   1802
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1891 TACCGGGACCGCTACCAGGACGTCACTTTGGGAGTTCCGAGGACGGGCTCTTACTCA   1950

Qy 1803 CTCAAGAAAGTGGTGATGATGATCCGACCGGAACCCCAAACACACTTCCACTAAGCCCAGCTCC   1862
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||

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Db        1951 CTCAAGAAAGTGGTGATGATGATCCGACCGAACCCCAACACCTTCCACTAAGCCAGCTCC 2010

Qy        1863 CCCTCCTGACCTCTCGTGGCCATTGCCAGGAGCCCACCCTGGTCACGCTGGCCACAGCAC 1922
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2011 CCCTCCTGACCTCTCGTGGCCATTGCCAGGAGCCCACCCTGGTCACGCTGGCCACAGCAC 2070

Qy        1923 AAAGAACAACTCCTCACCAGTTCATCCTGAGGCTGGGAGGACCGGGATGCTGGATTCTGT 1982
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2071 AAAGAACAACTCCTCACCAGTTCATCCTGAGGCTGGGAGGACCGGGATGCTGGATTCTGT 2130

Qy        1983 TTTCCGAAGTCACTGCAGCGGATGATGGAACTGAATCGATACGGTGTTTTCTGTCCCTCC 2042
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2131 TTTCCGAAGTCACTGCAGCGGATGATGGAACTGAATCGATACGGTGTTTTCTGTCCCTCC 2190

Qy        2043 TACTTTCCTTCACACCAGACAGCCCCTCATGTCTCCAGGACAGGACAGGACTACAGACAA 2102
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2191 TACTTTCCTTCACACCAGACAGCCCCTCATGTCTCCAGGACAGGACAGGACTACAGACAA 2250

Qy        2103 CTCTTTCTTTAAATAAATTAAGTCTCTACAATAAAAACA 2141
               ||||||||||||||||||||||||||||||||||||| |
Db        2251 CTCTTTCTTTAAATAAATTAAGTCTCTACAATAAAAAAA 2289

RESULT 10
US-10-152-405-267
; Sequence 267, Application US/10152405
; Publication No. US20030211571A1
; GENERAL INFORMATION:
;  APPLICANT: Baker,Kevin P.
;  APPLICANT:  Beresini,Maureen
;  APPLICANT:  DeForge,Laura
;  APPLICANT:  Desnoyers,Luc
;  APPLICANT:  Filvaroff,Ellen
;  APPLICANT:  Gao,Wei-Qiang
;  APPLICANT:  Gerritsen,Mary E.
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Sherwood,Steven
;  APPLICANT:  Smith,Victoria
;  APPLICANT:  Stewart,Timothy A.
;  APPLICANT:  Tumas,Daniel
;  APPLICANT:  Watanabe,Colin K
;  APPLICANT:  Wood,William
;  APPLICANT:  Zhang, Zemin
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P3330R1C383
;  CURRENT APPLICATION NUMBER: US/10/152,405
;  CURRENT FILING DATE:  2002-05-20
;  Prior Application removed - See File Wrapper or Palm
;  NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 267
;   LENGTH: 2290
;   TYPE: DNA
;   ORGANISM: Homo Sapien
US-10-152-405-267

  Query Match             98.1%;  Score 2132.6;  DB 13;  Length 2290;
  Best Local Similarity   99.8%;  Pred. No. 0;
  Matches 2135;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy           3 AAATGAGGCTGCTGCGGACGGCCTGAGGATGAACCCCAAGCCCTGGACCTGCCGAGCGTG 62
               ||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db         151 AAATGAGGCTGCTGCGGACGGCCTGAGGATGGACCCCAAGCCCTGGACCTGCCGAGCGTG 210

Qy          63 GCACTGAGGCAGCGGCTGACGCTACTGTGAGGGAAAGAAGGTTGTGAGCAGCCCCGCAGG 122
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         211 GCACTGAGGCAGCGGCTGACGCTACTGTGAGGGAAAGAAGGTTGTGAGCAGCCCCGCAGG 270

Qy         123 ACCCCTGGCCAGCCCTGGCCCCAGCCTCTGCCGGAGCCCTCTGTGGAGGCAGAGCCAGTG 182
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         271 ACCCCTGGCCAGCCCTGGCCCCAGCCTCTGCCGGAGCCCTCTGTGGAGGCAGAGCCAGTG 330

Qy         183 GAGCCCAGTGAGGCAGGGCTGCTTGGCAGCCACCGGCCTGCAACTCAGGAACCCCTCCAG 242
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         331 GAGCCCAGTGAGGCAGGGCTGCTTGGCAGCCACCGGCCTGCAACTCAGGAACCCCTCCAG 390

Qy         243 AGGCCATGGACAGGCTGCCCCGCTGACGGCCAGGGTGAAGCATGTGAGGAGCCGCCCCGG 302
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         391 AGGCCATGGACAGGCTGCCCCGCTGACGGCCAGGGTGAAGCATGTGAGGAGCCGCCCCGG 450

Qy         303 AGCCAAGCAGGAGGGAAGAGGCTTTCATAGATTCTATTCACAAAGAATAACCACCATTTT 362
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         451 AGCCAAGCAGGAGGGAAGAGGCTTTCATAGATTCTATTCACAAAGAATAACCACCATTTT 510

Qy         363 GCAAAGACCATGAGGCCACTGTGCGTGACATGCTGGTGGCTCGGACTGCTGGCTGCCATG 422
               |||| |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         511 GCAAGGACCATGAGGCCACTGTGCGTGACATGCTGGTGGCTCGGACTGCTGGCTGCCATG 570

Qy         423 GGAGCTGTTGCAGGCCAGGAGGACGGTTTTGAGGGCACTGAGGAGGGCTCGCCAAGAGAG 482
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         571 GGAGCTGTTGCAGGCCAGGAGGACGGTTTTGAGGGCACTGAGGAGGGCTCGCCAAGAGAG 630

Qy         483 TTCATTTACCTAAACAGGTACAAGCGGGCGGGCGAGTCCCAGGACAAGTGCACCTACACC 542
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         631 TTCATTTACCTAAACAGGTACAAGCGGGCGGGCGAGTCCCAGGACAAGTGCACCTACACC 690

Qy         543 TTCATTGTGCCCCAGCAGCGGGTCACGGGTGCCATCTGCGTCAACTCCAAGGAGCCTGAG 602
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         691 TTCATTGTGCCCCAGCAGCGGGTCACGGGTGCCATCTGCGTCAACTCCAAGGAGCCTGAG 750

Qy         603 GTGCTTCTGGAGAACCGAGTGCATAAGCAGGAGCTAGAGCTGCTCAACAATGAGCTGCTC 662
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         751 GTGCTTCTGGAGAACCGAGTGCATAAGCAGGAGCTAGAGCTGCTCAACAATGAGCTGCTC 810

Qy         663 AAGCAGAAGCGGCAGATCGAGACGCTGCAGCAGCTGGTGAAGGTGGACGGCGGCATTGTG 722
               ||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db         811 AAGCAGAAGCGGCAGATCGAGACGCTGCAGCAGCTGGTGGAGGTGGACGGCGGCATTGTG 870

Qy         723 AGCGAGGTGAAGCTGCTGCGCAAGGAGAGCCGCAACATGAACTCGCGGGTCACGCAGCTC 782
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         871 AGCGAGGTGAAGCTGCTGCGCAAGGAGAGCCGCAACATGAACTCGCGGGTCACGCAGCTC 930

Qy         783 TACATGCAGCTCCTGCACGAGATCATCCGCAAGCGGGACAACGCGTTGGAGCTCTCCCAG 842
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         931 TACATGCAGCTCCTGCACGAGATCATCCGCAAGCGGGACAACGCGTTGGAGCTCTCCCAG 990

Qy         843 CTGGAGAACAGGATCCTGAACCAGACAGCCGACATGCTGCAGCTGGCCAGCAAGTACAAG 902
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         991 CTGGAGAACAGGATCCTGAACCAGACAGCCGACATGCTGCAGCTGGCCAGCAAGTACAAG 1050

Qy         903 GACCTGGAGCACAAGTACCAGCACCTGGCCACACTGGCCCACAACCAATCAGAGATCATC 962
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1051 GACCTGGAGCACAAGTACCAGCACCTGGCCACACTGGCCCACAACCAATCAGAGATCATC 1110

Qy         963 GCGCAGCTTGAGGAGCACTGCCAGAGGGTGCCCTCGGCCAGGCCCGTCCCCCAGCCACCC 1022
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1111 GCGCAGCTTGAGGAGCACTGCCAGAGGGTGCCCTCGGCCAGGCCCGTCCCCCAGCCACCC 1170

Qy        1023 CCCGCTGCCCCGCCCCGGGTCTACCAACCACCCACCTACAACCGCATCATCAACCAGATC 1082
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1171 CCCGCTGCCCCGCCCCGGGTCTACCAACCACCCACCTACAACCGCATCATCAACCAGATC 1230

Qy        1083 TCTACCAACGAGATCCAGAGTGACCAGAACCTGAAGGTGCTGCCACCCCCTCTGCCCACT 1142
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1231 TCTACCAACGAGATCCAGAGTGACCAGAACCTGAAGGTGCTGCCACCCCCTCTGCCCACT 1290

Qy        1143 ATGCCCACTCTCACCAGCCTCCCATCTTCCACCGACAAGCCGTCGGGCCCATGGAGAGAC 1202
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1291 ATGCCCACTCTCACCAGCCTCCCATCTTCCACCGACAAGCCGTCGGGCCCATGGAGAGAC 1350

Qy        1203 TGCCTGCAGGCCCTGGAGGATGGCCACGACACCAGCTCCATCTACCTGGTGAAGCCGGAG 1262
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1351 TGCCTGCAGGCCCTGGAGGATGGCCACGACACCAGCTCCATCTACCTGGTGAAGCCGGAG 1410
```

; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William I
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P33031C88
; CURRENT APPLICATION NUMBER: US/10/127,852A
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; NUMBER OF SEQ ID NOS: 550

; SEQ ID NO 267
; LENGTH: 2290
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-127-852A-267

Query Match 98.1%; Score 2132.6; DB 13; Length 2290;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 2135; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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Qy      3 AAATGAGGCTGCTGCGGACGGCGGCGGGGTGAGGATGAACCCCAAGCCCTGCCGAGCGGTG   62
          ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db    151 AAATGAGGCTGCTGCCGGACGGCGGCGGGGTGAGGATGAACCCCAAGCCCTGCCGAGCGGTG  210

Qy     63 GCAGTGAGGCAGCGGCGTGACCGCTACTCTGAGGGAAAGAGAGGTTGTGAGCAGCGGCAGG  122
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    211 GCAGTGAGGCAGCGGCGTGACCGCTACTTGAGGGAAAGAGAGGTTGTGAGCAGCGGCAGG  270

Qy    123 ACCCCTGGCCAGCCCTGGCCCGGCCCCAGCCTCTGCGGCAGCCCCCGCAGTG  182
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    271 ACCCCTGGCCAGCCCTGGCCCGGCCCCAGCCTCTGCGGCAGCCCCCGCAGTG  330

Qy    183 GAGCCCAGTGAGGCAGGGCTGCTTGGCAGCCCACCGCCGCCTGCAACTCAGGAACCCTTCCAG  242
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    331 GAGCCCAGTGAGGCAGGGCTGCTTGGCAGCCCACCGCCGCCTGCAACTCAGGAACCCTTCCAG  390

Qy    243 AGGCCATGGACAGGCCTGCCCGCTGACGGCCCAGGGTGAAGCAATGTGAGGAGGCCGCGGG  302
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    391 AGGCCATGGACAGGCTGCCCGCTGACGGCCCAGGGTGAAGCAATGTGAGGAGGCCGCGGG  450

Qy    303 AGCCAACCAGGAGGGAGGAGAGGCTTTCATAGAGTTCTTATTCACAAAGAATAACCACCATTTT  362
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    451 AGCCAACCAGGAGGGAGGAGAGGCTTTCATAGAGTTCTTATTCACAAAGAATAACCACCATTTT  510

Qy    363 GCAAAGACCATGAGGCCACTGTCGTGGTCGGTCGGACTGTGCTGGTCCATG  422
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    511 ...
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RESULT 11
US-10-127-852A-267
Sequence 267, Application US/10127852A
Publication No. US20030203428A1
GENERAL INFORMATION:

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Qy   1263 AACACCAACCGCCTCATGCAGGTGCGTGGTGCGACCAGAGAACACCGACCCCGGGGGCCTGGACC  1322
          |||||||||||||||| ||||| ||||||||||||||||||| |||||||||||||||||||||
Db   1411 AACACCAACCGCCTCATCCAGGTGTGCGTGGTGCGACCAGAGAACACGGACCCCGGGGGCCTGGACC  1470

Qy   1323 GTCATCCAGAGACGCCCTGGATGGCTCGTGTTAACTTCTTCAGGAACTGGGAGACGTACAAG  1382
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1471 GTCATCCAGAGACCCTGGATGGCTCGTGTTAACTTCTTCAGGAACTGGGAGACGTACAAG  1530

Qy   1383 CAAGGGGTTTGGGAACATTGACGCGGAATACTGGCTCGGCCTGGGACCTGGACATTTACTGGCTG  1442
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1531 CAAGGGTTTGGGAACATTGACGCGGAATACTGGCTCGGCCTGGGACATTTACTGGCTG  1590

Qy   1443 ACGAACCAAGGCAAACTACAAACTCCTGGTTGACCATGGAGACTGGGTCCGGCGCGCAAAGTC  1502
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1591 ACGAACCAAGGCAAACTACAAACTCCTGGTTGACCATGGAGACTGGGTCCGGCGCGCAAAGTC  1650

Qy   1503 TTTGCAGAATACGGCCAGTTTCCGCCTGGAACCTGAGACGGCGAGTATTAATTAAGTGCGGCTG  1562
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1651 TTTGCAGAATACGGCCAGTTTCCCGCCTGGAACCTGAGACGGCGAGTATTAATTAAGTGCGGCTG  1710

Qy   1563 GGGCGGCTACCTATGGCAATCGCGGGTGACTCCTTTACATGCACAAACGGCAAGCAGTTCACC  1622
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1711 GGGCGGCTACCATGGCAATCGCGGGTGACTCCTTTACATGCACAAACGGCAAGCAGTTCACC  1770

Qy   1623 ACCCTGGACAGCAGAATCAATGATGTTCTACACAGAGAAAACTGTGCCCACTACCAGGAAGGGC  1682
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1771 ACCCTGGACAGCAGAATCAATGATGTTCTACACAGAGAAAACTGTGCCCACTACCAGGAAGGAGGC  1830

Qy   1683 TGGTGGGTATAAACGGCCTGTGCCCACTCCAAACCTCAAACCTGAGAGGGAGGTATTATAAGCTCGCGGCCAT  1742
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1831 TGGTGGGTATAAACGGCCTGTGCCCACTCCAAACCTCAAACCTGAGAGGGAGGTATTATAAGCTCGCGGCCAT  1890

Qy   1743 TACCGGAGCCGCTACCAGGAGAGTTCTACTGGGCTGAGTTCCGAGGAGGCTCTTACTCA  1802
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1891 TACGGGAGCCGCTACCAGGAGAGTTCTACTGGGCTGAGTTCCGAGGAGGCTCTTACTCA  1950

Qy   1803 CTCAAGAAAAGTGGTGATGATGAATCGGACCGGAGTCTACTGGGCTCACTAAGCCAGTCC  1862
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1951 CTCAAGAAAAGTGGTGATGATGAATCGGACCGGAGTCTACTGGGCTCACTAAGCCAGTCC  2010

Qy   1863 CCCTCCCTGACCTCTCGTGCCATTGCCAGGAGCCCCCTGGTTCACGCTGGCCACAGCGAC  1922
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2011 CCCTCCTTGACCTCTCGTGCCATTGCCAGGAGCCCCCTGGTTCACGCTGGCCACAGCGAC  2070

Qy   1923 AAAGAACAACTCCTCACCAGTTCATCCTGAGGCTGGAGGAGCCCACCGGATCGTGGATTTCTGT  1982
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2071 AAAGAACAACTCCTCACCAGTTCATCCTGGGAGGCTGGAGGAGCCCACCGGATCGTGGATTTCTGT  2130

Qy   1983 TTTCCGAAGTCACTGCAGCGGGATGGGAACTGAATCGATACGGTGTTTTTCGTCCCTCC  2042
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2131 TTTCCGAAGTCACTGCAGCGGGATGGGAACTGAATCGATACGGTGTTTTTCGTCCCTCC  2190

Qy   2043 TACTTTCCTTCACACAGACAGCCCCTCAGTGTCCAGGACAGGAGGGACTACAGACAA  2102
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2191 TACTTTCCTTCACACAGACAGCCCCTCATGTCCAGGACAGGAGGGACTACAGACAA  2250

Qy   2103 CTCTTTCTTTTAAATTAAATTAAGTCTCTACAATAAAAAACA  2141
          |||||||||||||||||||||||||||||||||||||||||
Db   2251 CTCTTTCTTTTAAATTAAATTAAGTCTCTACAATAAAAAA  2289
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[Sequence alignment between Qy (query) and Db (database), nucleotide positions 423–2289]

PRIOR APPLICATION NUMBER: 60/049911
PRIOR FILING DATE: 1997-06-18
PRIOR APPLICATION NUMBER: 60/056974
PRIOR FILING DATE: 1997-08-26
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059115
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059117
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059122
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059184
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059263
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/059352
PRIOR FILING DATE: 1997-09-19
PRIOR APPLICATION NUMBER: 60/059588
PRIOR FILING DATE: 1997-09-19
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 550

SEQ ID NO 267
LENGTH: 2290
TYPE: DNA
ORGANISM: Homo Sapien
US-10-127-900A-267

Query Match   98.1%;   Score 2132.6;   DB 13;   Length 2290;
Best Local Similarity   99.8%;   Pred. No. 0;   Mismatches 0;
Matches 2135;   Conservative 0;   Mismatches 4;   Indels 0;   Gaps 0;

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Db  1831. TGGTGGTATAACGCCTGTGCCCACTCCAACCTCAACGGGGTCTTGGTACCGCGGGGGGCCAT 1890

Qy  1743 TACCGGAGCCGCGTACCAGGACGGAGCTGTTACTGCTGAGTTCCGAGGAGAGGCTTCTTACTCA 1802
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1891 TACCGGAGCCGCGTACCAGGACGGAGTCTACTGCTGAGTTCCGAGGAGGGCCTCTTACTCA 1950

Qy  1803 CTCAAGAAAGTGGTGATGATGATCCGACCGGAACCCCAACACCTTCCACTAAGCCAGCTCC 1862
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1951 CTCAAGAAAGTGGTGATGATGATCCGACCGGAACCCCAACACCTTCCACTAAGCCAGCTCC 2010

Qy  1863 CCCTCCTGACCTCTCGTGGCCATTGCCACGAGCCCACCCTGGTCACGCTGGCCACAGCAC 1922
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2011 CCCTCCTGACCTCTCGTGGCCATTGCCACGAGCCCACCCTGGTCACGCTGGCCACAGCAC 2070

Qy  1923 AAAGAACAACTCCTCACCAGTTCATCCTGAGGCTGGGAGGCACGGAGGACGGAGATTCTGT 1982
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2071 AAAGAACAACTCCTCACCAGTTCATCCTGAGGCTGGGAGGCACGGAGGACGGAGATTCTGT 2130

Qy  1983 TTTCCGAAGTCACTGCACCGGATGAACTGAATCGAATACGGTGTTTTTCGTGTCCCTCC 2042
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2131 TTTCCGAAGTCACTGCACCGGATGAACTGAATCGAATACGGTGTTTTTCGTGTCCCTCC 2190

Qy  2043 TACTTTCCTTCACACCAGACAGCCCCTTCCAGGCACGGACAGGACTACAGACAA 2102
         |||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2191 TACTTTCCTTCACACCAGACAGCCCCTCATGTTCTCAGGACAGGACTACAGACAA 2250

Qy  2103 CTCTTTCTTAAATAAATTAAGTCTCTACAATAAAAAACA 2141
         |||||||||||||||||||||||||||||||||||||
Db  2251 CTCTTTCTTAAATAAATTAAGTCTCTACAATAAAAAAA 2289
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RESULT 13
US-10-128-685A-267

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Query Match             98.1%;  Score 2132.6;  DB 13;  Length 2290;
Best Local Similarity   99.8%;  Pred. No. 0;
Matches 2135;  Conservative  0;  Mismatches  4;  Indels  0;  Gaps  0;

Qy     3 AAATGAGGCTGTGCGGACGGCCGTGAGGGATGAAACCCCAGACCTGAGCCGACGGTG 62
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   151 AAATGAGGCTGTGCGGACGGCCGTGAGGGATGAAACCCCAGACCTGAGCCGACGGTG 210

Qy    63 GCACTGAGGCACGGGCTGACCGCTACTGTCGTGAGGGAAAGAAGGTTGTGAGCAGCCCCCAGG 122
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   211 GCACTGAGGCACGGGCTGACCGCTACTGTCGTGAGGGAAAGAAGGTTGTGAGCAGCCCCCAGG 270

Qy   123 ACCCCTGGCCAGCCCTTGGCCCCCCAGCCCTTCGCCGGGGAGCCCCTTCGTGGGGAGGCAGCAGTG 182
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   271 ACCCCTGGCCAGCCCTTGGCCCCCCAGCCCTTCGCCGGGGAGCCCCTTCGTGGGGAGGCAGCAGTG 330

Qy   183 GAGCCCAGTGAGGCAGGGCTCTTGCCAGCCACCGGCCCTGCAAACTCAGGAACCCCTCAG 242
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   331 GAGCCCAGTGAGGCAGGGCTCTTGCCAGCCACCGGCCCTGCAAACTCAGGAACCCCTCAG 390

Qy   243 AGGGCCATGGACAGGGCTCCCCCCTGACGGCCCAGGGTCAAGCATGTGAGGAGCCCCCGG 302
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   391 AGGGCCATGGACAGGGCTCCCCCCTGACGGCCCAGGGTCAAGCATGTGAGGAGCCCCCGG 450

Qy   303 AGCCAAGCAGCAGAGGGGAAGAGGCTTTCATAGAATTCTATTCACAGAGAATACCACACATTTT 362
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   451 AGCCAAGCAGCAGAGGGGAAGAGGCTTTCATAGAATTCTATTCACAGAGAATACCACACATTTT 510

Qy   363 GCAAAGACCCATGAGGCCACTGTGCGTGACATGCTGGTGTGGCTCGGAGCTGGCTGCCATG 422
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   511 GCAAAGACCCATGAGGCCACTGTGCGTGACATGCTGGTGTGGCTCGGAGCTGGCTGCCATG 570

Qy   423 GGAGCTGTTGCAGGCCAGGAGGACGGTTTTTGAGGGACTGAGGAGGGCTCGCGAGAGAG 482
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   571 GGAGCTGTTGCAGGCCAGGAGGACGGTTTTTGAGGGACTGAGGAGGGCTCGCGAGAGAG 630

Qy   483 TTCATTTACCTAAAACAGGTACAAGGCGGGGGAGTGCCAGGACAAAGTGCCACCTACACC 542
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   631 TTCATTTACCTTAAACAGGTACAAGGCGGGGGAGTGCCAGGACAAAGTGCACCTACACC 690

Qy   543 TTCATGTGTGCCCCAGCAGCGGGGGTGCCATCTGCGTCAACTCCAAGGAGCCTGAG 602
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   691 TTCATTGTGTGCCCCAGCAGCGGGGGTGCCATCTGCGTCAACTCCAAGGAGCCTGAG 750

Qy   603 GTGCTTCTGGAGAACCGAGTGCATAAGCAGGAGCTAGAGCTGCTCAACAATGAGCTGCTC 662
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   751 GTGCTTCTGGAGAACCGAGTGCATAAGCAGGAGCTAGAGCTGCTCAACAATGAGCTGCTC 810

Qy   663 AAGCAGAAGCCGCAGATCGAGACGTGCAGACGTGTGAAGGTGGACGTGGCCAGCATTGTG 722
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   811 AAGCAGAAGCCGCAGATCGAGACGTGCAGACGTGTGAAGGTGGACGTGGCCAGCATTGTG 870

Qy   723 AGCGAGGTGAAGCTGCTGCGCAAGGAGAGCAGCACAGACTCCGGGGTGACGGCAGCTC 782
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   871 AGCGAGGTGAAGCTGCTGCGCAAGGAGAGCCGCAACATGAACTCGGGGTCACGGCAGCTC 930

Qy   783 TACATGCCAGTCTCCTCGCACGAGATCATCCGCAAGCGCGGGGACAAACGCGTTGGAGCTCTCCCAG 842
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   931 TACATGCCAGTCTCCTCGCACGAGATCATCCGCAAGCGCGGGGACAAACGCGTTGGAGCTCTCCCAG 990
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Qy    843 CTGGAGAACAGCAGGATCCTTGGAAGCCAGGAAGCAGACGAGCACCGACTGCCGCCAAGTACAAG  902
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    991 CTGGAGAACAGCAGGATCCTTGGAAGCCAGGAAGCAGACGAGCACCGACTGCCGCCAAGTACAAG 1050

Qy    903 GACCTGGAGCACAAGTACCAGCACTGGCCCCACACTGGCCACGCAGAAGATCATC           962
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1051 GACCTGGAGCACAAGTACCAGCACTGGCCCCACACTGGCCACGCAGAAGATCATC          1110

Qy   1051 GACCTGGAGCACAAGTACCAGCACTGGCCCCACACTGGCCACAACAATCAGAGATCATC        1110
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1111 GGCCCAGCTTGAGGAGCACTGACCAGAGGTGACCCGTTCCCCCAGCCACCC              1170

Qy    963 GCCCAGCTTGAGGAGCACTGACCAGAGGTGACCCGTTCCCCCAGCCACCC               1022
          ||||||||||||||||||||||||||||||||||||||||||||||
Db   1111 GGCCCAGCTTGAGGAGCACTGACCAGAGGTGACCCGTTCCCCCAGCCACCC              1170

Qy   1023 CCCGCCTGCCCGCCCGCCCGGGTCTTCACCAACCACCCACCCACTGCCTGCCCACT          1082
          ||||||||||||||||||||||||||||||||||||||||||||
Db   1171 CCCGCCTGCCCGCCCGCCCGGGTCTTCACCAACCACCCATCATCAACCAGATC            1230

Qy   1083 TCTTACCAACGAGATCCACAGTGACCAGAACCTGAAGGTGCTGCCACCCCCTCTGCCCACT     1142
          |||||||||||||||||||||||||||||||||||||||||||||
Db   1231 TCTTACCAACGAGATCCACAGTGACCAGAACCTGAAGGTGCTGCCACCCCCTGCCCCACT     1290

Qy   1143 ATGCCCACTCTCACCACGCTCCCACTCTTCCACCGACAAGCCGTCGGCGCCCATGGAGAC      1202
          ||||||||||||||||||||||||||||||||||||||||||||||
Db   1291 ATGCCCACTCTCACCACGCTCCCACTCTTCCACCGACAAGCCGTCGGCGCCCATGGAGAGAC   1350

Qy   1203 TGCCTGCAGGCCCTGGAGGATGGGCCACGACACCAGAGTCCATTCCACTTACCTGGCTGAAGCCCGGAG 1262
          ||||||||||||||||||||||||||||||||||||||||||||||||
Db   1351 TGCCTGCAGGCCCTGGAGGATGGGCCACGACACCAGAGTCCATTCCACTGAAGCCCGGAG     1410

Qy   1263 AACACCAACCGCCTCATGCAGGTGTGGTGTCGACCAGAGACACCGACACCCGGGGACC       1322
          ||||||||||||||||||||||||||||||||||||||||||||
Db   1411 AACACCAACCGCCTCATGCAGGTGTGGTGACCAGACACCGGGACC                   1470

Qy   1323 GTCATCCAGAGACGCGCCTGGATGGCTCGTTAACTTCTTCAGGAANACTGGGAGACGTACAAG  1382
          ||||||||||||||||||||||||||||||||||||||||||
Db   1471 GTCATCCAGAGACCCTGGATGGCTCGTTAACTTCTTCAGGAANACTGGGAGACGTACAAG     1530

Qy   1383 CAAGGGTTTGGGAACATTGACCGGCGAATACTGGCGTGGGCCTGGAGAACACATTTACTGGCTG 1442
          ||||||||||||||||||||||||||||||||||||||||||
Db   1531 CAAGGGTTTGGGAACATTGACCGGCGAATACTGGCGTGGGCCTGGAGAACACATTTACTGGCTG 1590

Qy   1443 ACGAACCAAGGCAACTACATACAAACTCCTGGTGACCATGGAGGACTGGGTCCGGCGGCCAAAGTC 1502
          ||||||||||||||||||||||||||||||||||||||||||||
Db   1591 ACGAACCAAGGCAACTACATACAAACTCCTGGTGACCATGGAGGACTGGGTCCGGCGGCCAAAGTC 1650

Qy   1503 TTTGCAGAATACGCGCAGTTTCCGCCTGGAACCTGAGACGGAGTATTATAAGCTGCGGCTG      1562
          |||||||||||||||||||||||||||||||||||||||||
Db   1651 TTTGCAGAATACGCGCAGTTTCCGCCTGGAACCTGAGACGGAGTATTATAAGCTGCGGCTG     1710

Qy   1563 GGGGCCTACCATGCAATGCGGGGTGACTTCTTTACATGGCACAACGGCAAGCAGTTCACC      1622
          ||||||||||||||||||||||||||||||||||||||||||
Db   1711 GGGGCCTACCATGCAATGCGGGGTGACTCCTTTACATGGCACAACGGCAAGCAGTTCACC     1770

Qy   1623 ACCCTGGACAGAGATCAGAGTGTCTGCCCACTACCAGAGGAAGGGAGGC               1682
          |||||||||||||||||||||||||||||||||||||||
Db   1771 ACCCTGGACAGAGATCATGATTGCCCACTACCAGAGGAAGGGAGGC                  1830

Qy   1683 TGGTGGGTATTAAGCGCCTGTGTCCCACTCCAACCTCAACCGGGGTCTCGGGTACAGCGGGGCCAT 1742
          |||||||||||||||||||||||||||||||||||||||||||
Db   1831 TGGTGGGTATTAAGCGCCTGTGTCCCACTCCAACCTCAACCGGGGTCTCGGGTACAGCGGGGCCAT 1890

Qy   1743 TACCCGGAGCGCGCTACCAGGACGGAGAGTCTTACTGGGCTGAGTTCCGAGGAGGCTCTTACTCA  1802
          |||||||||||||||||||||||||||||||||||||||||
Db   1891 TACCCGGAGCGCGCTACCAGGACGGAGAGTCTTACTGGGCTGAGTTCCGAGGAGGCTCTTACTCA  1950

Qy   1803 CTCAAGAAAGTGGTGATGATGATCCGACGAACCCACCACCTTCCACTAAGCCAGTCC        1862
          ||||||||||||||||||||||||||||||||||||||||||
Db   1951 CTCAAGAAAGTGGTGATGATGATCCGACGAACCCACCACCTTCCACTAAGCCAGTCC        2010

Qy   1863 CCCTCCTTGACCTCTCGTTGCCCATTGCCAGGAGCCCACACCCTGGTCACGCTGGCCACAGCGAC 1922
          ||||||||||||||||||||||||||||||||||||||||||
Db   2011 CCCTCCTTGACCTCTCGTTGCCCATTGCCAGGAGCCCACACCCTGGTCACGCTGGCCACAGCAC  2070

Qy   1923 AAAGAACAACTCTCACCAGTTCATCCTTGAGGCGTGGGATGCTGGATTCTGT             1982
          ||||||||||||||||||||||||||||||||||||||||||
Db   2071 AAAGAACAACTCTCACCAGTTCATCCTTGAGGCGTGGGATGCTGGATTCTGT             2130

Qy   1983 TTTCCGAAGTCACTGCCAGCCGGATGAGGAACTGAATCGATACGGGTTGTTTTCTGTGTCCCTCC 2042
          ||||||||||||||||||||||||||||||||||||||||||
Db   2131 TTTCCGAAGTCACTGCCAGCCGGATGAGGAACTGAATCGATACGGGTTGTTTTCTGTGTCCCTCC 2190

Qy   2043 TACTTTCCTTCACACCAGACAGCGCCCCTCATGTCTCCAGGACAGGACAGGAGGACTACAGACAA 2102
          ||||||||||||||||||||||||||||||||||||||||||
Db   2191 TACTTTCCTTCACACCAGACAGCGCCCCTCATGTCTCCAGGACAGGACAGGAGGACTACAGACAA 2250

Qy   2103 CTCTTTTCTTTAAATAAAATTAAAGTCTCTACAAATAAAAAACA                     2141
          ||||||||||||||||||||||||||||||||
Db   2251 CTCTTTTCTTTAAATAAAATTAAAGTCTCTACAAATAAAAAAA                      2289
```

Query Match   98.1%; Score 2132.6; DB 13; Length 2290;
Best Local Similarity 99.8%; Pred. No. 0;

Matches 2135; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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Qy      3  AAATGAGGCTGCTGCGGAGGGCGGTGGAGGGGATGAACCCAAGCCTTGGACCTGCCGAGCCTG     62
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1  AAATGAGGCTGCTGCGGAGGGCGGTGGAGGGGATGAACCCAAGCCTTGGACCTGCCGAGCCTG     60
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RESULT 15
US-10-142-886-267
; Sequence 267, Application US/10142886
; Publication No. US20030203432A1
; GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: DeForge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin X.
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C236
CURRENT APPLICATION NUMBER: US/10/142,886
CURRENT FILING DATE: 2002-05-10
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 267
LENGTH: 2290
TYPE: DNA
ORGANISM: Homo Sapien
US-10-142-886-267

Query Match   98.1%; Score 2132.6; DB 13; Length 2290;
Best Local Similarity   99.8%; Pred. No. 0;
Matches 2135; Conservative   0; Mismatches   4; Indels   0; Gaps   0;

Qy   3 AAATGAGGCTGCTTGCGGACGGCCTGAGGAATGAACCCCAAGCCTTGGACGCCTGAGCGTG 62
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   151 AAATGAGGCTGCTTGCGGACGGCCTGAGGAATGAACCCCAAGCCTTGGACGCCTGAGCGTG 210

Qy   63 GCACTGAGGCCAGGCGGCGGCCTGAGCCTTACTGTGTGAGGGGAAAGAAGGTTGTGAGCTC 122
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   211 GCACTGAGGCCAGGCGGCGGCCTGAGCCTTACTGTGTGAGGGGAAAGAAGGTTGTGAGCTC 270

Qy   123 ACCCCTGGCCAGCGCCCTGGGCCCCAGCCTCTCGCCGGAGCCCTCGTGGAGGCAGAGCCAC 182
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   271 ACCCCTGGCCAGCGCCCTGGGCCCCAGCCTCTCGCCGGAGCCCTCGTGGAGGCAGAGCCAC 330

Qy   183 GAGCCCAGTGAGGCAGGGGCTGCTTGGCCAGCCCTTCTGCCGGAGCCCTCCTCGTGGAGTG 242
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   331 GAGCCCAGTGAGGCAGGGGCTGCTTGGCCAGCCCTTCTGCCGGAGCCCTCCTCGTGGAGTG 390

Qy   243 AGGCCCATGGACAGGCTGCCCCGCTCCAGGGTGAAGCAGTGTGAGGAGCCGCCCCCCGG 302
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   391 AGGCCCATGGACAGGCTGCCCCGCTCCAGGGTGAAGCAGTGTGAGGAGCCGCCCCCCGG 450

Qy   303 AGCCAAGCAGGAGGCGGAAGAGGCTTTCATAGATTCTATTCACAAAAGAATAAACCACCATT 362
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   451 AGCCAAGCAGGAGGCGGAAGAGGCTTTCATAGATTCTATTCACAAAAGAATAAACCACCATTT 510

Qy   363 GCAAAGACCATGAGCCCACTGTGCCTGACATGCTGGTGGCTCGGACTCCTGGTCCATG 422
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   511 GCAAGGACCATGAGCCCACTGTGCCTGACATGCTGGTGGCTCGGACTCCTGGTCCATG 570

Qy   423 GGAGCTGTTGCAGCGCCAGGAGGACGGTTTTGAGGGGCACTGAGGAGGGGCCAAGAGAG 482
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   571 GGAGCTGTTGCAGCGCCAGGAGGACGGTTTTGAGGGGCACTGAGGAGGGGCCAAGAGAG 630

Qy   483 TTCATTTACCTAAACAGGTTACAACGGGGGGCGGGGGCCAGTCCCAGGACACAAGTGCACCTACACC 542
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Qy   631 TTCATTTACCTAAACAGGTTACAACGGGGGGCGGGGGCCAGTCCCAGGACACAAGTGCACCTACACC 690

Qy   543 TTCATGTGTGCCCCAGCAGGGTCGCTCGGGTTGCCATCTGCGTCTCAACTTCCAAGGAGGCCTGAG 602
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   691 TTCATTGTGTGCCCCAGCAGGGTCGCTCGGGTTGCCATCTGCGTCTCAACTTCCAAGGAGGCCTGAG 750

Qy   603 GTGCTTCTTGGAGCAACCGGAGTGCATAAGCAGGAGGAGCTAGAGCTGCTCAACAATGAGCTGCTC 662
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   751 GTGCTTCTTGGAGAACCGGAGTGCATAAGCAGGAGGAGCTAGAGCTGCTCAACAATGAGCTGCTC 810

Qy   663 AAGCAGAAGCGGCGGCAGATCGAGACGTGCACCAGTGCTGGTGAAGGTGGAGCGGCGGCATTGTG 722
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   811 AAGCAGAAGCGGCGGCAGATCGAGACGTGCACCAGTGCTGGTGAAGGTGGAGCGGCGGCATTGTG 870

Qy   723 AGCGGAGGTGAAGCTGCTGCGCCAAGGGAACTCGCCGGGTGTCACGGAGCTC 782
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   871 AGCGGAGGTGAAGCTGCTGCGCCAAGGGAACTCGCCGGGTGTCACGGAGCTC 930

Qy   783 TACATCGCAGCTCCTGCACGGAGGATCATCCCGCACGAGATCACCCGCAACCAACGCTCTCCCAG 842
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   931 TACATGCAGCTCCTGCACGGAGATCATCCCGCACGAGATCACCCGCAACCAACGCTCTCCCAG 990

Qy   843 CTGGAGAACAGGATCCTTGAACCAGCAGCAGCAATGCTGCGAGCTGGCAGCAGTACAAG 902
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   991 CTGGAGAACAGGATCCTTGAACCAGCAGCAGTGCTGCGAGCTGGCAGCAGTACAAG 1050

Qy   903 GACCTGAGCACAAGTAGTACCAAGACCTGGCCACACTGGCCCACAACCAATCAGAATCATC 962
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1051 GACCTGAGCACAAGTAGTACCAAGACCTGGCCACACTGGCCCACAACCAATCAGAATCATC 1110

Qy   963 GCGGCAGCTTGAGGAGCACTGCGCAGAGGGTGCCCTGGCCAGGCCGGCCCTGGAAGCCACC 1022
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1111 GCGGCAGCTTGAGGAGCACTGCGCAGAGGGTGCCCTGGCCAGGCCGGCCCTGGAAGCCACC 1170

Qy   1023 CCGGCTGCCCGCCCGGCCCGGGGTCCACCACCCACTACAACCGCATCATCAACCAGATC 1082
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1171 CCGGCTGCCCGCCCGGCCCGGGGTCTACCACCACCCACTACAACCGCATCATCAACCAGATC 1230

Qy   1083 TCTACCAACGAGAGTCCAGAGTGACCAGGAACCTGAAGGTGCTGCCACCCCCCTGCCCACT 1142
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1231 TCTACCAACGAGAGTCCAGAGTCACCAGAACCTGAAGGTGCTGCCACCCCCCTGCCCACT 1290

Qy   1143 ATGCCCACTCTCCACCAGCCTCCACATTTCCACCGACAAGCCGTCGGGCCCCCATGGAGGAC 1202
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1291 ATGCCCACTCTCCACCAGCCTCCACATCTTCCACCGACAAGCCGTCGGGCCCCCATGGAGGAC 1350

Qy   1203 TGCCTGCAGGCCCCTGCGGATGGCCACGACACCAGCTCCATCTACCTGGTGGAAGCCGGAG 1262
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy   1263 AACACCCAACCCCCTCCATGCAGGTGTGGGTGGTGGACGACCAGAGACAGAGACACGGACC 1322
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Qy   1323 GTCATCCAGAGACCGCCTGGGAATGGCTCTGTTGTTAACTTCTTCAGGGAACTGGGTACAAG 1382
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Qy   1383 CAAGGGTTTGGGAACATTGACGGCGGAATACTGGCTGGCCTGGAGAAGAACATTACTGGCTG 1442
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Qy   1443 ACGAAACCAAGCCAACTACAAAACTCCCGGGTGACCATGGAGGAGCGGAGGACTGAGGAGAC 1502
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Qy   1503 TTTGCAGAATACGCCAGTTTCCGCCTGGGAACCTGAGCAGAGTGAGTATATAAGCTGCGG 1562
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Qy   1563 GGGCGCTTACCATGGCCAATGCCGGGTGACTCCTTACATGGCACAAGGCAACACAGTTCACC 1622
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Db  1711  GGGCGCGCTACCCATGGGCAATGCGGGGTGACTCCTTTACATGGCACAACGGCAAGCAGTTCACC 1770

Qy  1623  ACCCTGGACAGAGATCATGATTGTCTACACAGGAAAACTGTGCCCACTTACCCAGAAGGGGAGGC 1682
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Qy  1743  TACCGGGAGGCCGGCTACCCAGGACGGGAGTCTACTGGGCTGAGTTCCGAGGAGGCTTCTTACTCA 1802
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Qy  1863  CCCTCCTTGACCTCTCGTGGCCATTGCAGGAGCCCCACCCTGGTCACCGTGGCCACAGCAC 1922
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Db  2011  CCCTCCTTGACCTCTCGTGGGCCATTGCCAGGAGCCCCACCCTGGTCACGGCTGGCCACAGCAC 2070

Qy  1923  AAAGAACAAACTCCTCACCAGTTCATCCTGAGGCTGGGAGGACCGGGATGCTGGGATTCTGT 1982
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Db  2071  AAAGAACAAACTCCTCACCAGTTCATCCTGAGGCTGGGAGGACCGGGATGCTGGGATTCTGT 2130

Qy  1983  TTTCCGAAGTCACTGCAGCGGATGATGGAACTGAATCGATACGGGTGTTTTCTGTCCCTCC 2042
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Qy  2043  TACTTTCCTTCACACCAGACACCCCTCCATGTCTCCAGGACAGGAGGACTACAGACAA 2102
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Qy  2103  CTCTTTCTTTAAATAAATTAAGTCTCTTACAATAAAAAACA 2141
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Search completed: August 6, 2004, 20:44:37
Job time : 987 secs

OM nucleic - nucleic search, using sw model

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

Run on: August 6, 2004, 13:47:28 ; Search time 5559 Seconds
(without alignments)
11673.056 Million cell updates/sec

Title: US-10-018-386-1
Perfect score: 2173
Sequence: 1 gaaaatgaggctgctgcgga.........aaaaaaaaaaaaaaaaaaaa 2173

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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25:  em_gss_rod:*
26:  em_gss_phg:*
27:  em_gss_vrl:*
28:  gb_gss1:*
29:  gb_gss2:*
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SUMMARIES

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1345.4	61.9	2062	11	AK037265	AK037265 Mus muscu
2	1039.4	47.8	1201	9	AL527015	AL527015 AL527015
3	989.6	45.5	1201	9	AL523842	AL523842 AL523842
4	939.8	43.2	1201	9	AL572386	AL572386 AL572386

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 5   931.8    42.9   3560    11    AK041888    AK041888 Mus muscu
 6   908.6    41.8   1201     9    AL547465    AL547465 AL547465
 7   885.2    40.7   1201     9    AL546299    AL546299 AL546299
 8   873.8    40.2   1201     9    AL554832    AL554832 AL554832
 9   870.0    40.1   1111    12    BM906705    BM906705 AGENCOURT
10   865.4    39.8    929    13    BQ711105    BQ711105 AGENCOURT
11   865     39.8    881    13    BQ879104    BQ879104 AGENCOURT
12   826.8    38.0   1195     9    AL525269    AL525269 AL525269
13   825.2    38.0    884    13    BQ952353    BQ952353 AGENCOURT
14   817.4    37.6   1201     9    AL527059    AL527059 AL527059
15   816.4    37.6    870    14    CD516561    CD516561 AGENCOURT
16   777.2    35.8    797    14    CF113488    CF113488 UI-HF-FQ0
17   777      35.8    875    13    BQ651478    BQ651478 AGENCOURT
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21   733.2    33.7    812    12    BI765043    BI765043 603051189
22   732.8    33.7    752    13    BQ717905    BQ717905 AGENCOURT
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28   701      32.3    683    10    BE745986    BE745986 601573433
29   691.6    31.8    700    12    BG676460    BG676460 602622918
30   686.6    31.6    738    12    BI768582    BI768582 603056901
31   677      31.2    683    13    BX482997    BX482997 DKFZp686B
32   671.4    30.9    682    14    CA411602    CA411602 UI-H-EU1-
33   659.6    30.4    666    14    CF131252    CF131252 UI-HF-FQ0
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43   592.4    27.3    881    14    CB193085    CB193085 AGENCOURT
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ALIGNMENTS

RESULT 1
AK037265
LOCUS   AK037265   2062 bp   mRNA   linear   HTC 19-SEP-2003
DEFINITION Mus musculus 16 days neonate thymus cDNA, RIKEN full-length
            enriched library, clone:A130002A02 product:ANGIOPOIETIN-RELATED
            PROTEIN 2 PRECURSOR, full insert sequence.
ACCESSION   AK037265
VERSION   AK037265.1 GI:26332099
KEYWORDS   HTC; CAP trapper.
SOURCE   Mus musculus (house mouse)
ORGANISM   Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
AUTHORS   Carninci,P. and Hayashizaki,Y.
TITLE   High-efficiency full-length cDNA cloning
JOURNAL   Meth. Enzymol. 303, 19-44 (1999)
MEDLINE   99279253
PUBMED   10349636-
REFERENCE   2
AUTHORS   Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
            Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
TITLE   Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL   Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE   20499374
PUBMED   11042159

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REFERENCE   3
  AUTHORS   Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
            Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,
            Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,
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            Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M.,
            Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J.,
            Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
    TITLE   RIKEN integrated sequence analysis (RISA) system--384-format
            sequencing pipeline with 384 multicapillary sequencer
  JOURNAL   Genome Res. 10 (11), 1757-1771 (2000)
   MEDLINE   20530913
   PUBMED    11076861
REFERENCE   4  (bases 1 to 2062)
  AUTHORS   The RIKEN Genome Exploration Research Group Phase II Team and the
            FANTOM Consortium.
    TITLE   Functional annotation of a full-length mouse cDNA collection
  JOURNAL   Nature 409, 685-690 (2001)
REFERENCE   5
  AUTHORS   The FANTOM Consortium and the RIKEN Genome Exploration Research
            Group Phase I & II Team.
    TITLE   Analysis of the mouse transcriptome based on functional annotation
            of 60,770 full-length cDNAs
  JOURNAL   Nature 420, 563-573 (2002)
REFERENCE   6  (bases 1 to 2062)
  AUTHORS   Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P.,
            Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W.,
            Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T.,
            Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T.,
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            Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S.,
            Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A.,
            Muramatsu,M. and Hayashizaki,Y.
    TITLE   Direct Submission
  JOURNAL   Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
            Physical and Chemical Research (RIKEN), Laboratory for Genome
            Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
            RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
            Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp,
            URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
            Fax:81-45-503-9216)
  COMMENT   cDNA library was prepared and sequenced in Mouse Genome
            Encyclopedia Project of Genome Exploration Research Group in Riken
            Genomic Sciences Center and Genome Science Laboratory in RIKEN.
            Division of Experimental Animal Research in Riken contributed to
            prepare mouse tissues.
            Please visit our web site for further details.
            URL:http://genome.gsc.riken.go.jp/
            URL:http://fantom.gsc.riken.go.jp/.
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Qy         50 --------CCTTCCGAGCGTGGCACTGAGGCGAGCGGGCGCTGACGGCTTACTGTGAGGGAAAGAA 101

Db        110 CCCAGGACCTGCAAGCAAGCAATGCACTAAGGCAGTGTCGCGGAGCCACACTGTGAGGGAGAGCA 169

Qy        102 GGTTGTGGAGCAGCCCGCAGAGCCCCTGGGCCCAGCCCCTTGCCCGGAGCCC 161

Db        170 GGTTGGGGAGCAGCCCCGGGGTGCAACCAGAGGCCAGCCTCATCCCTAGGAGCTTCAGAGAGCA 229

Qy        162 TCTGTGGAGGCAGAGCCCAGTGGGCCAGCCAGCGGGCGCTGGCTGGCACCCA---CCGGC 219

Db        230 TAGACTG-----CTGCCAGTGAGGGCCCAGTGAGGCAGGGCTGCTCGGGCGGCCAGTCCAGC 284

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AL527015/c

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Qy   1720 GGGGTCTGGTTACCGGGGGGGCCATTACCCGGAGGAGGGGAGTCTACTGGGGCTG 1779
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Qy   1780 AGTTCCGGAGCGGCTCTTACTCACTCGGAAAGTGGTGATGATGATATCCGACCGAACCCCCA 1839
Db   1836 AGTTCCGGAGCGGCTCTTACTCACTCGGAGAGTGGTGGTGATGATGATTCGGCCCCAACCCCA 1895
Qy   1840 ACACCTTCCACTAAGCCACGCTCCCCCT 1866
Db   1896 ACACCTTCCACTAAGCTCTCCTGCCT 1922

Query Match 47.8%;  Score 1039.4;  DB 9;  Length 1201;
Best Local Similarity 94.38%;  Pred. No. 4.7e-128;
Matches 1096;  Conservative 20;  Mismatches 41;  Indels 5;  Gaps 4;

Qy    985 AGAGGGGTTGCCCTCCGGCCCAGGCCGCCCGTCCCCCAGCCCCATGAGAGACTGCCTTGCACGGGGTCT 1044
Db   1162 RGACAYKSCAGAGGGCVTYSGCSAGCCCKCCCCAGCACCCCGGTGCCCGCCCGG--TT 1105
Qy   1045 ACCAACCACCCACCTACAACCGCATCATCAACCAGATCTCTACCAACGAGATCCAGAGTG 1104
Db   1104 TACMAMCACCCCACCTAMAMCCGCWTCTTCACCAAGAGTTTTTTCCC-AGRKATCCAGRKTG 1046
Qy   1105 ACCAGAACCTGAAGGTGCTGCCACCCCCTCTGCCCACTCTCACCACGCCTCC 1164
Db   1045 ACCAGAACCTGAAGGGGGTGCCACCCCYTCTGCAAAACTWTATGCCCAYTCTCACCACGCCTCC 986
Qy   1165 CATCTCACCACAACGCGGTGGGGCCCCCCATGAGAGACTGCCTTGCACGGGGATG 1224
Db   1045 CATTTTCACCGACAAAGCCGGTCGGGCCCCCCATGAGAGACTGCCTTGCACGGGGATG 986
Qy    985 CATTTTCACCGACAAAGCCGGTCGGGCCCCCCATGAGAGACTGCCTTGCACGGGGATG 926
Qy   1045 ACCAACCACCCACCTACAACCGCATCATCAACCAGATCTCTACCAACGAGATCCAGAGTG 1104
Db   1162 RGACAYKSCAGAGGGCVTYSGCSAGCCCKCCCCAGCACCCCGGTGCCCGCCCGG--TT 1105
Qy   1225 GCCACGACCACCAGCTCCATCTACCTGGTGAAGCCGCGGGAGGAGAACACCAACACCGCCCTGACGTGGGATG 1284
Db   1285 TGTGGTGCGACCAGAGACACGACCCCGGGGGCTGGACGTCATCCAGACGCGCTGGTTTAACTTCTTCAGG 1344
Qy    925 GCCACGACCACCAGCTCCATCTACCTGGTGAAGCCGGGAGGAGAACACCAACACCGCCCTGACGTGGGATG 866
Db    865 TGTGGTGCGACCAGAGACACGACCCCGGGGGCTGGACGTCATCCAGACGCGCTGGTTTAACTTCTTCAGG 806
Qy   1345 GCCCTGTTAAACTTTCTTCAGGAACTGGGACGTTGGGAACATTGACG 1404
Db    865 GCTCTGTTAACTTTCTTCAGGAACTGGGGAGACGTACAAGCAAGGGTTTGGGACATTGACG 806
Qy   1896 ACACCTTCCCACTAAGCTCTCCTGCCT 1922
Db    805 GCTCTGTTAACTTCTTCAGGAACTGGGAGACGTACAAGCAAGGGTTTGGGACATTGACG 746
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ORIGIN

RESULT 3
AL523842/c

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LOCUS       AL523842               1201 bp    mRNA    linear   EST 22-MAY-2003
DEFINITION  AL523842 Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED Homo sapiens
            cDNA clone CS0DC003YP19 3-PRIME, mRNA sequence.
ACCESSION   AL523842
VERSION     AL523842.2  GI:31042103
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1201)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT     On Feb 13, 2001 this sequence version replaced gi:12787335.
            Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr; Web : www.genoscope.cns.fr
            Library was constructed by Life Technologies, a division of
            Invitrogen. This sequence belongs to sequence cluster 4821.r For
            more information about this cluster, see
            http://www.genoscope.cns.fr/
            cgi-bin/cluster.cgi?seq=CS0DC003CH10NP1&cluster=4821.r. Contact :
            Feng Liang Email : fliang@lifetech.com URL :
            http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
            Faraday Avenue Genoscope sequence ID : CS0DC003CH10NP1.
FEATURES             Location/Qualifiers
     source          1..1201
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="CS0DC003YP19"
                     /tissue_type="NEUROBLASTOMA COT 25-NORMALIZED"
                     /clone_lib="Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED"
                     /note="1st strand cDNA was primed with a NciI-oligo(dT)
                     primer. Five prime end enriched, double-strand cDNA was
                     digested with Not I and cloned into the Not I and EcoR V
                     sites of the pCMVSPORT 6 vector. Library was normalized."
ORIGIN

Query Match     45.5%;  Score 989.6;  DB 9;  Length 1201;
Best Local Similarity   91.6%;  Pred. No. 1.8e-121;
Matches 1030;  Conservative 37;  Mismatches 53;  Indels 4;  Gaps 3;
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Alignment (Query vs Database):

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Qy  1012 CCCAGCCACCCCCCCGGCGTTGCCCCCGGGGGGGTCTACCAACCCCACCCCCACCTACAACCCGCATCA 1071
         |||      : | | |:|        |:||    |||||  : |    :|||||:      |:|
Db  1120 CCCTCCCCAGCMCCCCGSTGCCCGCCCCGGTTTCAACCCACCC--AAAACGSATCT 1063

Qy  1072 TCAACCAGATCTCTACCAACGAGAGATCCAGAGTGACCAGAACCTGAAGGTGCTGCCACCCC 1131
         |||:|||||| | ||||| :|||||||||||||:|||||     :|||| | |||||| |||
Db  1062 TAAACCAG--TTTTTACCAACGRGATCCAGRKGKRACCAGAACCTGGRG--GCTGCCACCCC 1005

Qy  1132 CTCTGCCCACTATTGCCCACTCTTCACCAGCCTCCATCTTCACCCGACAAGCCGTCGGGGCC 1191
         | ||||||  |||||| | ||||:||||||||||    |||:|| :||||| ||:|||| ||
Db  1004 CTYTGCCCACTATKGCCAACYYCACCAGCCTCCCNTCTTCGTTAACTTCTTCAGGAACTGGCC 945

Qy  1192 CATGGAGAGAGACTGCCCTGCCAGGCGCCCTGGAGGATGGCCACGACGACCAGCTGATCTGG 1251
         |||||||||||||:| || |||||||||| ||||||||| |||||||:|||||||  ||:|||
Db   944 CATGGAGAAAACTGCCKGCCAGGGGCCCTGGAGGGGGCGACGACGACCKGCTCCATCTWCCTGG 885

Qy  1252 TGAAGCCGGAGAACACAACACCGCCTCATCGAGGTGTTGGTTCGGACCACAGAGACACGGACCCCG 1311
         |||:|||||||||||||||||||||||| |||| ||||||||||||||||||||||||||:||:
Db   884 TGAAGCCGGAGAACACCAACCCCCCTCATGCAGKTGTGGTGGACCAGARACACGACCCCG 825

Qy  1312 GGGGGCTGGACCCGTCAGGAGACGACGCCTGGAATGGGCTCGTTAACTTCTTCAGGAACTGGG 1371
         |||||||||||||| ||||||||| | || :||  |  |  |||  ||||||||||||||||
Db   824 GGGGGCTGGACCGTCATCMAGRAGACGGCCTGGAATGGCGTCGTTAACTTCTTCAGGAACTGGG 765

Qy  1372 AGACGCAGCAAGCAAAGGGGTTTGGGAACATTGACGGCGGCAAAAACTGGCTGGGGCCTGGAGAACA 1431
         |:|  |||||||||||||||||||||||  |||||| |:| ||||||  ||| ||| ||||||||||
Db   764 AGACGAACAAGCAAAGGGGTTTGGGAACATTGACGGCCGCAAAAACTGGCTGGGGCCTGGAGAACA 705

Qy  1432 TTTACTGGCTGACGAACCAAGCGACTACACAAACTCCTGGTGACCATGGAGACTGGTCCG 1491
         |:||||||||||||||||:|:||   ||||||||||||||| ||| || |||| |||||||
Db   704 TTWACTGGCTGACGAACCAAGCGACAACTACACAAACTCCTTWACGTGGCGCACAACGGCA 645

Qy  1492 GCCGCAAAGTCTTTGCAGAATACGGCCAGTTTCCGCCGCTGGAACCTGAGACCCAGTATTATA 1551
         ||||||||||| |||||||||||||||||||||||:||:||||||||||||||| |||||:|:|
Db   644 GCCGCAAAGTCTTTGCAGAATACGGCCAGTTTCCGCCGCTGGAACCTGAGACGGAGTATKATA 585

Qy  1552 AGCTGCGGCGTGGGGGCGCCTACCATGGCAATGCGGGGGTGACCTCCTTTACATGGCACGGGCA 1611
         |||:|:||||||||||| |||||||||||||||:|||||| |||||||||||||| ||||||||
Db   584 AGCTGCGGCCTGGGGGCGCCTACCATGGCAATGCGGGGTTAACTCCTTTACGTGGCACACGGCA 525

Qy  1612 AGCAGTTCACCACCTGGACAGAGATCAGATCATGATGTGTTACACAGAGAAACTGTGCCCACTACC 1671
         |:||||||||||||  |||:|||||||||||||| |||||:|||||||||:||:|||||||||||||
Db   524 AGCAGTTCACCACCTGGACAGAGATCATGATGTCNACACGGAGAAAACTGTGCCCACTACC 465

Qy  1672 AGAAGGGGAGGCTGGTGGTGTATAACGGCCTGTTGCCCACTCCAACCTCAACGGGGGTCTGGTACC 1731
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   524 ...
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First alignment set (left column):

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Qy  1405 GCGAATACTGGCTGGGCCTGGGAACACATTTACTGGCTGACGACCAAGCCAACTACAAAC 1464
         |||||||||||||||||||||||||||||||||||||||||||:||:|||||||||||||
Db   745 GCGAATACTGGCTGGGCCCTGGAGAACACATTTACTGGCTGACGACCAAGCCAACTACAAAC 686

Qy  1465 TCCTGGTGACCATGGAGACTGGTCCGGCCGCGCAAAGTCTTTGCAGAATACGGCCAGTTTCC 1524
         |:||:|||||||||||||||||||||||:||||||||||||||||||||||||||||||||||
Db   685 TCCTGGTGACCATGGAGGACTGGTCCGGCCGCGCAAAGTCTTTGCAGAAATACGGCCAGTTTCC 626

Qy  1525 GCCGCTGGAACCTGAGACGGAGTATTATAACGGCCTGCGGCGTGGGCCTACCATGGCAATGCGGG 1584
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   625 GCCTGGAACCTGAGACGGAGTATTATAACGGCCTGCGGCGTGGGCCTACCATGGCAATGCGGG 566

Qy  1585 GTGACTCCTTTACATGGCACAACGGCAGCCGCAAGCAGTTCACCACCCTGGGACAGAGGATCATGATG 1644
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   565 GTGACTCCTTTACATGGCACAACGGCAGCCGCAAGCAGTTCACCACCCTGGGACAGAGGATCATGATG 506

Qy  1645 TCTACACAGGAAACTGTGCCCACTACCAGGCGGCTGGTGGTGTATAACGGCCTGTGCCC 1704
         |||||||||||||||||||||||||||||||||:||||||||||||||||||||||||||
Db   505 TCTACACAGGAAACTGTGCCCACTACCAGAAGGGGAGGCTGGTGGTGTATAACGGCCTGTGCCC 446

Qy  1705 ACTCCAACCTCAACGGGGGTCTGGTTACCCGGGGGGGCCCATTACCGGCCTACCAGGACG 1764
         ||||||||||:||||:||||||||||||:||||||| |||||||||||||||||||||||||
Db   445 ACTCCAACCTCAACGGGGGTCTGGTTATAACCGGAGCGGGGCCCATTACCGGCCTACCAGGACG 386

Qy  1765 GAGTTACTGGGGGCTGAGTTCCGAGGAGGGGCTTCTTACTCAC-TCAAGAAAGTGGTTGATGATG 1823
         |||:||||||||||:||:||||||||||||||||||:||||||| |||||||||||||||||||||
Db   385 GAGTTACTGGGGCTGCTCACTCACTTCAAGAAAGTGGTGATGATG 326

Qy  1824 ATCCGACCGAACCCCAACACCTTCCACTAAGCCAGTCCCCCTTCGACCTCTGCGGGCC 1883
         |||:||||||||:| ||:|||||||||:|||||||||||||||||||||||||||||||
Db   325 ATCCGACCGAACCCCAACACCTTCCACTAAGCCAGTCCCCCTTCGACCTCTGCGGGCC 266

Qy  1884 ATTGCCAGGAGCCCACCTGGTCACGCTGGCCACAGAACTCTTCACCAGT 1943
         |||||||||||||||||||||||||||||||||||||||||||||||||
Db   265 ATTGCCAGGAGCCCACCTGGTCACGCTGGCCACAGAACTCTTCACCAGT 206

Qy  1944 TCATCCTGAGGCTGGAGGACCCGGGATGCTGGATTCTGTTTCCGGAGTCACTGCAGCGG 2003
         |||||||||||||||||||:||||||||||||||||||||||||||||||||||||||||
Db   205 TCATCCTGAGGCTGGGGGACCCGGGATGCTGGATTCTGTTTCCGGAGTCACTGCAGCGG 146

Qy  2004 ATGATGGAACTGAATCGATCGGATACCGGTGTTTTTCTGTCCCTCCCCTACTTCACCAGACA 2063
         |||||||||||||||:||:|||||||:||||||||||||||||||||||||||||||||||||
Db   145 ATGATGGAACTGAATCGATCGGGTTTTTCTGTCCCCTCCCAACTTCCTTCACACCAGACA 86

Qy  2064 GCCCCTCATGTCTCCAGAGCAGGAGACTACAGAGACAGGACAAGCCGTCGGGGCG 2122
         |||||||||||||||||||||||||||||:|||||||||| ||||||||||||||
Db    85 GCCCCTCATGTCTCCAGAGCAGGAGACTAC---TTTAAATAAAATTA 26

Qy  2123 AGTCTCTACAAATAAAAACAA 2144
         |||:||||:|||||||  : |:
Db    25 AGTATCTAAAATAAAANNNVAM 4
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RESULT 4
AL572386/c

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LOCUS       AL572386              1201 bp    mRNA    linear    EST 31-MAY-2003
DEFINITION  AL572386 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
            clone CS0DI011YP14 3-PRIME, mRNA sequence.
ACCESSION   AL572386
VERSION     AL572386.2  GI:31293769
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1201)
  AUTHORS   Li,W.B., Gruber,C., Jesse,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT     On Feb 16, 2001 this sequence version replaced gi:12930602.
            Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr
            Library was constructed by Life Technologies, a division of
            Invitrogen. This sequence belongs to sequence cluster 4821.r For
            more information about this cluster, see
            http://www.genoscope.cns.fr/
            cgi-bin/cluster.cgi?seq=CS0DI011DH07NP1&cluster=4821.r. Contact :
            Feng Liang Email : fliang@lifetech.com URL :
            http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
            Faraday Avenue Genoscope sequence ID : CS0DI011DH07NP1.
FEATURES             Location/Qualifiers
     source          1..1201
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="CS0DI011YP14"
                     /tissue_type="PLACENTA COT 25-NORMALIZED"
                     /clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
                     /note="1st strand cDNA was primed with a Not-oligo(dT)
                     primer. Five prime end enriched, double-strand cDNA was
                     digested with Not I and cloned into the Not I and EcoR V
                     sites of the pCMVSPORT 6 vector. Library was normalized."
ORIGIN
```

Query Match 43.2%; Score 939.8; DB 9; Length 1201;
Best Local Similarity 89.0%; Pred. No. 6, 7e-115;
Matches 1031; Conservative 37; Mismatches 82; Indels 9; Gaps 6;

[Sequence alignment block of Qy (query) and Db (database) rows with numbered nucleotide sequences — positions 44 through 2135 for the query and corresponding database positions 140 through 2004.]

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Qy    2005  TGATGGAACTGAATCGATACGGTGTTTTCTGTCCTCCTACTTTCTTCACCACGACAG  2064
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     139  TGATGGAACTGAATCGATACGGTGTTTTCTGTCCTCCTACTTTCTTCACCACGACAG   80

Qy    2065  CCCCTCATGTCTCCAGGACGCAGGAGGACTACAGACAACTCTTTCTTTAAATTAAATTAAG  2124
            |:|::|:|||||||||||||||||||||||||||||||||||||||||||||||
Db      79  CCCCMCMTRNCNCCAGGACAGAGCAGACARRACAGACARTNCNG-CGNNAAGTKAATNAKG   21

Qy    2125  TCTTCACHATAAAAACACA  2143
            |||||||||||||
Db      20  NCACAAXAANNKAATVANM   2
```

RESULT 5

LOCUS   AK041888   3560 bp   mRNA   linear   HTC 19-SEP-2003

DEFINITION   Mus musculus 3 days neonate thymus cDNA, RIKEN full-length enriched
             library, clone:A630044F14 product:ANGIOPOIETIN-RELATED PROTEIN 2
             PRECURSOR, full insert sequence.

ACCESSION   AK041888

VERSION   AK041888.1 GI:26088710

KEYWORDS   HTC; CAP trapper.

SOURCE   Mus musculus (house mouse)

ORGANISM   Mus musculus
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE   1
  AUTHORS   Carninci,P. and Hayashizaki,Y.
  TITLE   High-efficiency full-length cDNA cloning
  JOURNAL   Meth. Enzymol. 303, 19-44 (1999)
  MEDLINE   99279253
  PUBMED   10349636

REFERENCE   2
  AUTHORS   Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
             Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
  TITLE   Normalization and subtraction of cap-trapper-selected cDNAs to
             prepare full-length cDNA libraries for rapid discovery of new genes
  JOURNAL   Genome Res. 10 (10), 1617-1630 (2000)
  MEDLINE   20499374
  PUBMED   11042159

REFERENCE   3
  AUTHORS   Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
             Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,
             Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,
             Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,
             Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M.,
             Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J.,
             Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
  TITLE   RIKEN integrated sequence analysis (RISA) system--384-format
             sequencing pipeline with 384 multicapillary sequencer
  JOURNAL   Genome Res. 10 (11), 1757-1771 (2000)
  MEDLINE   20530913
  PUBMED   11076861

REFERENCE   4
  AUTHORS   The RIKEN Genome Exploration Research Group Phase II Team and the
             FANTOM Consortium.
  TITLE   Functional annotation of a full-length mouse cDNA collection
  JOURNAL   Nature 409, 685-690 (2001)

REFERENCE   5
  AUTHORS   The FANTOM Consortium and the RIKEN Genome Exploration Research
             Group Phase I & II Team.
  TITLE   Analysis of the mouse transcriptome based on functional annotation
             of 60,770 full-length cDNAs
  JOURNAL   Nature 420, 563-573 (2002)

REFERENCE   6 (bases 1 to 3560)
  AUTHORS   Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P.,
             Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W.,
             Hayashida,K., Hayatsu,N., Hiraoka,K., Hiraoka,T., Hirozane,T.,
             Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T.,
             Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M.,
             Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M.,
             Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N.,
             Okazaki,Y., Saito,R., Saito,H., Sakai,C., Sakai,K., Sakazume,N.,
```

COMMENT   cDNA library was prepared and sequenced in Mouse Genome
             Encyclopedia Project of Genome Exploration Research Group in Riken
             Genomic Sciences Center and Genome Science Laboratory in RIKEN.
             Division of Experimental Animal Research in Riken contributed to
             prepare mouse tissues.
             Tissues were provided by Dr. John Todd (Dept. of Medical Genetics
             Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome
             Trust/MRC building Addenbrookes Hospital Cambridge) whose
             assistance we gratefully acknowledge.
             Please visit our web site for further details.
             URL:http://genome.gsc.riken.go.jp/
             URL:http://fantom.gsc.riken.go.jp/.

FEATURES   Location/Qualifiers
     source   1..3560
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                     /mol_type="mRNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="A630044F14"
                     /tissue_type="thymus"
                     /clone_lib="RIKEN full-length enriched mouse cDNA library"
                     /dev_stage="3 days neonate"
     misc_feature   1..3560
                     /note="ANGIOPOIETIN-RELATED PROTEIN 2 PRECURSOR
                     (SWISSPROT|Q9R045, evidence: FASTY, 99.6%ID, 100%length,
                     match=1479)"

TITLE   Direct Submission
JOURNAL   Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
               Physical and Chemical Research (RIKEN), Laboratory for Genome
               Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
               RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
               Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp,
               URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
               Fax:81-45-503-9216)

               Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T.,
               Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S.,
               Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A.,
               Muramatsu,M. and Hayashizaki,Y.

ORIGIN

Query Match   42.9%; Score 931.8; DB 11; Length 3560;
Best Local Similarity 81.9%;
Matches 1149; Conservative 0; Mismatches 217; Indels 37; Gaps 5;

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Qy      3  AAATGAGGCTGCTGCGGACAGGCGTGAGGATGAACCCCAAAGCCCTGGA------------   49
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Db     46  AACTGAGGCTGCTGCGTCGTCGGATCGGAATCGGACCCCAAGCCCTGAGTGGTGTGTTGGA  105

Qy     50  --------CCTGCCGACGTGGCACTGAGGCAGCGCGCGCTGACCGCTACTGTGAGGGAAAGAA  101
                   ||||||||||||||||||||||  ||||||||  |||||||||||||||||||
Db    106  CCCAGGAGCACCTGCAAGAGCAGCATGCACTPAAGGCAGCTCGCGGACCACACTGTGAGGCAGCA  165

Qy    102  GGGTTGTGAGCAGCCCCGCAGAGACCCCTGGGCCCAGCCCTGGGCCCCAGCCTCTGCCGGAGCCC  161
           ||||| ||||||||  ||||||||||||||||| ||||| ||||||||||||||||||
Db    166  GGGTTGGGAGCAGCCCCCCGTGACCCACAGAGCCAGCCCTCATCCCTAGGAGCTTCAGAGAGCA  225

Qy    162  TCTGTGGAGGCAGAGCCCAGTGGAGCCCCAGTGTAGGAGGCCAGGGCAGGTTGGCAGCCA--CCGGC  219
           ||| |||||||||||||| ||||| ||  |||||  | || | |||||||||||   |||
Db    226  TAGACTG-----CTGCCAGCGTGAGGCCCAGTGAGCCAGGGCCATGGGCAGGGCTTGGCAGCCAGT  280

Qy    220  CTGCAACTCAGGAACCCCTCCAGAGGCAGCAGGCTGCCCCGCGTGACGGCGCAGGGGGTG  279
           |||||| ||||||||||| |||||||| ||||| ||||| ||||||||||||||||||
Db    281  CTGAGACTCGGGACCTTCCTCGGAGCCCACGGCCAGGCTGTCGCTGATGG-CACCGTG  339

Qy    280  AAGCATCTGAGGAGCCGCCCCCCGCCCCCGGAGCCCAAGCAGAGGGGGGAAGAGGGAA  339
           || |||| |||||||||||||||||||  | ||||||||||||||||||||| ||||
Db    340  AGGCAGTGAAGCGGCTCGTCCAGGGCCAAGCAGGGGAGAGAGAAGGAGAGGCTTTCA  391

Qy    340  TCACAAAGAATAACCCACCATTTTGCAAAGAACCATGAGGGCCACTGTGCGTGACATGCTGGT  399
           ||||||| ||||| |||||||||||||||||||||||||||| |||||||||||||||||||
Db    392  TCATAAAGAGCAACCAACCAGCACACTGCAAGGACCATGAGGCCCACTGTGTRATGACCTACTGGT  451
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RESULT 6
AL547465
LOCUS       AL547465     1201 bp    mRNA    linear   EST 31-MAY-2003
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```
Qy    400 GGCTTCGGGACTGCTGCTGGGCTTGGGGTAGGGTGTTGCGAGGGCCAGGAGGGACGGTTTTTGAGGGCA 459
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    452 GGCTTGGGACTGCTGCTGGGCCTACGGTCTGGGAGTGGCCCCAGGAGGGCTGACGTTGAGGGCA 511

Qy    460 CTGAGGAGGGGCTCGCCACAGAGAGTTCATTTACTTAAACAGGTACAAGGCAGT 519
          |||||||||||||||||||||||||||||||||||||||||||
Db    512 CAGAGGATGGTTCACAGAGAGTACATTTACCTCAACGGTACAAGGCGGGTGAGT 571

Qy    520 CCCAGGACAAGTGCACTACACCTTTCATTGTGTGCCCCACCACGCGGGGTCACGGTTGCCATCT 579
          ||||||||||||||||||||||||||||||||||||||||||||
Db    572 CCCCGACAAGTGCAACCTACACTTTCATTGTCCCCAGGAGCGGGGGCAGGGTGAGT 631

Qy    580 GCGTCAACTTCCAAGGAGCCTGAGGTGCTTCTCGAGGAGCAGGAGCAGGAGGAGCTAG 639
          ||||||||||||||||||||||||||||||||||||||||
Db    632 GTGTCAACTTCCAAGGAGCCTGAGGTGCCACCTGGTGTGCACAAGCAGCAGGAGCTGG 691

Qy    640 AGGTGCTCAACACAATGAGCTGTGCTCAGCAGAGAAGAGCCAGATCGAGACGGTGCAGCAGCTGG 699
          |||||||||||||||||||||||||||||||||||||||||
Db    692 AGCTGCTCAACAATGAGCTGCTTAAGCAGAGGAGCGGCAGAATCGAGAGCCTGCAGCAGCTGG 751

Qy    700 TGAAGGTGGACGGCGCATTGTGACGAGGGTGAAGCTCGCCAAGGACAGCGGCAACA 759
          ||||||||||||||||||||||||||||||||||||||||
Db    752 TAGAGGTTGAGCGGAGGCATCGTGAGCGTGGAAGCTGCTGGAGGACGGCGCAACA 811

Qy    760 TGAACTCCGGGGTTCACGCAGCTTCCTGCACGACGATCATCCGCAAGCGGGG 819
          |||||||||||||||||||||||||||||||||||
Db    812 TGAACTTCGAGACTCACGCAGCTGCATGCAACGTCCTCTACGGAATCAGAAAGGGAG 871

Qy    820 ACAAGGCGGTTGGAGCTCTCCCAGCTGGAGAACAGGAGGATCCTGAAGCAGCAGCGACATGC 879
          |||||||||||||||||||||||||||||||||||||
Db    872 ACAATGCCGCTGGAGGCTCTCCCAGCTGGAGGACAGCTGAAGCGGCCACAGCACATGC 931

Qy    880 TGCAGCTGGCCAGCGAAGTACAAGGACTGGAGCGAGTACAGCACACCTGGCCACACTGG 939
          ||||||||||||||||||||||||||||||||||||
Db    932 TGCAGCTGGCAAGCGACATGGGACCAAGGGCCACACGTTCCAGCACCTGGCCTATGCTGG 991

Qy    940 CCCACAACCAATCAGAGAATCATTGCGGCAGCTTGAGGAGGCACTCCACGAGGGTGCCCCTCGG 999
          |||||||||||||||||||||||||||||||||||
Db    992 CACACAACCAATCAGATGAGGTCATTGCTCAGCTCGAAGAGGCACGTGCCGACGCGGTACCTGCAG 1051

Qy   1000 CCAGGCCCGTCCCCAGCCACCCCGCCCCCTGCCCGCGCCCCCGGGTTCTCTACCACCACCACCT 1059
          |||||||||||||||||||||||||||||||||||||
Db   1052 CCAGGCCTATGCCCCCAGCACCCCCAGCGCTCCACGTCGGGTCTACCACCACCAACCACCT 1111

Qy   1060 ACAACCCGCATCATCAACCAGATCTCTACCAACGGAGATCCAGAGTTGACCAGAACCTGAAGG 1119
          |||||||||||||||||||||||||||||||||||||
Db   1112 ACAACCCGCCATCATCAACCAGATTTCACCCAAGGAGTGACCAGAATCTGAAGG 1171

Qy   1120 TGCTGGCCACCCCCTTCTGCCCACTATGCCCACTCTCCACTCTTCCACCGACA 1179
          |||||||||||||||||||||||||||||||||||
Db   1172 TGCTCGCCCGCGCCTTCCCGCCGCCACTGCGTCCCAGTGTCCCATCTTCCACTGATA 1231

Qy   1180 AGCCGTCGGGGCCCCGGGAGGCCCATGGAGGAGACTGCGTGCAGGGATGGCCGCACGACACCCAGTG 1239
          ||||||||||||||||||||||||||||||||||||
Db   1232 AGCCACACAGGTCCATGGAGAGACTGCCTGCAAGCCCTGGCCGGAGGCCAGTG 1291

Qy   1240 CCATCTACCTGGTTGAACGCGGGGAGAACAACACCGCCTCATCAGGTTTGGTCGGACCAGA 1299
          |||||||||||||||||||||||||||||||||||
Db   1292 CCATCTACCTGGTTGAAGCCTGAGAATCACAGGGCCACCGCTGATCCAGGTGTGTTGGACCAGA 1351

Qy   1300 GACCACGACCCCCCGGGGGCTGGACCGTCATCCAGGATGGCTGGATTCCT 1359
          ||||||||||||||||||||||||||||||||||||
Db   1352 GACCATGACCCTGAGGTTGGACTGTCATCCAGAGACGCCTGCGATGGCCTGCTGTGTCAACTTCT 1411

Qy   1360 TCAGGAACTGGGGAGACCTACAAG 1382
          |||||||||||||||||||
Db   1412 TCAGGAACTGGGGAGACCTATAAG 1434
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```
DEFINITION  AL547465 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
            clone CS0DI01lYP14 5-PRIME, mRNA sequence.
ACCESSION   AL547465
VERSION     AL547465.2  GI:31269296
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1201)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT     On Feb 15, 2001 this sequence version replaced gi:12881558.
            Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
            Library was constructed by Life Technologies, a division of
            Invitrogen. This sequence belongs to sequence cluster 4821.r For
            more information about this cluster, see
            http://www.genoscope.cns.fr/
            cgi-bin/cluster.cgi?seq=CS0DI01lDH07QP1&cluster=4821.r. Contact :
            Peng Liang Email : fliang@lifetech.com URL :
            http://fulllength.invitrogen.com/ InVitrogen Corporation 1600
            Faraday Avenue Genoscope sequence ID : CS0DI01lDH07QP1.
FEATURES             Location/Qualifiers
     source          1..1201
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="CS0DI01lYP14"
                     /tissue_type="PLACENTA"
                     /clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
                     /note="1st strand cDNA was primed with a NotI-oligo(dT)
                     primer. Five prime end enriched, double-strand cDNA was
                     digested with Not I and cloned into the Not I and EcoR V
                     sites of the pCMVSPORT 6 vector. Library was normalized."
ORIGIN
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Query Match           41.8%;  Score 908.6;  DB 9;  Length 1201;
Best Local Similarity 91.7%;
Matches  981;  Conservative  30;  Mismatches  52;  Indels  7;  Gaps  5;
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Qy      3 AAATGAGGCTGCCTGGGGACCGGCCGTCCGAGGGATGAAACCCCAAGCCCCTGACCTTGCCGAGCGTG 62
          ||||||||||||||||||||||||||||||||||||
Db     69 AAATGAGGCTGCTGCGCACGGCGTCAGGGATGAACCCCCAAGCCCTGACCTCCGAGCGTG 128

Qy     63 GCACTGAGGCAGGCGGCTGACGCTACTGTGAGGGAAAGAAGGTTGTGAGCGAGCCCCGCCCAGG 122
          |||||||||||||||||||||||||||||||||||
Db    129 GCACTGAGGCAGCGGCTGACGCTACTGTGAGGGAAAGAAGGTTGTGAGCGAGCCCCGCCCCA-G 187

Qy    123 ACCCCTGGCCAGCCCCTGGCCCCCAGCCCTTCTGCCGACCCTCTTGTCGGGCAGCAGCCAGTG 182
          ||||||||||||||||||||||||||||||||||||
Db    188 ACCCCTGGCCCAGCCCTTGGCCCCCAGCCCTTCTGCCGGAGCCCTTCTGTGGAGGCCAGTG 247

Qy    183 GAGCCCCAGTGAGGCCAGGGGCGTGCTTGGCCAGCCCCACCCGCCGGGAGCCCTGACGGTG 242
          ||||||||||||||||||||||||||||||||||||
Db    248 GAGCCCAGTGAGGCCAGGGCCTTGGCCAGCCACCCGCCGGGAGCCCTGACGGTG 307

Qy    243 AGGCCATGGACAGGCTGCCCCCGCGCTACCGCCCCAGGGTGAAGCAGTGTGGAGGCCCCG 302
          ||||||||||||||||||||||||||||||||||||
Db    308 AGGCCATGGACAGGCTGCCCCGCTACCGGCCAGGGTGAAGCATGTGAGGAGACGCCCCG 367

Qy    303 AGCCAAGCAGGAGGAGAGGGCTTTCATGAGATTCTTATTCACAAAGAATAACCACCATTT.362
          |||||||||||||||||||||||||||||||||||
Db    368 AGCCAAGCACGAGGGGAAGGGCTTCATCAGATTCTTATTCACAAAGAATAACCACCATTT 427

Qy    363 GCAAAGACCATGAGGCCACTGTCGCTGACATGCTGGTCGGACTGGCTGGCTGGCTGCCATG 422
          |||||||||||||||||||||||||||||||||||
Db    428 GCAAGGACCATGAGGCCACTGTGCGTGACATGCTGGTTGGCTCGGACTGGCTGGCTGCCATG 487

Qy    423 GGAGCTGTTGCAGGCCCAGGAGGACGGGTTTGAGGGCACTGAGGAGGGCTGCCGCAAGAGAG 482
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RESULT 7

AL546299

LOCUS   AL546299   1201 bp   mRNA   linear   EST 31-MAY-2003
DEFINITION   AL546299 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
             clone CS0DI031YF21 5-PRIME, mRNA sequence.
ACCESSION   AL546299
VERSION   AL546299.2 GI:31268133
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
  ORGANISM   Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 1201)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE   Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT   On Feb 15, 2001 this sequence version replaced gi:11287279.
             Contact: Genoscope
             Genoscope - Centre National de Sequencage
             BP 191 91006 EVRY cedex - France
             Email: seqref@genoscope.cns.fr; Web : www.genoscope.cns.fr
             Library was constructed by Life Technologies, a division of
             Invitrogen. This sequence belongs to sequence cluster 4821.r For
             more information about this cluster, see
             http://www.genoscope.cns.fr/
             cgi-bin/cluster.cgi?seq=CS0DI031CC11QP1&cluster=4821.r. Contact :
             Feng Liang Email : fliang@lifetech.com URL :
             http://fullength.invitrogen.com/ InvitroGen Corporation 1600
             Faraday Avenue Genoscope sequence ID : CS0DI031CC11QP1.
FEATURES   Location/Qualifiers
     source   1..1201
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="CS0DI031YF21"
                     /tissue_type="PLACENTA COT 25-NORMALIZED"
                     /clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
                     /note="1st strand cDNA was primed with a NotI-oligo(dT)
                     primer. Five prime end enriched, double-strand cDNA was
                     digested with Not I and cloned into the Not I and EcoR V
                     sites of the pCMVSPORT 6 vector. Library was normalized."
ORIGIN

Query Match   40.7%; Score 885.2; DB 9; Length 1201;
Best Local Similarity   90.3%; Pred. No. 1.1e-107;
Matches   914; Conservative   34; Mismatches   63; Indels   1; Gaps   1;

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RESULT 8
LOCUS       AL554832                1201 bp    mRNA    linear    EST 31-MAY-2003
DEFINITION  AL554832 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
            clone CS0DI087YH21 5-PRIME, mRNA sequence.
ACCESSION   AL554832
VERSION     AL554832.2  GI:31276642
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1201)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT     On Feb 15, 2001 this sequence version replaced gi:1289989.
            Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr
            Library was constructed by Life Technologies, a division of
            Invitrogen. This sequence belongs to sequence cluster 4821.r For
            more information about this cluster, see
            http://www.genoscope.cns.fr/
            cgi-bin/cluster.cgi?seq=CS0DI087YH21QP1&cluster=4821.r Contact :
            Feng Liang Email : fliang@lifetech.com URL :
            http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
            Faraday Avenue Genoscope sequence ID : CS0DI087YH21QP1.
FEATURES             Location/Qualifiers
     source          1..1201
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="CS0DI087YH21"
                     /tissue_type="PLACENTA COT 25-NORMALIZED"
                     /clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
                     /note="1st strand cDNA was primed with a NotI-oligo(dT)
                     primer. Five prime end enriched, double-strand cDNA was
                     digested with Not I and cloned into the Not I and EcoR V
                     sites of the pCMVSPORT 6 vector. Library was normalized."
ORIGIN

Query Match
Best Local Similarity   40.2%;  Score 873.8;  DB 9;  Length 1201;
87.8%;   Pred. No. 3.5e-106;
Matches 921;  Conservative 53;  Mismatches 68;  Indels 7;  Gaps 3;

Qy   15 TCGGGACGGGGCCTTGAGGATTGAACACCCAAGCCCTTGGACTGCCGGAGCCTGAGCCAG   74
         ||||||  | || |||||||| |||||||||||||||||||||||||||||||||||||
Db   69 TCGGGACGGCCCTTGAGGATGGAACACCCAAGCCCTTGGACTGCCGGAGCCTGAGGCAG  128

Qy   75 CGGCTGAGCGCTACTGTGAGGGAAGAAGGTTTGTGAGCAGCCTGCCGGACCCCTGGGCCAG  134
         ||||||| || ||||| ||||| |||||| ||||||||||||||||||||||||||||
Db  129 CGGCTGACGCGCTACTGTGRAGGGAAGAAGGTTGTGACAGCCCCGCGAGGACCCCTGGGCCAG  188

Qy  135 CCCTGGCGCCCCAGCCTCTCGCGGAGCCCTTCGTGTGGGAGGGAGAGGCCAGTGAGCCCAGTGAG  194
         |||||||||||||||||||| || ||||||||||||||||||||||||||||||||||
Db  189 CCCTGGCCCCAGCCTTCTGCCGAGGCCCTGTGTGGAGGGCGAGAGGCCAGTGGAGCCCAGTGAG  248

Qy  843 CTGGAGAACAGGATCCTGAACAGCCAGCGAGCCGACAAGCTGCAGCGTGGCCAGCAAGTACAG  902
         ||||||||||||||||||||||||||||||      |||| |||   ||||||||||||
Db  932 CTGGAGAACAGGATCCTGAACAGCCAGAAGCCGACAGCTGCA-STGGCCAGCAAGTAMAG  990

Qy  903 GACCTGGAGACAAGTACCACACACTGGCCACACTGGCCCACACCAATCAGGATCATC  962
         |||  | |||  | ||
Db  991 GACTGGGGAGGACAARTACCACACACTGGGCMWACTGGCGCMWMCRATMRARAYATCSSCKKTT  1050

Qy  963 GCCCAGCGCTTGAGGAGCGCACTGCAGAGGGGTGCCCTGCCCCTCGGCACGCGTCCCC  1014
         ||||| ||| || || | |  :|  |:
Db 1051 GAGGAGCCTGCMAAGGTKXYCYCGSCMRGSBCYKKYMAAMAWMACCCSCRNCCCC  1102
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RESULT 9
LOCUS       BM906705                1111 bp    mRNA    linear    EST 12-MAR-2002
DEFINITION  AGENCOURT_6621548 NIH_MGC_125 Homo sapiens cDNA clone IMAGE:5724698
            5', mRNA sequence.
ACCESSION   BM906705
VERSION     BM906705.1  GI:19357084
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Qy  195 GCAGGGCTGCTTGGCACCCAGCCACCCGCCCTGCCAACTCAGGAACCCCTTCCAGATGGGACA  254
         |||||| ||||| || |||   | ||| ||   || || |||||||||||||||||||||
Db  249 GCAGGGCTGCTTGGCACCCAGCCGCCACCCGGCCCTGCCAACTCAGGAACCCCTTCCAGAGGGCCATGGACA  308

Qy  255 GGCTGCCCCGCTGACCGCCCCAGGGTGAAGCATGTGAAGTGAGAGGGCGCGGCCCCGGGAGGA  314
         |||||||| ||||||||| ||||| | |||||| || |||||||||||||||||||||
Db  309 GGCTGCCCCGCTGACCGCCCCAGGGTGAAGCATGTGAAGGGTGAGGGCCATGGACA  368

Qy  315 GGGAAGAGGCTTTCATAGATTCTTATTCACAAAGGATAAACACACATTTTGCAAAGACCATG  374
         |||||||||||| ||| |||| ||||| || |||||||||| ||||||||||||||||
Db  369 GGGAAGAGGCTTTCATAGATTCTTATTCACAAAGGATAAACACCATTTTGCAAGGACCATG  428

Qy  375 AGGCCACTTGTTGCGTGACATGCTTGGTGGTGGCCTCGGACTGCCTCGGACTGGGGAGGCTGTTGCA  434
         ||| |||| | |||| |||||||||||| || |||  |||||||||||||||||||||
Db  429 AGGCCACTGTTGCGTGACATGCTTGGTGGTGGCCTCGGACTGCCTCCATGGGGGAGGCTGTTGCA  488

Qy  435 GGGCCAGGAGGACGGGTTTTGAGGGCACTGAGGAGGCCGCCAAGAGTTCATTTACCTA  494
         |||||||||||| ||||||| |||||||||||||||||||||||| ||||||||||
Db  489 CAGCCAGGAGGACGGGTTTTGAGGGCACTGAGGGTGGCCTCAACTCCAAGGAGTCGAGGTCAATGGACA  548

Qy  495 AACAGGTACAAGCGGGGGCGGGGGGAGTCCCAGACAAGTGCACCTACACCTTCATTGTGCCC  554
         |||||||||||| | ||||||||||| || ||||||||||||||||||||||||||||
Db  549 AACAGGTACAAGCGGGCGGAATACCAGGACAAGTGCACCTACACCTTCATTGTGCCC  608

Qy  555 CAGCAGCGCGG-GTCACGGGTGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGTGGA  613
         |||||||| || |||||| || |  |  :||:
Db  609 CAGCAGCGCGGGGTCACGGGTGCCATCCGTCCAACTCCGTCAGCCAGCAGGCAGGAGGGCTCTTCGGA  668

Qy  614 GAACCGGAGTGCATAAGCAGGAGGAGCTAGAGCTGCTCAACAATGAGCTGCTCAAGCAGCAGCG  673
         |||||||| |||| |||||||||||| |||||||||||||||||||||||||||||||
Db  669 GAACCGGAGTGCATAAGCAGGAGGAGCTAGAGCTGCTCAACAATGAGCTGCTCAAGCAGCAGCG  728

Qy  674 GCAGATCGAGAGCGCTGCAGCTGGTGGAGTGGAGCGGGGGCCATTGTGAGCGGAGGTGAA  733
         |||||| ||||| || || ||||| |||| |||||||||||||||||||||||||||
Db  729 GCAGATCGAGAGCGGCTGCAGCTGGTGCTGGGGCCATTGTGACGGAGGTGGAA  788

Qy  734 GCTGCGTCGGCCAAGGAGAGCCGCGAAACATGAATCGCGGGGTCACGCGAGCGGCTCACATCGAGCT  793
         |||| ||||| ||||||||| || |||||  ||||||||| |||||||||||||||||
Db  789 KCTTKCTCGCTCAAGGAGAGCCCGCAACAKKAACKCKCGGGGTCACGCGAGCGGCTCTACACKGAACGGCK  848

Qy  794 CCTGCACGAGATCATCGGACAACACCGGTGGAGCTCTCCCAGCTCTGGAGAACAG  853
         | |||||| |||||||||  | |  |  ||||||||||||||||||||||||||
Db  849 CCKGCACGAGAGCAKCCGCWAGCGGAGCACGCGTKWGKCKCKCCCATCTGGAGAGCAG  908

Qy  854 GATCCTGAACAGCAGCCGACTAGCCCGGTGGCACTGGGCCGAGTCAACGTGCAGTACAAGGAGACCTTGAGCA  913
         || ||||||||| |||| ||| || | ||| ||||||||||||||||||||||||||
Db  909 GAXCCSKGWACCARAMAGCCGAMAKGCKGGACCKGGAGCW  968

Qy  914 CAAGTACCAGCAGCACCTGGCCCACAACTGGGCCGCCAACAATCAGAAGATCATCGGGGCAGCTTGA  973
         ||||||| |||| |||||||||| |  | ||| | | |||||| ||||||||||||||
Db  969 YAAKK-CYAGCMCCKGCCMATGGCCC------AYAACAACCAGWAAGHRCGGCGCGTTG  1022

Qy  974 GGAGCACTGCCAGAGGGGTGCCCTCGGCCAGGACCGGTCCCCAGCCCACCCCCCCGCTGCCCC  1033
         || || || || |||||| |||||| || |   || |||||||||||||||||||||||
Db 1023 ARGAGCMTKCCARARGGGGSCSCBGCCATGGGGGSCARCCACCCCGCKKCCCSCCK  1082

Qy 1034 GCCCCGGGTCTTACCACCACCCCCACCTTACA  1062
         ||||| || |||| |||| || |||||||||
Db 1083 GGGYDACAACACCWWYTCAACCYTCTTCA  1111
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REFERENCE   1 (bases 1 to 1111).
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
            National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE   Unpublished (1999)
JOURNAL
COMMENT   Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Invitrogen
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM12714 row: g column: 03
            High quality sequence start: 3
            High quality sequence stop: 640.
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source   1..1111
            /organism="Homo sapiens"
            /mol_type="mRNA"
            /db_xref="taxon:9606"
            /clone="IMAGE:5724698"
            /lab_host="DH10B"
            /clone_lib="NIH_MGC_125"
            /note="Organ: ovary (pool of 3); Vector: pCMV-SPORT6;
            Site 1: EcoRV (destroyed); Site 2: NotI; RNA source pool
            of three ovaries, from females ranging in age from 38 to
            49 yo. Library is oligo-dT primed and directionally cloned
            (EcoRV site is destroyed upon cloning). Average insert
            size 2.1 kb, insert size range 1-3.5 kb. Library is
            normalized and enriched for full-length clones and was
            constructed by C. Gruber (Invitrogen). Research Genetics
            tracking code 036."
ORIGIN

Query Match   40.1%; Score 870.6; DB 12; Length 1111;
Best Local Similarity 92.2%; Pred. No. 9.6e-106;
Matches 987; Conservative 0; Mismatches 69; Indels 15; Gaps 6;

Qy   3 AAATGAGGCTGCTTCGCGACGGCGGCGCCCTGAGGATGAACCCCAAGCCCTGAGACCTGCCGAGCGTG 62
          ||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db   39 AAATGAGGCTGCTTCGCGACGGGCCCTGAGGATGGACCCCAAGCCCTGAGACCTGCCGAGCGTG 98

Qy   63 GCACTGAGGCAGGCGGCCTGACGCTACTGTGAGGGGAAAGAAGGTTGTGAGCAGCAGCCCGAGG 122
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   99 GCACTGAGGCAGGCGGCTGACGCTACTGTGAGGGGAAAGAAGGTTGTGAGCAGCAGCCCGAGG 158

Qy   123 ACCCCTGGCCAGCCCCAGCCTCTGCCCGACGGACCCTCTGTTGGAGGCAGAGCCAGTG 182
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   159 ACCCCTGGCCCAGCCCCAGCCTCTGCCGGAGGCCCTCTGTTGGAGGCAGAGCCAGTG 218

Qy   183 GAGCCCCACTGAGGCAGGGCGCTGCTTGGCAGCCACCGGCCGCCTGCCAACTCAGGAACCCCTCCAG 242
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   219 GAGCCCCAGTGAGGCAGGGCGTGCTTGGCACCACCGGCCGCCTGCAACTCAGGAACCCCTCCAG 278

Qy   243 AGGCCCATGGAACAGGCCTGCCCCGCGTTGACCGCGCCAGGGTGAAGCAATGTGAGGAGCCCGGGCCCGG 302
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   279 AGGCCCATGGACAGGCCTGCCCCGCGTTGACCGCGCCAGGGTGAAGCATGTGAGGAGCCCGGGCCCGG 338

Qy   303 AGCCAAGCAGGAGGGAAGGAGGCTTTCATAGATTTCTATTCACAAAGAATAACCACCACCATTTT 362
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   339 AGCCAAGCAGGAGGAAGGAGGCTTTCATAGATTTCTATTCACAAAGAATAACCACCACCATTTT 398

Qy   363 GCAAAGACCATGAGGCCACTGTGCGTGGGTGGTGGCTCCGACTGCTGGCGTGCCATG 422
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   399 GCAAGGACCATGAGGCCACTGTGCCTGACATGCTGGTGGCTCCGACTGCTGGCTGGCCATG 458

Qy   423 GGAGCTGGTTGCAGCCCAGAGACGGGTTTTTGAGGGGACTTCGCCAAGACAG 482
          ||||||||||||||||||||||||||||||||||||||||||||||
Db   459 GGAGCTGGTTGCAGGCCCAGAGGACGGGTTTTTGAGGGGGCTTCGCCAAGAGAG 518

Qy   483 TTCATTTACCTAAACACAGGTACAACGCGGCGCGGGGGCGGGGGTCCCAGGACAGAAGTGCACCTACACC 542
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   519 TTCATTTACCTAAACACAGGTACAACGCGGCGCGGGGGCGGGGGTCCCAGGACAGAAGTGCACCTACACC 578

Qy   519 TTCATTTACCTAAACACAGGTACAACGCGGCGCGGGGGCGGGGGTCCCAGGACAGAAGTGCACCTACACC 578
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   543 TTCATTGTGCCCCAGCAGCGGGTCACGGGTTGCCATCTGCCTCAACTCCAAGGAGGAGGCTGAG 602

Qy   579 TTCATTGTGTGCCCCAGCAGCGGGTCACGGGTTGCCATCTGCCTCAACTCCAAGGAGGAGGCTGAG 638
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   603 GTGCTTCTGGAGAACCGAGTCATTAAGACAGGAGAGCTAGAGAGCGGTGCCATCTGGCTCAACAATGAGGAGCTC 662

Qy   639 GTGCTTCTGGAGAACCGAGTCCATTAAGACAGGAGAGCTAGAGAGCGGTGCCATCTGGCTCAACAATGAGGAGCTC 698
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Db   663 AAGCAGAAGCGGCACATCAGACGCTGCCAGCGTGGTGGAAGGCTAGAGCAATTGTG 722

Qy   699 AAGCAGAAGCGGCAGATCGAGACCCTGCCAGCGTGGTGGAAGGCTAGAGCAATTGTG 758
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Db   723 AGCGGAGGTGAAGCTGCTGCGGGCAAAGAGAGCCCGCACACATGAACTCGGCGGGTCAGCAGCT 781

Qy   759 AGCGGAGGTGAAGCTGCTGCGGGCAAAGAGAGCCCGCACACATGAACTCGGCGGGTCAGCAGCT 818
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Db   782 CTACATCAGCTGCCTGCACGAGGATCCTGAACCAGAACAGCCAGCCGACGACATGCGCAAGCGGG 840

Qy   819 CTACATCAGCTGCCTGCACGAGGATCATCCGCCAGCGAACAACCGGTTGGAGTCTCCC 878
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Db   841 AGCTGGAGAACGCAGGACGATCCTGGAACCAACAGCAGCCAGACGAGCGGGTGGGCACT 900

Qy   841 AGCTGGAGAACAGCAGGATCCTGAACCAGAACAGCCAGCCGACATGCTGCAGTGTGCGCAGCAGCTACA 900
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Db   879 AGCTGGAGTAACAGATCCTGGAACCAACAGCAGCAGGCAGCATGTTCGCACCTTGCCGCAGCAGCTACA 938

Qy   879 AGCTGGAGTAACAGATCCTGGAACCAACAGCAGCAGGCAGCATGTTCGCACCTTGCCGCAGCAGCTACA 938
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Db   901 AGGA-CCTGGAGCACAAGTACACCAGCACCTGCCCACACTGGGCCCACAA-CCAATCAGAGAT 958

Qy   901 AGGA-CCTGGAGCACAAGTACACCAGCACCTGCCCACACTGGGCCCACAA-CCAATCAGAGAT 958
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Db   939 AGGACCCTGGAGGCACAAGTCCCGCCCCTGGGCCCCATTGGCCCCAACCAATCAAAAAT 998

Qy   939 AGGACCCTGGAGGCACAAGTCCCGCCCCTGGGCCCCATTGGCCCCAACCAATCAAAAAT 998
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Db   959 CATCGCGGCAGC--TTGAGGAGCACTGCCCAGAGGG----------TGCCCTCGGGCCAGGCCC 1007

Qy   959 CATCGCGGCAGC--TTGAGGAGCACTGCCCAGAGGG----------TGCCCTCGGGCCAGGCCC 1007
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Db   999 CTTTCCCCCACCTTGAGGAAGCACTCCCAAAAGGGTGGCCCCCTCGGCCCCAAGGCCGGTTCC 1058

Qy   999 CTTTCCCCCACCTTGAGGAAGCACTCCCAAAAGGGTGGCCCCCTCGGCCCCAAGGCCGGTTCC 1058
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Db   1008 GTCCCCCAGCCACCCCCCTTTGTGCCCTGCCCCGGGGTTCACCACCCAC 1058

Qy   1008 GTCCCCCAGCCACCCCCCTTTGTGCCCTGCCCCGGGGTTCACCACCCAC 1058
          ||||||||||||||||||||||||||||||||||
Db   1059 CCAAGCCACCCCCCTTTGTGCCCTGCCCCGGGGTTACCAAAACCCCCCCCC 1109

Qy   1059 CCAAGCCACCCCCCTTTGTGCCCTGCCCCGGGGTTACCAAAACCCCCCCCC 1109

RESULT 10
BQ711105

LOCUS   BQ711105   929 bp   mRNA   linear   EST 16-JUL-2002
DEFINITION AGENCOURT_7976097 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6214550
            5', mRNA sequence.
ACCESSION   BQ711105
VERSION   BQ711105.1 GI:21850004
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 929)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
            National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE   Unpublished (1999)
JOURNAL
COMMENT   Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Mark Watson
            cDNA Library Preparation: Rubin Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM2382 row: a column: 15
            High quality sequence stop: 542.
FEATURES   Location/Qualifiers
source   1..929
            /organism="Homo sapiens"
            /mol_type="mRNA"
            /db_xref="taxon:9606"
            /clone="IMAGE:6214550"
            /lab_host="DH10B (phage-resistant)"

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                                                  /clone_lib="NIH_MGC_113"
                                                  /note="Organ: spleen; Vector: pCTB7; Site_1: XhoI; Site_2:
                                                   EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                                                   into EcoRI/XhoI sites using the following 5' adaptor:
                                                   GGCACGAG(G). Library constructed by Ling Hong in the
                                                   laboratory of Gerald M. Rubin (University of California,
                                                   Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
                                                   Superscript II RT (Life Technologies). Note: this is a
                                                   NIH_MGC Library."

ORIGIN
Query Match    39.8%;  Score 865.4;  DB 13;  Length 929;
Best Local Similarity   97.6%;  Pred. No. 4.9e-105;
Matches 908;  Conservative   0;  Mismatches  19;  Indels   3;  Gaps   3;
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Qy    460 CTGAGGAGGGCTCGCCAACAGAGAGTTCATTTACCTAAACAGGTACAAGCGGCGGGGCCGGGCGAGT 519
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Db      1 CTGAGGAGGGCTCGCCAACAGAGAGTTCATTTACCTAAACAGGTACAAGCGGCGGGGCCGGGCGAGT 60

Qy    520 CCCAGGACAAAGTGCACCTACACCTTCATTGTGCCCCAGCAGTCACGGGTGCCATCT 579
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 CCCAGGACAAAGTGCACCTACACCTTCATTGTGCCCCAGCAGTCACGGGTGCCATCT 120

Qy    580 GCGTCAACTCCAAGGAGGCCTGAGGTGCTTCTGGAGAACCGAGTGCATAAGCAGGAGCTAG 639
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 GCGTCAACTCCAAGGAGGCCTGAGGTGCTTCTGGAGAACCGAGTGCATAAGCAGGAGCTAG 180

Qy    640 AGCTGCTCAACAATGAGCTGCTCAAGCAAGCCGGCAGATCGAGACGGTCAGCAGCTGG 699
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 AGCTGCTCAACAATGAGCTGCTCAAGCAAGCCGGCAGATCGAGACGGTCAGCAGCTGG 240

Qy    700 TGGAAGGTGGACGCGGGCAATTGTGAGCGAGGTGAAGCTGCGCCAAGGAGACCCGCAACA 759
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 TGGAAGGTGGACGCGGGCATTGTGAGCGAGGTGAAGCTGCGCCAAGGAGAGCCGCAACA 300

Qy    760 TGAACTCGCGGGTTCACGCAGCTCTTACATTGCACATGCACGACGGATCATCCCGCAAGCGGG 819
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Db    301 TGAACTCGCGGGTCACGCAGCTCTTACATGCACATGCACGACGGATCATCCCGCAAGCGGG 360

Qy    820 ACAACGCGTTGGAGCTCTCCCAGCTGGAGAACAGGATCCTGAACCAGACAGCCGACATGC 879
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Db    361 ACAACGCGTTGGAGCTCTCCCAGCTGGAGAACAGGATCCTGAACCAGACAGCCGACATGC 420

Qy    880 TCGAGCTGGCCAGCAAGTACAAGGACACTGGAGCACCTGGGCCACACTGG 939
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 TCGAGCTGGCCAGCAAGTACAAGGACACTGGAGCACCTGGGCCACACTGG 480

Qy    940 CCCACAACCAATCAGAGATCATCGGCGAGCTTGAGGACCACTCCCAGAGGGGTGCCCTCGG 999
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 CCCACAACCAATCAGAGATCATCGGCGAGCTTGAGGACCACTCCCAGAGGGGTGCCCTCGG 540

Qy   1000 CCAGGCCCGTCCCCAGCCACCCCCCGCCCCCGCCCCGCCCGTCTTACCACACACCACCT 1059
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 CCAGGCCCGTCCCCAGCCACCCCCCGCCCCCGCCCGTCTTACCACACACCACCT 600

Qy   1060 ACAACCCGGATCCATCAACCAGATCTCTTAGCCAAGAGTGACCAGAACCTGAAGG 1119
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 ACAACCCGGATCCATCAACCAGATCTCTTAGCCAAGAGTGACCAGAACCTGAAGG 660

Qy   1120 TGCTGCCACACCCCCTCGCCCACTATGCCCACTCTCACCAGCCTCCAACTTCCACCGACA 1179
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 TGCTGCCACACCCCCTCGCCCACTATGCCCACTCTCACCAGCCTCCAACTTCCACCGAC 720

Qy   1180 AGCCGTGCGGGCCCCATGAGAGACTGCCTGGAGGATGGCCACACACAGCT 1239
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 AGCCGTGCGGGCCCATGAGAGACTGCCTGGAGGATGGCCACACACAGCT 780

Qy   1240 CCATCTACCTGGTTGAAGCGCGGAGAAACACCAACCCGCCTCATGCAGGTGTGGTCGGACCAGA 1299
          |||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Db    781 CCATCTACCTGGGGAAGCCGGAG-ACACGACCGCCTCATGCGAGGTGTGGGTCGGACCA-CAGA 838

Qy   1300 GACACGACCCCCGGGGGTCGGACCGTCATCCCAGAG-ACGCCTCGGATGGCTCTGTTAACTTC 1358
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ORIGIN
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RESULT 11
LOCUS       BQ879104                881 bp    mRNA    linear    EST 16-AUG-2002
DEFINITION  AGENCOURT_8118172 Lupski_dorsal_root_ganglion Homo sapiens cDNA
            clone IMAGE:6181203 5', mRNA sequence.
ACCESSION   BQ879104
VERSION     BQ879104.1  GI:22271112
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 881)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr James R. Lupski
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM13565 row: d  column: 04
            High quality sequence stop: 671.
FEATURES             Location/Qualifiers
     source          1..881
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6181203"
                     /sex="male"
                     /tissue_type="dorsal root ganglia"
                     /dev_stage="adult, 36 yr"
                     /lab_host="DH10B"
                     /clone_lib="Lupski dorsal root ganglion"
                     /note="Vector: pCMV-SPORT6 (Life Technologies); Site_1:
                     NotI; Site_2: SalI; cDNA made by oligo-dT priming.
                     Directionally cloned using the following adaptors:
                     5'-TCGACCCACGCGTCCG-3' and
                     5'-GACTAGTTCTAGATCCGGAGGCCGCGGCCCT(15)-3'. Size selected >
                     1 kb for average insert length 1.7 kb. This is a primary
                     library, non-amplified. Library constructed by Life
                     Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor
                     College of Medicine) and is available through Life
                     Technologies."
ORIGIN
Query Match    39.8%;  Score 865;  DB 13;  Length 881;
Best Local Similarity   98.9%;  Pred. No. 5.6e-105;
Matches 871;  Conservative   0;  Mismatches  10;  Indels   0;  Gaps   0;
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Db    839 GACACGACCCCCGGGGGTCGGACCGTCATCCCAAAGAACGCCCTGGATGGCTCTCGNNTACTTC 898
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Qy   1359 TTCAGGAACTGGGAGACAGGTACAAGCCAAGGG 1388
          ||||||||||||||||| |||
Db    899 TTCAGGAACTGGGAACNTCCCAAGCAAGGG 928

Qy     30 GATGAACCCCAAGCCCTGGACCTGCCGGACCTGGCCACTGAGGCAGGGGCTGACGTACTG 89
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 GATGAACCCCAAGCCCTGGACCTGCCGGACCTGGCCACTGAGGCAGGGGCTGACGTACTG 60

Qy     90 TGAGGGAAAGAAGGTTGTGAGCAGCCCCGCAGGACCCGCCGCACCCTGGCCCCCAGCCT 149
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 TGAGGGAAAGAAGGTTGTGAGCAGCCCCGCAGGACCCGCCGCACCCTGGCCCCCAGCCT 120

Qy    150 CTGCCGGAGCCCTCTGTGGAGGCAGAGCCCAGTGGAGCCCAGTGGAGCCAGGGGCTGTTGGC 209
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 CTGCCGGAGCCCTCTGTGGAGGCAGAGCCCAGTGGAGCCCAGTGGAGCCAGGGGCTGTTGGC 180
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Qy   210 AGCCACCGGGCCTGCAACTCAGGAACCCCTTCCAGAGCGACGCAGAGCAGGCTGCCCCGCTGAC 269
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Db   181 AGCCACCGGGCCTGCAACTCAGGAACCCCTTCCAGAGCGACGCAGAGCAGGCTGCCCCGCTGAC 240

Qy   270 GGGCCAGGGTGAAGCATGTGAGGAGCCGCGGCCGGAGGGAGGGAGGAGAGAGGCTTTCA 329
         
Db   241 GGGCCAGGGTGAAGCATGTGAGGAGCC 300

Qy   330 TAGAGTTGAGGAGGGGCTGGCTCAGCTGTGAGCCAGGGCACTGGGAGCCACTGTGGGGTG 389
Db   301 TAGAGTTCTATTCACAAGAATAACCACCATTTTGCAAGGACCCATGAGGCCACTGTCGGTG 360

Qy   390 ACATGCTGGTGTCGTCGGACTGTGTTGGCTGGCCCATGGGAGCCCCAGGAGGGAGGACGGT 449
Db   361 ACATGCTGGTGCCGGCTCGGACTGTGTTGGCAGGCCCATGAGGCCCAGGAGGGAGGACGGT 420

Qy   450 TTTGAGGGCCACTCAGGAGGAGGGCTCGCCAAGAGAGTTCATTTACCTAAACAGGTTACAAGCGG 509
Db   421 TTTGAGGGCCACTCAGGAGGAGGGCTCGCCAAGAGAGTTCATTTACCTAAACAGGTTACAAGCGG 480

Qy   510 GCGGGGCGGAGTCCCAGGACAAGTGCACCTTACACCTTCATTGTGCCCGAGCACGGCACGCACG 569
Db   481 GCGGGGCGGAGTCCCAGGACAAGTGCACCTTACACCTTCATTGTGCCCGAGCACGGCACGCACG 540

Qy   570 GGTGCCATCTGCGGTCAACTCCAAGGAGGTGCTTCTGGAGGTGCCTGAGGTGCATAAG 629
Db   541 GGTGCCATCTGCGGTCAACTCCAAGGAGGTGCTTCTGGAGGTGCCTGAGGTGCATAAG 600

Qy   630 CAGGAGCTAGAGCTGCTCAACAATGAGCTGCTCAAGCACAGGGCAGATCGAGACCGCTG 689
Db   601 CAGGAGCTAGAGCTGCTCAACAATGAGCTGCTCAAGCACAGGGCAGATCGAGACCGCTG 660

Qy   690 CACGCAGTCGCTTGAAGGTGGACGGCGCATTGTGAGCGAAGGTGCGTGGGCCAGGAG 749
Db   661 CAGGAGCTGTGGAGGTGACGGCGCATTGTGAGCGAAGGTGCGTGGGCCAGGAG 720

Qy   750 AGCCGCGCAACATGAACTCCCGGGGTCACGCGGCTCTTCCCAGCTGGAGAATCCTGTGCACCAGGACA 809
Db   721 AGCCGCGCAACATGAACTCCCGGGGTCACGCGGCTCTTCCCAGCTGGAGAATCCTGTGCACCAGGACA 780

Qy   810 CGCAAGCGGGACAACGCGGTTGGAGCTTCACGCGGGTCTACACGCACCTGCTCTGAACCAGGACA 869
Db   781 CGCAAGCGGGACAACGCGGTTGGAGCTTCTCCGACTCGAACAGGGACTCTGAACCAGACA 840

Qy   870 GCCCACACAGCTGCGAGCTGGCCACAAGTACACAAGGACACCTGGA 910
Db   841 GCCGACACATGCTGCGACCTGCCGCAAGTACACCAGGGACCTGA 881
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Query Match    38.0%;  Score 826.8;  DB 9;  Length 1195;
Best Local Similarity  86.2%;  Pred. No. 5.7e-100;
Matches 859;  Conservative 76;  Mismatches 58;  Indels 4;  Gaps 4;

Qy  1160 CCTCCCATCTTCCACCGACAAAGCCCGTCGGGCCCCATGGACGGAGGAGGACTCCTGGGAGGATCA 1219
Db   995 SCTCCCATTTTCCACCRACAA-SCSTCGGSGCSCCCATGGAAKAAAATKCCCTGCAGGCCCTGGW 937

Qy  1220 GGAATGGCCACCACACAGCTCCATCTCACCTCGGTGAAGCCCGGAGAACACCAACCGCCTCAT 1279
Db   936 GGWTGBCTACTACACCAGCCTCCATSTRYYTCGGTGWRAGCCCKGWGTACACCWACCSCCTCAT 877

Qy  1280 GCAGGTGTTGGTGCGACCAGAGACAGACAGCCCCGGGGCTGGACCGTCATCCAGAGACGCGCCT 1339
Db   876 KCAGGSKKT-GKGCGGAAMADRRACACCAACCCCGGGKCCTGGACCGSTCATCCAGAGACKXCCT 818

Qy  1340 GGATGGCTCTGTTAACTTCTTCAGGAACTGGGAGACGAAGCAAGGGTTTGGGGAACAT 1399
Db   817 GSATGGSCTTCTGTTTACTTCTTCAGGTAYAGCGGGGAGACGCAYAAGCAAGGGTTTGGGGAACAT 758

Qy  1400 TGACGGCGGAATACTGGGCTGGGCCTGGAGAACCATTTACTGGCTGACGAAGCCAGGGCAACTA 1459
Db   757 TGACGGCGGAATACTGGCTGGGCCTGGAGMACATTTACTGGCTGACGAACCAAGGCAACTA 698

Qy  1460 CAAACTCCTCGTTGACCATGGAGACAGCTGGTGGCTTCGGGCCGGCCGGCGCAAATAGGCCAG 1519
Db   697 YAKAYTCCTCGGTGACCATGGAGACAGGTCCGCCCGCCAAAGTCTKTGCAGAATAGGCCCAG 638

Qy  1520 TTTCCGGCCTGGAACCTGAGGAGCGGAGTATTATTAAAGCTGGGCGGCTCCATGTGCCA 1579
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Qy  1580 TGCGGGGTGACTCCTTTACATGGCACAAGCGGCAGTTCACCACCCTGACAGACAGGATCA 1639
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Qy  1640 TGATGGTCTACACAGGAAACTGTGCCCACTACACAGGAAGGAGGAGGKAGKYTGTTGGGTTATAACGCCTG 1699
Db   518 KGAIGTCTACAYAGKAAACTGGCCCACTACCACCAGGAAGGKAGKYTGTTGGGTTATAACGCCTG 459

Qy  1700 TGCCCACTCCAACCTCAACGCGGGGTCTGGTACCGCGCGGGGCCATTACCGGACCGGCTACCA 1759
Db   458 TGCCCACTCCAACCTCMACGGGGTTCTGKTACCGYGGGGCCCATTACCKGACCACCCTGACAGACAGATCA 399

Qy  1760 GGACGGAGTCTACTGGGCTGAGTTCCGAGAGGCGTCTTACTCACTCAAAGAAAGTGGTGAT 1819
Db   398 GGACGGAGTCTATTGGGCKGAGKKYCGATGAGTCTCTTAACTCACTTAAGAAAGTKTTGAT 339

Qy  1820 GATGATCCGACGGAACCCCAACACACTTCCACTAAGCCAGTCCCCCCTCCCTGACCCTCTCGT 1879
Db   338 GATGATCCGACGACGAACCCCAACACACTTCCAYTAAGCCAGTCCCCCCTCCCKCCCTCGT 279

Qy  1880 GGCCATTGCCAGGAGCCCACCCTGGTCACGCTGGCCACAGCACAAAGAACAACTCCTCAC 1939
Db       ||||||||||||||||||||||||||
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FEATURES   Location/Qualifiers
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                     /db_xref="taxon:9606"
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                     /tissue_type="CS0DC011YL19"
                     /clone_lib="Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED"
                     /note="NEUROBLASTOMA COT 25-NORMALIZED"
                     /note="lst strand cDNA was primed with a NotI-oligo(dT)
                     primer. Five prime end enriched, double-strand cDNA was
                     digested with Not I and cloned into the Not I and EcoR V
                     sites of the pCMVSPORT 6 vector. Library was normalized."
ORIGIN

RESULT 12
ALS25269/c
LOCUS   ALS25269   1195 bp   mRNA   linear   EST 22-MAY-2003
DEFINITION ALS25269 Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED Homo sapiens
            cDNA clone CS0DC011YL19 3-PRIME, mRNA sequence.
ACCESSION   ALS25269
VERSION   ALS25269.2 GI:31043524
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 1195)
AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE   Full-length cDNA libraries and normalization
JOURNAL   Unpublished (2001)
COMMENT   On Feb 13, 2001 this sequence version replaced gi:12788762.
            Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr; Web.: www.genoscope.cns.fr
            Invitrogen. This sequence was constructed by Life Technologies, a division of
            Invitrogen. This sequence belongs to sequence cluster 4821.r For
            more information about this cluster, see

RESULT 13
BQ952353

LOCUS   BQ952353   884 bp   mRNA   linear   EST 21-AUG-2002
DEFINITION AGENCOURT_8963557 Lupski_sciatic_nerve Homo sapiens cDNA clone
            IMAGE:6200431 5', mRNA sequence.
ACCESSION   BQ952353
VERSION   BQ952353.1   GI:22367831
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 884)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
TITLE   National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
COMMENT   Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. James R. Lupski
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: 11AM13615 row: e column: 08
            High quality sequence stop: 624.
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                     /dev_stage="adult, 70 yr"
                     /lab_host="DH10B"
                     /clone_lib="Lupski_sciatic_nerve"
                     /note="Vector: pCMV-SPORT6 (Life Technologies); Site_1:
                     NotI, Site_2: SalI; cDNA made by oligo-dT priming.
                     Directionally cloned using the following adaptors:
                     5'-TCGACCCACGCGTCCG-3', and
                     5'-GACTAGTTCTAGATCGCGAGCGGCCGCCCGGGCCCT(15)-3'. Size selected >
                     1 kb for average insert length 1.87 kb. This is a primary
                     library, non-amplified. Library constructed by Life
                     Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor
                     College of Medicine) and is available through Life
                     Technologies."
ORIGIN

Query Match   38.0%;   Score 825.2;   DB 13;   Length 884;
Best Local Similarity   98.8%;
Matches 866; Conservative 0; Mismatches 15; Indels 3; Gaps 3;

Db 278 GGCCATTGCCAGGAGCCACCCTGGTCACGTGCACGCAGCACAAAGAACAAACTCCTCAC 219
Qy 1940 CAGTTCATCCTGAGGCGTCGGGAGGACCCGGGGATCGTCGGATTCTGTTTTTCGGAAGTCACTGCA 1999
Db 218 CAGTTCATCCTGAGGCGTCGGGAGGACCCGGGGATCGTCGGATTCTGTTTTTCGGAAGTCACTGCA 159
Qy 2000 GCGGATGATGGAAACTGAAATCGATACGGTGTTGTTTTTCTGTCCCTACTTTCCTT-CACACC 2058
Db 158 GCGGATGATGGAAACTGAAATCGATACGGTGTTGTTTTTCTGTCCCTACTTTCCTT-CACACC 99
Qy 2059 AGACACGCCCTCATGTGTTCCAGGACAGGACTACAGACCAACCTTCTTCTTTACACACC 2118
Db   98 AGACACGCCCTCATTGTCWMCAGRACAGRAMAGRACAACACAGAMAACTACMATCTTTRAAAA 39
Qy 2119 ATTAAGTTCTTCTACAATAAAAACACACAACTGCAAAGTAA 2155
Db   38 AAAAAAAAAAAAAAAAAAAAAAAVVVAAAAMAAAAVA 2

RESULT 14
AL527059

LOCUS   AL527059   1201 bp   mRNA   linear   EST 23-MAY-2003
DEFINITION AL527059 Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED Homo sapiens
            cDNA clone CS0DC017YL03 5-PRIME, mRNA sequence.
ACCESSION   AL527059
VERSION   AL527059.2   GI:31064913
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Qy 667 AGAAGCGGCAGATCGAACGCTGCAGCAGTGTGGTAAGGTGGACCGGCGGGCATTGTGAGCG 726
Db   1 AGAAGCGGCAGATCGAGAGCCGCTGCAGGAGTCGCACCAGCTGGTGGACGGCGGGCATTGTGAGCG 60
Qy 727 AGGTGGAGCTGCTGCGGCAAGGAGAGGGCGGCAACACATGAACTCGCGGGGTCACCGCAGCTCTACA 786
Db   61 AGGTGAAGCTGTCTGGGCAAGGAGAGCAGCGCAACATGAACTCGCGGGTCACCGCAGCTCTACA 120
Qy 787 TGCAGCTCCTGCACGAGGATCATCCCGACGAGACGGCCAAGGCCGGTTGGAGCTCTCCCAGCTGG 846
Db 121 TGCAGCTCCTGCACGAGGATCATCCCGACCAAGGCCAAGGCCGTTGGAGCTCTCCCAGCTGG 180
Qy 847 AGAACAGGAATCCTGAACCAGCAGCCGACAATGCCGACGCTGCAGCAAGTACAAGAGGACC 906
Db 181 AGAACAGGAATCCTGAACCAGCAGCCGACAATGCCGACGCTGCAGCAAGTACAAGAGGACC 240
Qy 907 TGGAGCACAAGTACCAGCACCTGGCCACACTGGGCCCACCAACAATCAGAGAATCATCGCGC 966
Db 241 TGGAGCACAAGTACCAGCACCTGGCCACACTGGGCCCACCAACAATCAGAGAATCATCGCGC 300
Qy 967 AGCTTGAGGAGCACTTGGCCAGAGGGGGTGCCCTTCGGGCCCAGGCCCGTGCTCCCCAGCACCCCCCG 1026
Db 301 AGCTTGAGGACCACTTGGCCAGAGGGGGTCCCCTGGCCCAGGCCCGTGCTCCCCAGCACCCCCG 360
Qy 1027 CTGCCCCGGCCCCGGGGTCTTACCAACCACCAACTACACACCCGGATCATCAACCAGATCTA 1086
Db 361 CTGCCCCGGCCCCGGGGTTCTTACCAACCACCACCTACACACCCGGATCATCAACCAGATCTA 420
Qy 1087 CCAACGGATCCAGAGTGACCAGAACCTGAAGGTGCTGCCACCCCCCTCTGCCCACTATGC 1146
Db 421 CCAACCAGATCCAGAGTGACCAGAACCTGAAGGTGCTGCCACCCCCTCTGCCCACTATGC 480
Qy 1147 CCACTCTCACCCAGCCTCCCATCTTCCACCACAACAACCGGTGGGCCCATGAGACGACTGCC 1206
Db 481 CCACTCTCACCCAGCCTCCCATCTTCACCACAACAACCGGTGGGCCCATGAGACGACTGCC 540
Qy 1207 TGCAGCCCCTGGAGGATGGGCCACGACAGCTCCATCTCCATCTTCACCTGGTGAACCGGAACA 1266
Db 541 TGCAGCGCCCTGGAGGATGGGCCACGACAGCTCCATCTCTACCTGGTGAACCGGAGAAACA 600
Qy 1267 CCAACCGGCTTCATGCAGGTGTTGGTGGCGGACACACAGAGACCCCCGGGGGGCCTGGACCGGTCA 1326
Db 601 CCAACCGGCTCATGCAGGTGTTGGTGGCGACCAGAGACACCCCCGGGGGGCCTGGACCGGTCA 660
Qy 1327 TCCAGGACACGGCCTGGATGGGCTCTGTTAACTTCTTCAGGGAACTGGGGAGGACTACAAGCAAG 1386
Db 661 TCCAGGACACGGCCTGGATGGGCTCTGTTAACTTCTTCAGGGAACTGGGGAGGACTACAAGCAAG 720
Qy 1387 GG-TTTGGGGAACCATTGACGCGGGAATACTGCGTGGGCGCTGGAGGAACATTACTGGCGTGACG 1445
Db 721 GGTTTTGGGGACCATTGAATGGCGAATACTGCGTGGGGGAACATTACTGGGTGACG 780
Qy 1446 AACCAAGGCAACTACAAACTCCCTGTTGACCATGGAGGACTGGGTCCGGCAAAAGTCTTT 1505
Db 781 ACCAAAGGC-ACTACAAACTCCTGGGACATGGACTGGGTCCGGCAAGTCTTT 839
Qy 1506 GCAGGAATACGGCCAG-TTTCCGCCTGGAACCTGAGAGCGGAGTATT 1548
Db 840 GCAGAATACGCCCAGNTTTCGCCCTGGAAACTGAAAGCGGAGTATT 883

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REFERENCE   1  (bases 1 to 1201)
AUTHORS     Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE       Full-length cDNA libraries and normalization
JOURNAL     Unpublished (2001)
COMMENT     On Feb 13, 2001 this sequence version replaced gi:12790552.
            Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr; Web : www.genoscope.cns.fr
            Library was constructed by Life Technologies, a division of
            Invitrogen. This sequence belongs to sequence cluster 4821.r For
            more information about this cluster, see
            http://www.genoscope.cns.fr/
            cgi-bin/cluster.cgi?seq=CS0DC017CF02QP1&cluster=4821.r. Contact :
            Feng Liang Email: fliang@lifetech.com URL :
            http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
            Faraday Avenue Genoscope sequence ID : CS0DC017CF02QP1.
FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="CS0DC017YL03"
                     /tissue_type="NEUROBLASTOMA COT 25-NORMALIZED"
                     /clone_lib="Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED"
                     /note="1st strand cDNA was primed with a NotI-oligo(dT)
                     primer. Five prime end enriched, double-strand cDNA was
                     digested with Not I and cloned into the Not I and EcoR V
                     sites of the pCMVSPORT 6 vector. Library was normalized."
ORIGIN
Query Match        37.68%;   Score 817.4;  DB 9;  Length 1201;
Best Local Similarity   92.38%;   Pred. No. 1e-98;
Matches  956;  Conservative   29;  Mismatches   37;  Indels   14;  Gaps   12;

Qy         3  AAATGAGGCTGCTGCGGACGGGGCTGAGGATGAACCCCTTGGACTTGCCGACGGTG   62
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Db        88  AAATGAGGCTGCTGCGGACGGGGCTGAGGATGAACCCCTTGGACTTGCCGACGGTG  147

Qy        63  GCACTGAGGCAGGCAGGCGGCTGACGCTACTGTGAGGGAAAGAGAGGTTGTGAGCAGCCCCCGCAGG  122
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       148  GCACTGAGGCAGGCAGGCGGCTGACGCTACTGTGAGGGAAAGAGAGGTTGTGAGCAGCCCCCGCAGG  207

Qy       123  ACCCCTGGCCCACCCCTTGCCCCAGCCTTCTGCGCGGACGCCCTCTGTGTGGAGGGCAGAGCCAGTG  182
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       208  ACCCCTGGCCCAGCCCTGCCCCAGCCTTCTGTGGAGGCAGAGCCAGTG  267

Qy       183  GACCCCAGTGAGGCAGGCGGCTGCTTGGGCAGCC-ACCGGCCTTGCAACTTCAGGGACCCCCTCCA  241
              |||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db       268  GACCCCAGTGAGGCAGGCGGCTGCTTGGGCAGCCAACCGGCCCTGCAACTTCAGGGACCCCTCCA  327

Qy       242  GAGGCCATGGACCAGGCTTGCCCCGCGCCCGACGGGCCCAGGGTGAAGCAGGCCATGTGAGGAGCGCGGGCCG  301
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       328  GAGGCCATGGACCAGGCTTGCCCCGCGCCCCGACGGGCCCAGGGTGAAGCATGTGAGGACCGGCGCCCG  387

Qy       302  GACCCAGCCAGGAGGGAAGAGGCCTTCAATAGATTCTATTCACAAAGAATAACCACCATTT  361
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       388  GACCCAGCCAGGAGGGGAAGAGCCTTTCAATAGATTCTATTCACAAAGAATAACCACCATTT  447

Qy       362  TGCAAAGACCATGAGGCCACTGTGCGTGCGTGGCTCGGACTGCTGCTGCCAT  421
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db       448  TGCAAGGACCATGAGGCCACTGTGCGTGACATGCTGGTCGGACTGCTGCCAT  507

Qy       422  GGG-AGCTGTTCCAGGCC-AGGAGGAGGTTTTGAGGGC-ACTGAGGAGGGCCTCGCCCAAG  478
              ||| ||||||||||||||  ||||||||||||||||| ||||||||||||||||||||||
Db       508  GGGAAGCTGTTGCAGGCCCAAGAGGACGGTTTTGAGGGCACTGAGGAGGGCCTCGCCCAAG  567

Qy       479  AGAGTTCATTTACCTAAACAGTTACAAGCGGACGTCCCAGACAAGTGCACCTA  538
              |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       568  AGAGTTCATTTACCTAAACAGTTACAAGCGGACGTCCCAGACAAGTGCACCTA  627

Qy       539  CACCTTCAATGTGCCCCAGCAGCGGGCGGGGTCACGGGTCGCCATCTGGCTCAACTCCAAGGAGCC  598
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       628  CACCTTCAATGTGCCCCAGCAGCGCGGGGTCACGGGTGCCATCTGGCTCAACTCCAAGGAGCC  687

Qy       599  TGAGGTGCTTCTGAGAACCCGAGGTGCATAAGCAGGAGGTTCAGGATTGCTGCTCAACAATGAGCT  658
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Db       688  TGAGGTGCTTCTGGAGAACCGAGGTGCATAAGCAGGAGGTTCAGGATTGCTGCTCAACAATGAGCT  747

Qy       659  GCTCAAGCACAAAGCCGGCAGATCGGACGCGTTGCAGCCGCTCGGTCTTGGTTGAAGGTTGGACCGGCAT  718
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       748  GCTCAAGCACAAAGCCGGCAGATCGGACGCGTTGCAGCCGCTCGGTCTTGGTTGAAGGTTGGACCGGCAT  807

Qy       719  TGTGAGCGAGGTGAAGCTGCTTCGCCGAAGGAGGAGCCCCAACATGAATCCGGCAGGGGTTCAGGCA  778
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Db       808  TGTGARCGAGGTGAAGCTGCTGCCGAAGGAGAGCGCCAACATGAACCTCGGCACG-M  866

Qy       779  GCTCTACATCCCAGTCTCCTGACCGAGAATCATCCCGAAGCGGGGACAACGGCGTTGGAGCTCTC  838
              ||||||||||||||||||  ||||||||||||||||||  :|||||||||||::||||||||||
Db       867  GCTTCTACATGGCAGCTTCTGCCACAGAATCAT-CGCAAGCGGGGA-MACGGCGTTGGAGCTCTC  924

Qy       839  CCAGCTGGAGAAACAGGATTCCTGACCAGCAGCCCACCATGCTTGCAGCTGCCCAGCAAGTA  898
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Db       925  CCAGCTGGAARACAAGGAT-CTGAACCAACAAMGCCGAMATGCTGCAGCTGGCCAGCTG  983

Qy       899  CAAGGACCTTGGAGCACAAGTACCAGCCACACTTGGCCACCACTGGCCCCACAACCAAATACAGAGAT  958
              |||||||||||||||||||||||||||:||||:|||||||||||||||||||||||:|:|:||||||
Db       984  MAAGGA-CTGGAGCCGMAAGTGCCACCA-CTGGGCCGMACWTGGCCAMAAMYAAATCARA-AT  1040

Qy       959  CATCGCGCAGCTTGAGGGAGGCGACTGCCAGGAGGGTGCCCTCGGCCAGGCCGCCGGTCCCCAGCC  1018
              ||||||||||||:|||||:|||||||||||||::|:||||||||||||||||||||||||||||
Db      1041  TATCGCGCMWTTGNAGGRSMCTGCMAAAGGTG----CCTCGGCMAGGCCCGTKBCARCAMC  1097

Qy      1019  ACCCCCGCGTCCCCCCG  1034
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Db      1098  CCCCsGCCCsCCCGG  1113
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RESULT 15
CDS16561
LOCUS       CDS16561              870 bp    mRNA        linear
DEFINITION  AGENCOURT 14366052 NIH_MGC_181 Homo sapiens cDNA clone
            IMAGE:30408400 5', mRNA sequence.
ACCESSION   CDS16561
VERSION     CDS16561.1  GI:31448279
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 870)
AUTHORS     NIH-MGC http://mgc.nci.nih.gov/,
TITLE       National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL     Unpublished (1999)
COMMENT     Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Michael Brownstein
            cDNA Library Preparation: Invitrogen Corp
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: NDAM491  row: e  column: 17
            High quality sequence stop: 692.
FEATURES             Location/Qualifiers
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                     /clone="IMAGE:30408400"
                     /tissue_type="White Matter"
                     /dev_stage="Unknown"
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ORIGIN

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             /lab_host="DH10B-Ton A ( T1 and T5 phage resistances)"
             /clone_lib="NIH_MGC_181"
             /note="Vector: pCMV-SPORT6.1; Site 1: NotI; Site 2: EcoRV
             (destroyed); Library is oligo-dT primed and directionally
             cloned (EcoRV site is destroyed upon cloning). Average
             insert size 1.42 kb. Library was constructed by
             (Invitrogen). Note: this is a NIH_MGC Library."

Query Match    37.6%; Score 816.4; DB 14;  Length 870;
Best Local Similarity  98.9%;  Pred. No. 1.5e-98;
Matches  843; Conservative  0; Mismatches  6;  Indels  3;  Gaps  2;
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Qy    16 GCGGACAGGCCTGAGGATGAACCCCAAGCCCTGACCTGCCGAGCGTGGCACTGAGGCAGC 75
         |||||||||||||||||| |||||||||||||||||||||||||||||| ||||||||||
Db     1 GCGGACAGGCCTGAGGATGGACCCCAAGCCCTGACCTGCCGAGCGTGGCCACTGAGGCAGC 60

Qy    76 GGCTGAGCGCTACTGTGAGGGAAAGAAGTTTGTGAGCAGCCCCGCAGGACCCCTGGCCAGC 135
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61 GGCTGAGCGCTACTGTGAGGGAAAGAAGTTGTGAGCAGCCCCGCAGGACCCCTGGCCAGC 120

Qy   136 CCTGGCCCCCAGCCTCTCTGCCGGAGGCCCTTCTGTGGAGGCCAGAGGCCAGTGGAGG 195
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy   196 CAGGGGCTGCTTGGGCACCACCACGCGGCCCTGCAACTCAGGAACCCCTCAGAGGCCATGG 255
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 CAGGGGCTGCTTGGGCACCACCACGCGGCCCTGCAACTCAGGAACCCCTCAGAGGCCATGG 240

Qy   256 GCTGCCCCGCTGACCGGCCCAGGGTGAAGCATGTGAGGAGCGCCCCCCGGGAGCCAAGCAGGAG 315
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 GCTGCCCCGCTGACCGGCCCAGGGTGAAGCATGTGAGGAGCGCCCCCCGGGAGCCAAGCAGGAG 300

Qy   316 GGAAGAGGCTTTCATAGATTCTATTCACAAAGAATAACCACCATTTTGCAAAGACCATGA 375
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 GGAAGAGGCTTTCATAGATTCTATTCACAAAGAATAACCACCATTTTGCAAAGACCACATGA 360

Qy   376 GGCCACTGTGCGGTGACATGCCTGGGTGCCTCGGACTGTGCTGGGCTGCCTGGGAGGCTGTTGCAG 435
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Db   361 GGCCACTGTGCGGTGACATGCTGGGTGCCTCGGACTGCTGGGCTGCCTGGGAGCTGTTGCAG 420

Qy   436 GCCAGGAGGACGGTTTTGAGGGCACTGAGAGGAGGGCTCGGCCAAGAGAGTTCATTTACTTAA 495
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Qy   496 ACAGGTACAAGGCGGCGGGGGGGAGTCCCAGGACAAGTGCACCTCACCTTCATTGTGCCCC 555
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Qy   556 AGCAGCGGGGTCACGGGGTGCCAATCTGGGTCAACTCCAAGGACCCTGAGGGTGCTTCTGGAGA 615
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Qy   616 ACCGAGGTGCAATAAGCAGGAGCTAGAGCTGCTTCAAGAGCTGCTCAAATGAGCTGGAAGCGGC 675
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Db   601 ACCGAGGTGCAATAAGCAGGAGCTAGAGCTGCTTCAAACAATGAGCTGGAAGCGGC 660

Qy   676 AGATCGAGACCGCTGCAGCAGCTGGGTGAAAGGTGGACGGGCGGCATTGTTGAGGGAGGTGAAGC 735
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Db   661 AGATCGAGACCGCTGCACCAGCTGGGTCACCGGGCATTGTGGCCAGGGTGAAGC 720

Qy   736 TGCTGCGGCAAGGAGAGCCGCAACATGAACTCGGCGGGGTCACCGGGTCACCGCCTTCACATGCAGCTCC 795
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Db   721 TGCTGCGGCAAGGAGAGACCCGCAACATCGGCGGGGTCACCGGCTTCACATGCAGCTCC 780

Qy   796 TGCACGGAGCATCCGCAAGCGGGACAAC GGCGTTGGAGCTCTCCCAGCTGG--AGAACA 852
         |||||||||||||||||||||||||||| |||||||||||||||||||||||  ||||||
Db   781 TGCACGGAGATCATCCCGCAAGCCGGACAACNGCGTTGGAGCTCTCCCAGCTGGGAGAAACA 840

Qy   853 GGATCCTGAACC 864
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Db   841 GGATCCTGAAAC 852
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